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(54) Title: CELL VISUAL CHARACTERISTIC-MODIFYING SEQUENCES

(57) Abstract: The present invention relates generally to peptides, polypeptides or proteins having one or more amino acids or one or more amino acid sequences which exhibit color-facilitating properties, either on their own or following interaction with one or more other amino acids and to nucleic acid molecules encoding same. Such peptides, polypeptides and proteins are referred to herein as "color-facilitating molecules" or "CFMs". The present invention further provides genetic constructs for use in genetically modifying eukaryotic or prokaryotic cells and more particularly eukaryotic tissue so as to alter their visual characteristics or capacity for exhibiting same to a human eye in the absence of excitation by an extraneous non-white light or particle emission. The present invention, therefore, extends to eukaryotic or prokaryotic cells and more particularly eukaryotic tissue, which are genetically modified to produce CFMs and which thereby exhibit altered visual characteristics in the absence of excitation by an extraneous non-white light or particle emission. In one particular embodiment, the CFMs are used to alter the visual characteristics of plants and even more particularly flower color. In another embodiment, the present invention provides gels or coatings or similar biomaterials in the form of a biomatrix comprising the CFMs such as for use as a UV sink, in a sun screen, in cosmetics, as an expression marker or other reporter molecule or for use as a photon trap to increase light intensity.

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CELL VISUAL CHARACTERISTIC-MODIFYING SEQUENCES

FIELD OF THE INVENTION

The present invention relates generally to peptides, polypeptides or proteins having one or more amino acids or one or more amino acid sequences which exhibit color-facilitating properties, either on their own or following interaction with one or more other amino acids and to nucleic acid molecules encoding same. Such peptides, polypeptides and proteins are referred to herein as "color-facilitating molecules" or "CFMs". The present invention further provides genetic constructs for use in genetically modifying eukaryotic or prokaryotic cells and more particularly eukaryotic tissue so as to alter their visual characteristics or capacity for exhibiting same to a human eye in the absence of excitation by an extraneous non-white light or particle emission. The present invention, therefore, extends to eukaryotic or prokaryotic cells and more particularly eukaryotic tissue, which are genetically modified to produce CFMs and which thereby exhibit altered visual characteristics in the absence of excitation by an extraneous non-white light or particle emission. In one particular embodiment, the CFMs are used to alter the visual characteristics of plants and even more particularly flower color. In another embodiment, the present invention provides gels or coatings or similar biomaterials in the form of a biomatrix comprising the CFMs such as for use as a UV sink, in a sun screen, in cosmetics, as an expression marker or other reporter molecule or for use as a photon trap to increase light intensity.

BACKGROUND OF THE INVENTION

Reference to any prior art in this specification is not, and should not be taken as, an acknowledgment or any form of suggestion that this prior art forms part of the common general knowledge in Australia or any other country.

All-protein chromophores (pigments) have been isolated from the phylum Cnidaria (also known as Coelenterata). This phylum contains four classes: Scyphozoa, Cubozoa,

Anthozoa and Hydrozoa. The first all-protein chromophore to be isolated, Green Fluorescent Protein (GFP), was cloned and sequenced from cDNA of the Hydrozoan *Aequorea victoria*, commonly called jellyfish.

Similar all-protein chromophores have been isolated from Anthozoans. Matz *et al.* (*Nature Biotechnol. 17:* 969-973, 1999), used degenerative primers based on *Aequorea victoria* GFP nucleotide sequence to PCR amplify cDNA isolated from four of the five orders of Anthozoa: Stolonifera, Actiniaria, Zoanthidea, and Corallimorpharia. Lukyanov *et al.* (*Journal of Biological Chemistry 275:* 25879-25882, 2000) used the same methodology to isolate a non-fluorescent all-protein chromophore from Actiniaria. However, the methodology used was unable to isolate all-protein chromophores from the fifth order, Scleractinia.

The Scleractinia are corals that form architecture for coral reefs. They are otherwise known as "true" or "reef-building" corals. International Patent Publication No. WO 00/46233 and Dove *et al.* (*Coral Reefs 19:* 197-204, 2000) both relate to isolation of an all-protein chromophore derived from Scleractinia pigment protein from coral tissue (PPCT).

All-protein chromophores isolated to date display a range of spectral properties which effect apparent color in specific environments. Color may be determined by absorption and/or fluorescence properties of the molecules as well as qualities of incident light. Spectral properties include absorption, excitation and emission energies, molar extinction coefficients, quantum yields and maturation parameters. In many cases, a simple amino acid substitution can have a dramatic effect on the polypeptide spectral parameters (e.g. Tsien, *Ann. Rev. Biochem. 67:* 509, 1998; Lukyanov *et al.*, 2000, *supra*). However, useful modifications of a particular molecule are limited, as directed and random mutagenesis of specific all-protein chromophores has failed to produce desired spectral features (Tsien, 1998, *supra*). The result is that all-protein chromophores isolated from different sources are finding specific application niches.

One all-protein chromophores, primarily used as molecular marker, is GFP. This protein, when excited with either UV or blue light (maximally at 396 nm or 475 nm) emits green fluorescence (maximally at 500 nm) [Heim *et al., Proc. Natl. Acad. Sci. USA 91:* 12501-12504, 1994]. GFP mutants that are altered in their maximal excitation and emission characteristics have been generated by random mutagenesis (Crameri *et al., Nature Biotechnology 14:* 315-319, 1996). Other GFP mutants have been generated that have increased solubility and fluorescence (Davis and Vierstra, Soluble derivatives of green fluorescent protein (GFP) for use in *Arabidopsis thaliana.* Weeds of the World, The International Electronic Arabidopsis Newsletter ISSN 1358-6912, (Ed. Mary Anderson) vol 3ii, 1996). The fluorescence of GFP and its mutants has been exploited for non-invasive analysis and monitoring of biological samples in plants and other organisms for research purposes (Haseloff *et al., Proc. Natl. Acad. Sci USA 94:* 2122-2127, 1997; Hu and Cheng, *FEBS Letters 369:* 331-334, 1995; Wang and Hazelrigg, *Nature 369:* 400-403, 1994). The use of these fluorescent GFPs, mutants and homologs as fluorescent marker pigments visible upon excitation by light of specific wavelengths is well documented (e.g. U.S. Patent Nos. 6,027,881 and 5,958,713; Japanese Patent No. 11266883; International Patent Publication No. WO97/11094; U.S. Patent No. 5,625,048; International Patent Application No. PCT/US99/29472 and International Patent Publication No. PCT/AU00/00056).

In contrast to other fluorescent proteins, the fluorescence of GFP is due to amino acid interaction within the molecule, generally after folding. A contiguous fluorophore-defining amino acid sequence of Ser-Tyr-Gly is modified upon folding to produce an extended aromatic system which imparts the characteristic green fluorescence to the mature protein (Cody *et al., Biochemistry 32:* 1212-1218, 1993; Ormö *et al., Science 273:* 1392-1395, 1996; Yang *et al., Nature Biotechnol. 14:* 1246-1251, 1996). As stated above, GFP like molecules have been identified for nonbioluminscent Anthozoa species (Matz *et al.*, 1999, *supra*) which provides evidence that GFP-like proteins are not necessarily components of bioluminescent systems but may just determine fluorescent coloration in animals (Lukyanov *et al.*, 2000, *supra*). Other weakly fluorescent GFP homologs have been identified from *Acropora formosa* and *Acropora digitifera* (Dove *et al., Biol. Bull. 189:*

288-297, 1995; Hoegh-Guldberg and Dove, 2000, *supra*; Salih *et al., Nature 408:* 850-853, 2000).

All-protein chromophores are now finding application as molecular markers for monitoring polypeptide expression and localization in the fields of biochemistry, molecular and cell biology.

The present invention now describes novel all-protein chromophores (or CFMs) as well as novel and useful applications of same.

For example, the flower industry strives to develop new and different varieties of flowering plants, in particular through the manipulation of flower color. While classical breeding techniques have been used with some success to produce a wide range of colors for most of the commercial varieties of flowers, this approach has been limited by the constraints of a particular species' gene pool. For this reason, it is rare for a single species to have a full spectrum of colored varieties. The development of blue varieties of major cut flower species such as rose, chrysanthemum, tulip, lily, carnation and gerbera, for example, has proved difficult and would offer a significant opportunity in both the cut flower and ornamental markets.

Flower color is predominantly due to three types of pigment: flavonoids, carotenoids and betalains. Of the three, the flavonoids are the most common and contribute to a range of colors from yellow to red to blue. The flavonoid molecules which make the major contribution to flower color are the anthocyanins which are glycosylated derivatives of cyanidin, delphinidin, petunidin, peonidin, malvidin and pelargonidin and are localized in the vacuole. Carotenoids are natural pigments that confer yellow, orange and red colors to flowers and fruit. In plants, these pigments are localized in chromoplasts in flowers, leaves, fruit and roots.

Novel colors in ornamental plant and flowering plant species may be generated by modifying the anthocyanin pathway to produce novel anthocyanins and aurones (Davies *et*

al., Plant Journal 13: 259-266, 1998) and to alter ratios of anthocyanins to co-pigments (Holton *et al., Plant Journal 4:* 1003-1010, 1993). Alternatively, the carotenoid biosynthetic pathway can be modified to produce novel flower colors (Mann *et al., Nature Biotech. 18:* 888-892, 2000). The levels of anthocyanin production can also be increased by the expression of heterologous anthocyanin pathway gene regulatory factors (e.g. see Borevitz *et al., Plant Cell 12:* 2383-2393, 2000).

These approaches have been used with some, albeit limited, success and alternative novel approaches are constantly being sought.

In work leading up to the present invention, the inventors sought, *inter alia*, to identify novel color-facilitating molecules (CFMs) and to use same to modify the visual characteristics of eukaryotic or prokaryotic organisms by introducing into eukaryotic or prokaryotic cells, genetic material encoding CFMs which impart a color visible to a human eye in the absence of excitation by extraneous non-white light or particle emission. In a preferred embodiment, the CFMs are proteins such as GFPs or their relatives, such as non-fluorescent GFP-homologs. The use of CFMs to modulate the color of plants or plant parts such as flowers and seeds, represents a new approach to developing plant varieties having altered color characteristics. Other uses contemplated herein for the CFMs include their use as expression markers or as general reporter molecules, as a photon trap, UV sink and in sun screen or cosmetic or may be embedded in a gel matrix and be used to convert less visible light to wavelengths which are more visible. All such compositions are encompassed by the term "biomatrix".

SUMMARY OF THE INVENTION

Throughout this specification, unless the context requires otherwise, the word "comprise", or variations such as "comprises" or "comprising", will be understood to imply the inclusion of a stated element or integer or group of elements or integers but not the exclusion of any other element or integer or group of elements or integers.

Nucleotide and amino acid sequences are referred to by a sequence identifier number (SEQ ID NO:). The SEQ ID NOs: correspond numerically to the sequence identifiers <400>1, <400>2, etc. A sequence listing is provided after the claims.

The present invention provides peptides, polypeptides and proteins having one or more amino acid sequences which exhibit color-facilitating properties, either on their own or following interaction with one or more amino acids as well as nucleic acid molecules encoding same. Preferably, the peptides, polypeptides and proteins or their nucleic acid molecules are derived from one or more *Anemonia majano, Anemonia sulcata, Clavularia* sp, *Zoanthus* sp, *Discosoma* sp (e.g. *Discosoma striata*), *Aequorea* sp (e.g. *Aequorea victoria*), *Anthozoa* sp, *Cassiopea* sp, (e.g. *Cassiopea xamachana*), *Millepora* sp, *Acropora* sp (e.g. *Acropora aspera* and *Acropora nobilis)*, *Montipora* sp, *Porites murrayensis*, *Pocillopora damicormis*, *Pavona descussaca*, *Acanthastrea* sp, *Platygyra* sp or *Caulastrea* sp. These peptides, polypeptides and proteins are referred to as "color-facilitating molecules" (CFMs) and may be in isolated form, be produced within or on a cell or may form part of a biomatrix.

Accordingly, in one aspect of the present invention, there is provided an isolated nucleic acid molecule comprising a nucleotide sequence encoding a color-facilitating molecule (CFM) which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to said cell when visualized by a human eye in the absence of excitation by extraneous non-white light or particle emission.

The present invention also provides an isolated CFM comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to said cell when visualized by a human eye in the absence of excitation by extraneous non-white light or particle emission.

The preferred CFM comprises the amino-terminal end of the polypeptide set forth in SEQ ID NOs: 5, 6, 7, 8 or 9.

Particularly preferred CFMs comprise amino acid sequences selected from SEQ ID NOs:10, 11, 12, 13, 14, 15, 16, 17 or 18.

Even more preferably, the CFM is encoded by a nucleotide sequence set forth in any one of SEQ ID NOs:19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 189, 191, 193, 195, 197, 199 and 201 or a nucleotide sequence capable of hybridizing to one of the above sequences or a complementary form thereof under low stringency conditions or a nucleotide sequence having at least about 60% similarity to any one of the above sequences.

Amino acid sequences corresponding to the above nucleotide sequences correpond to SEQ ID NOs:20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 190, 192, 194, 196, 198, 200 and 202 as well as an amino acid sequence having at least about 60% similarity to any one of the above sequences.

The CFM may be in isolated form or part of a biomatrix wherein the biomatrix includes a cell, solid support, gel or bioinstrument. The CFMs are particularly useful in generating

eukaryotic or prokaryotic cells exhibiting altered visual characteristics as well as biomatrices in the form of sun screen, UV traps, photon traps and illuminescent intensifiers.

In a particularly preferred embodiment, the present invention provides transgenic plants and parts thereof including flowers, roots, leaves, stems, fruit and fibers exhibiting an altered visual characteristic.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1 shows a representation of multiple alignment of encoded amino acid sequences having SEQ ID NOs:20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68 70, 72, 74, 76, 78, 80, 82, 84 and 86, representing polypeptides comprising an N-terminal SVIAK (SEQ ID NO:5) sequence.

Figure 2 shows corresponding nucleotide sequence alignments of nucleic acid molecules, having SEQ ID NOs:19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83 and 85, encoding the polypeptides shown in Figure 1.

Figure 3 shows a representation of multiple alignment of encoded amino acid sequences having SEQ ID NOs:88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166 and 168, for polypeptides comprising an N-terminal (M)SVIAT (SEQ ID NO:6), SGIAT (SEQ ID NO:7), SVIVT (SEQ ID NO:8) and SVSAT (SEQ ID NO:9) sequences.

Figure 4 shows corresponding nucleotide sequence alignments of nucleic acid molecules, having SEQ ID NOs:87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165 and 167, encoding the polypeptides shown in Figures 3A-3D.

Figure 5 shows a representation of an alignment of amino acid sequences having SEQ ID NOs:170, 172, 174, 176, 178 and 180, for polypeptides comprising an N-terminal SVIAK sequence (SEQ ID NO:5) and a stop codon corresponding to amino acid residue 14.

Figure 6 shows corresponding nucleotide sequence alignments for nucleic acid molecules, having SEQ ID NOs:169, 171, 173, 175, 177 and 179, encoding the polypeptides shown in Figure 5.

Figure 7 is a nucleotide sequence alignment of SEQ ID NO:19 and SEQ ID NO:169, being nucleic acid sequences encoding polypeptides without and with a stop codon corresponding to amino acid residue 14, respectively.

Figure 8 shows a representation of multiple alignment of amino acid sequences for polypeptides comprising an N-terminal SVIAK sequence (SEQ ID NO:5), including SEQ ID NOs:20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68 70, 72, 74, 76, 78, 80, 82, 84 and 86, as well as sequences Aapat-1 (SEQ ID NO:181) and Aapat-2 (SEQ ID NO:182) which are disclosed in International Patent Publication No. WO 00/46233.

Figure 9 shows amino acid sequence alignments of pigment polypeptides from coral tissue, grouped according to their N-terminal 5-amino acid sequence. The name and SEQ ID NO for each peptide is indicated, as well as the "Type" to which each has been assigned based on the identity of the 29 amino acids which are located within 5 Angstroms of the "QYG" fluorophore. These 29 individual, non-contiguous amino acid residues are also indicated, as are the individual non-contiguous variable amino acids residues throughout the polypeptides shown.

Figure 10 is a diagrammatic representation of a generic bacterial expression vector based on pQE-30 (Qiagen), into which is inserted an ~0.7kb cDNA; depending on the source of the cDNA clone, each plasmid is designated as follows: pCGP2915 - A10 clone from *Acropora* sp.; pCGP2916 - A11 clone from *Acropora* sp.; pCGP2917 - A12 clone from *Acropora* sp.; pCGP2918 - A8 clone from *Acropora* sp. (SEQ ID NO:189); pCGP2920 - D10 clone from *Discosoma* sp. (SEQ ID NO:191); pCGP2922 - T3 clone from *Tubastrea* sp. (SEQ ID NO:195); pCGP2924 - S3 clone from *Sinularia* sp. (SEQ ID NO:193); pCGP2919 - D1 clone from *Discosoma* sp. (SEQ ID NO:197); pCGP2921 - T1 clone from

Tubastrea sp. (SEQ ID NO:201); pCGP2923 - S1 clone from *Sinularia* sp. (SEQ ID NO:199). Abbreviations are as follows: bla = β-lactamase gene; ColE1ori = plasmid origin of replication. The locations of restriction endonuclease recognition sites for *Pst*I, *Hin*dIII and *Bam*HI are also marked. Refer to Example 3 for further details.

Figure 11 is a graphical representation of examples of absorption scans of five "Type 1" (refer to text in Example 2 and Tables 6 and 7 for further detail) colored proteins showing extinction coefficients ($\varepsilon_{\lambda max}$) based on the method of Whitaker and Granum, 1980 (*Anal. Biochem.* **109**:156-159) for calculating protein concentration. x-axis = relative absorption; y-axis = wavelength (nm); (a) Rtms5.pep (SEQ ID NO:166), where ε_{592} = 111,000 M^{-1} cm^{-1}; (b) LGasv-C.pep (SEQ ID NO:44) where ε_{591} = 53,000 M^{-1} cm^{-1}; (c) Ce61-7sv.pep (SEQ ID NO:38) where $\varepsilon_{591.5}$ = 104,000 M^{-1} cm^{-1}; (d) PPd57-2ms.pep (SEQ ID NO:140) where ε_{593} = 67,000 M^{-1} cm^{-1}; (e) Mims-C.pep (SEQ ID NO:126) where ε_{589} = 48,000 M^{-1} cm^{-1}.

Figure 12 a graphical representation of examples of absorption scans of three "Type 2" (**A**) and two "Type 12" (**B**) (refer to text in Example 2 and Tables 6 and 7 for further detail) colored proteins, showing extinction coefficients ($\varepsilon_{\lambda max}$) based on the method of Whitaker and Granum (*Anal. Biochem. 109:* 156-159, 1980) for calculating protein concentration. x-axis = relative absorption; y-axis = wavelength (nm); **(A)** (a) PMms-B.pep (SEQ ID NO:130) where $\varepsilon_{579.5}$ = 39,000 M^{-1} cm^{-1}; (b) LGAsv-D.pep (SEQ ID NO:46) where ε_{579} = 72,400 M^{-1} cm^{-1}; (c) rtsv-2.pep (SEQ ID NO:84) where $\varepsilon_{579.5}$ = 75,000 M^{-1} cm^{-1}; **(B)** (d) Misv-F.pep (SEQ ID NO:54) where ε_{579} = 111,000 M^{-1} cm^{-1}; (e) Acasv-C.pep (SEQ ID NO:78) where $\varepsilon_{579.5}$ = 32,300 M^{-1} cm^{-1}.

Figure 13 a graphical representation of examples of absorption scans of two "Type 6" (refer to text in Example 2 and Tables 6 and 7 for further detail) colored proteins, showing extinction coefficients ($\varepsilon_{\lambda max}$) based on the method of Whitaker and Granum (*Anal. Biochem. 109:* 156-159, 1980) for calculating protein concentration. x-axis = relative absorption; y-axis = wavelength (nm); (a) LGAms-5.pep (SEQ ID NO:116) where $\varepsilon_{583.5}$ = 71,000 M^{-1} cm^{-1}; (b) Rtms-1.pep (SEQ ID NO:162) where ε_{584} = 44,000 M^{-1} cm^{-1}.

Figure 14 a graphical representation of (A) Absorption spectra and (B) Chromatogram of gel filtrated protein elution, both showing 95% confidence intervals for N = 5, for raw phosphate buffer extract of two colour morphs of *Acropora aspera* (dark blue pigmented morph; cream morph). In (A), the estimation of blue-purple pocilloporin concentration per surface area of coral tissue is based on an extinction coefficient range of 50,000 – 100,000 $M^{-1}cm^{-1}$. In (B), the chromatogram of gel filtrated protein elution is determined from 235 nm chromatograms and 280 nm chromatograms, applying the equation: 235nm -280 nm)/ 2.51 (Whitaker and Granum, 1980, *supra*). The total area under the graph represents the total soluble protein. Blue-purple pocilloporin concentration is based on the difference between areas under the blue and cream graph in the range of pocilloporin elution (24 - 26.5 min).

Figure 15 is a representation of multiple alignment of encoded amino acid sequences from T1 (SEQ ID NO:202), D1 (SEQ ID NO:198), S1 (SEQ ID NO:200), T3 (SEQ ID NO:196), D10 (SEQ ID NO:192), S3 (SEQ ID NO:194) and A8 (SEQ ID NO:190).

Figure 16 is a representation of multiple alignment of encoded amino acid sequences from SVIAK (SEQ ID NO:5)-containing peptides T1 (SEQ ID NO:202), D1 (SEQ ID NO:198), S1 (SEQ ID NO:200), T3 (SEQ ID NO:196), D10 (SEQ ID NO:192), S3 (SEQ ID NO:194) and A8 (SEQ ID NO:190), together with the SVIAK (SEQ ID NO:5)-containing peptides shown in Figure 1, having SEQ ID NOs:20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68 70, 72, 74, 76, 78, 80, 82, 84 and 86.

Figure 17 is a diagrammatic representation of the yeast expression plasmid pCGP3269. The T1 cDNA (SEQ ID NO:201) cloned in a sense orientation behind the yeast glyceraldehyde 3-phosphate dehydrogenase promoter (PGAP) in the expression vector pYE22m. Abbreviations are as follows: TRP1 = Trp1 gene, TGAP = terminator sequence from the yeast glyceraldehyde 3-phosphate dehydrogenase gene, IR1 = inverted repeat of 2 μm plasmid, pBR322 = origin of replication from *E. coli*. A selection of restriction enonuclase recognition sites are also marked. Refer to Example 7 for further details.

Figure 18 is a diagrammatic representation of the yeast expression plasmid pCGP3270. The A8 cDNA (SEQ ID NO:189) cloned in a sense orientation behind the yeast glyceraldehyde 3-phosphate dehydrogenase promoter (PGAP) in the expression vector pYE22m. Abbreviations are as follows: TRP1 = Trp1 gene, TGAP = terminator sequence from the yeast glyceraldehyde 3-phosphate dehydrogenase gene, IR1 = inverted repeat of 2 μm plasmid, pBR322 = origin of replication from *E. coli*. A selection of restriction enonuclase recognition sites are also marked. Refer to Example 7 for further details.

Figure 19 is a diagrammatic representation of a plasmid, designated pCGP2756, which comprises a multiple cloning site from pNEB193 (New England Biolabs) between the CaMV (Cauliflower Mosaic Virus) 35S promoter and CaMV 35S terminator sequences. Abbreviations are as follows: Amp = ampicillin resistance gene; p35S = a promoter region from the CaMV 35S gene; t35S = a terminator fragment from the CaMV 35S gene. A selection of restriction endonuclease recognition sites are also marked. Refer to Example 9 for further details.

Figure 20 is a diagrammatic representation of the binary plasmid pCGP2757, which comprises the CaMV35S expression cassette of pCGP2756 (Figure 19) and a *SuRB* selectable marker gene. Abbreviations are as follows: TetR = the tetracycline resistance gene; LB = left border; RB = right border; *SuRB* = the coding region and terminator sequence from the acetolactate synthase gene from tobacco; p35S = a promoter region from the cauliflower mosaic virus (CaMV) 35S gene; t35S = a terminator fragment from the CaMV 35S gene; pVS1 = a broad host range origin of replication from a plasmid from *Pseuodomonas aeruginosa;* pACYC ori = modified replicon from pACYC184 from *E. coli*. Selected restriction endonuclease recognition sites are also marked. Refer to Example 9 for further details.

Figure 21 is a diagrammatic representation of the binary plasmid pCGP2765, which comprises the A8 cDNA from *Acropora* sp. (SEQ ID NO:189) cloned into the binary vector pCGP2757 (Figure 20). Abbreviations are as follows: TetR = the tetracycline

resistance gene; LB = left border; RB = right border; *SuRB* = the coding region and terminator sequence from the acetolactate synthase gene from tobacco; p35S = a promoter region from the cauliflower mosaic virus (CaMV) 35S gene; t35S = a terminator fragment from the CaMV 35S gene; pVS1 = a broad host range origin of replication from a plasmid from *Pseudomonas aeruginosa;* pACYC ori = modified replicon from pACYC184 from *E. coli*; A8 = cDNA from *Acropora* sp. (SEQ ID NO:189). Selected restriction endonuclease recognition sites are also marked. Refer to Example 9 for further details.

Figure 22 is a diagrammatic representation of the binary plasmid pCGP2769, which comprises the D1 cDNA from *Discosoma* sp. (SEQ ID NO:197) cloned into the binary vector pCGP2757 (Figure 20). Abbreviations are as follows: TetR = the tetracycline resistance gene; LB = left border; RB = right border; *SuRB* = the coding region and terminator sequence from the acetolactate synthase gene from tobacco; p35S = a promoter region from the cauliflower mosaic virus (CaMV) 35S gene; t35S = a terminator fragment from the CaMV 35S gene; pVS1 = a broad host range origin of replication from a plasmid from *Pseuodomonas aeruginosa;* pACYC ori = modified replicon from pACYC184 from *E. coli*; D1 = cDNA from *Discosoma* sp. (SEQ ID NO:197). Selected restriction endonuclease recognition sites are also marked. Refer to Example 9 for further details.

Figure 23 is a diagrammatic representation of the binary plasmid pCGP2770, which comprises the S1 cDNA from *Sinularia* sp. (SEQ ID NO:199) cloned into the binary vector pCGP2757 (Figure 20). Abbreviations are as follows: TetR = the tetracycline resistance gene; LB = left border; RB = right border; *SuRB* = the coding region and terminator sequence from the acetolactate synthase gene from tobacco; p35S = a promoter region from the cauliflower mosaic virus (CaMV) 35S gene; t35S = a terminator fragment from the CaMV 35S gene; pVS1 = a broad host range origin of replication from a plasmid from *Pseudomonas aeruginosa;* pACYC ori = modified replicon from pACYC184 from *E. coli*; S1 = cDNA from *Sinularia* sp. (SEQ ID NO:199). Selected restriction endonuclease recognition sites are also marked. Refer to Example 9 for further details.

Figure 24 is a diagrammatic representation of the binary plasmid pCGP2772, which comprises the T1 cDNA from *Tubastrea* sp. (SEQ ID NO:201) cloned into the binary vector pCGP2757 (Figure 20). Abbreviations are as follows: TetR = the tetracycline resistance gene; LB = left border; RB = right border; *SuRB* = the coding region and terminator sequence from the acetolactate synthase gene from tobacco; p35S = a promoter region from the cauliflower mosaic virus (CaMV) 35S gene; t35S = a terminator fragment from the CaMV 35S gene; pVS1 = a broad host range origin of replication from a plasmid from *Pseudomonas aeruginosa;* pACYC ori = modified replicon from pACYC184 from *E. coli*; T1 = cDNA from *Tubastrea* sp. (SEQ ID NO:201). Selected restriction endonuclease recognition sites are also marked. Refer to Example 9 for further details.

Figure 25 is a diagrammatic representation of the plasmid pCGP1116, which comprises a promoter fragment from a chalcone synthase (CHS) gene from *Rosa hybrida* cv. Kardinal. Abbreviations are as follows: Rose CHS = Rose chalcone synthase promoter fragment; ori = origin of replication; Amp = ampicillin resistance gene; Several restriction endonuclease recognition sites are also marked. Refer to Example 10 for further details.

Figure 26 is a diagrammatic representation of the binary plasmid pCGP3255. The CaMV35S promoter of the 35S expression cassette of pCGP2757 (Figure 20) has been replaced with the rose chalcone synthase promoter fragment from pCGP1116 (Figure 25) Abbreviations are as follows: rCHS = rose chalcone synthase promoter fragment; TetR = the tetracycline resistance gene; LB = left border; RB = right border; *SuRB* = the coding region and terminator sequence from the acetolactate synthase gene from tobacco; p35S = a promoter region from the cauliflower mosaic virus (CaMV) 35S gene; t35S = a terminator fragment from the CaMV 35S gene; pVS1 = a broad host range origin of replication from a plasmid from *Pseudomonas aeruginosa;* pACYC ori = modified replicon from pACYC184 from *E. coli.* Refer to Example 10 for further details.

Figure 27 is a diagrammatic representation of the bianry plasmid pCGP2782. The T1 cDNA from *Tubastrea* sp. (SEQ ID NO:201) was cloned into binary vector pCGP3255

(Figure 26) behind the rose chalcone synthase promoter fragment. Abbreviations are as follows: rCHS = rose chalcone synthase promoter fragment; TetR = the tetracycline resistance gene; LB = left border; RB = right border; *SuRB* = the coding region and terminator sequence from the acetolactate synthase gene from tobacco; p35S = a promoter region from the cauliflower mosaic virus (CaMV) 35S gene; t35S = a terminator fragment from the CaMV 35S gene; pVS1 = a broad host range origin of replication from a plasmid from *Pseudomonas aeruginosa;* pACYC ori = modified replicon from pACYC184 from *E. coli*; T1 = cDNA from *Tubastrea* sp. (SEQ ID NO:201). A selection of restriction endonuclease recognition sites is also marked. Refer to Example 10 for further details.

Figure 28 is a diagrammatic representation of the binary plasmid pCGP2773. The D1 cDNA from *Discosoma* sp. (SEQ ID NO:197) was cloned into binary vector pCGP3255 (Figure 26), behind the rose chalcone synthase promoter fragment. Abbreviations are as follows: rCHS = rose chalcone synthase promoter fragment; TetR = the tetracycline resistance gene; LB = left border; RB = right border; *SuRB* = the coding region and terminator sequence from the acetolactate synthase gene from tobacco; p35S = a promoter region from the cauliflower mosaic virus (CaMV) 35S gene; t35S = a terminator fragment from the CaMV 35S gene; pVS1 = a broad host range origin of replication from a plasmid from *Pseuodomonas aeruginosa;* pACYC ori = modified replicon from pACYC184 from *E. coli*; D1 = cDNA from *Discosoma* sp. (SEQ ID NO:197). A selection of restriction endonuclease recognition sites is also marked. Refer to Example 10 for further details.

Figure 29 is a diagrammatic representation of the binary plasmid pCGP2774. The S1 cDNA from *Sinularia* sp. (SEQ ID NO:199) was cloned into binary vector pCGP3255 (Figure 26), behind the rose chalcone synthase promoter fragment. Abbreviations are as follows: rCHS = rose chalcone synthase promoter fragment; TetR = the tetracycline resistance gene; LB = left border; RB = right border; *SuRB* = the coding region and terminator sequence from the acetolactate synthase gene from tobacco; p35S = a promoter region from the cauliflower mosaic virus (CaMV) 35S gene; t35S = a terminator fragment from the CaMV 35S gene; pVS1 = a broad host range origin of replication from a plasmid

from *Pseudomonas aeruginosa;* pACYC ori = modified replicon from pACYC184 from *E. coli*; S1 = cDNA from *Sinularia* sp. (SEQ ID NO:199). A selection of restriction endonuclease recognition sites is also marked. Refer to Example 10 for further details.

Figure 30 is a diagrammatic representation of the binary plasmid pCGP2780, which is plasmid pCGP2757 (Figure 20) from which has been removed a ~290 base-pair *SalI* fragment to allow the creation of a unique *Bam*HI restriction endonuclease site. Abbreviations are as follows: TetR = the tetracycline resistance gene; LB = left border; RB = right border; *SuRB* = the coding region and terminator sequence from the acetolactate synthase gene from tobacco; p35S = a promoter region from the cauliflower mosaic virus (CaMV) 35S gene; t35S = a terminator fragment from the CaMV 35S gene; pVS1 = a broad host range origin of replication from a plasmid from *Pseudomonas aeruginosa;* pACYC ori = modified replicon from pACYC184 from *E. coli* A selection of restriction endonuclease recognition sites is also marked. Refer to Example 11 for further details.

Figure 31 is a diagrammatic representation of the binary plasmid pCGP2784, which is comprised of the ~0.2 kb chloroplast transit-peptide from the small subunit of ribulose bisphosphate carboxylase gene (RBCase) from *Nicotiana sylvestris*, cloned into the multiple cloning site of pCGP2780 of Figure 30. Abbreviations are as follows: TetR = the tetracycline resistance gene; LB = left border; RB = right border; *SuRB* = the coding region and terminator sequence from the acetolactate synthase gene from tobacco; p35S = a promoter region from the cauliflower mosaic virus (CaMV) 35S gene; t35S = a terminator fragment from the CaMV 35S gene; pVS1 = a broad host range origin of replication from a plasmid from *Pseudomonas aeruginosa;* pACYC ori = modified replicon from pACYC184 from *E. coli*; TSSU = chloroplast transit-peptide from the small subunit of RBCase of *Nicotiana sylvestris*. Selected restriction endonuclease recognition sites are also marked. Refer to Example 11 for further details.

Figure 32 is a diagrammatic representation of the binary plasmid pCGP2781, which is plasmid pCGP2772 (Figure 24) from which has been removed a ~290 base-pair *SalI*

fragment to allow the creation of a unique *Bam*HI restriction endonuclease site. Abbreviations are as follows: TetR = the tetracycline resistance gene; LB = left border; RB = right border; *SuRB* = the coding region and terminator sequence from the acetolactate synthase gene from tobacco; p35S = a promoter region from the cauliflower mosaic virus (CaMV) 35S gene; t35S = a terminator fragment from the CaMV 35S gene; pVS1 = a broad host range origin of replication from a plasmid from *Pseuodomonas aeruginosa;* pACYC ori = modified replicon from pACYC184 from *E. coli.* T1 = T1 cDNA from *Tubastrea* sp. (SEQ ID NO:201). Selected restriction endonuclease recognition sites are also marked. Refer to Example 11 for further details.

Figure 33 is a diagrammatic representation of the binary plasmid pCGP2785, which is comprised of the ~0.2 kb chloroplast transit peptide from the small subunit of ribulose biphosphate carboxylase (RBCase) from *Nicotiana sylvestris* inserted into the CaMV 35S expression cassette of binary vector pCGP2781 (Figure 32), upstream of the T1 cDNA. Abbreviations are as follows: TetR = the tetracycline resistance gene; LB = left border; RB = right border; *SuRB* = the coding region and terminator sequence from the acetolactate synthase gene from tobacco; p35S = a promoter region from the cauliflower mosaic virus (CaMV) 35S gene; t35S = a terminator fragment from the CaMV 35S gene; pVS1 = a broad host range origin of replication from a plasmid from *Pseuodomonas aeruginosa;* pACYC ori = modified replicon from pACYC184 from *E. coli.* T1 = T1 cDNA from *Tubastrea* sp. (SEQ ID NO:201); TSSU = chloroplast transit peptide from the small subunit of RBCase from *Nicotiana sylvestris.* Selected restriction endonuclease recognition sites are also marked. Refer to Example 11 for further details.

Figure 34 is a diagrammatic representation of the binary plasmid pCGP2787 which is comprised of the ~0.2 kb chloroplast transit peptide from the small subunit of ribulose biphosphate carboxylase (RBCase) from *Nicotiana sylvestris* inserted into the Rose CHS expression cassette of binary vector pCGP2782 (Figure 27), upstream of the T1 cDNA. Abbreviations are as follows: TetR = the tetracycline resistance gene; LB = left border; RB = right border; *SuRB* = the coding region and terminator sequence from the acetolactate

synthase gene from tobacco; p35S = a promoter region from the cauliflower mosaic virus (CaMV) 35S gene; t35S = a terminator fragment from the CaMV 35S gene; rCHS = rose chalcone synthase promoter fragment; pVS1 = a broad host range origin of replication from a plasmid from *Pseuodomonas aeruginosa;* pACYC ori = modified replicon from pACYC184 from *E. coli.* T1 = T1 cDNA from *Tubastrea* sp. (SEQ ID NO:201); TSSU = chloroplast transit peptide from the small subunit of RBCase from *Nicotiana sylvestris.* Selected restriction endonuclease recognition sites are also marked. Refer to Example 11 for further details.

Figure 35 is a diagrammatic representation of the plasmid pCGP3257, which is comprised of the basic chitinase N-terminal endoplasmic reticulum (ER) transit peptide signal sequence from *Arabidopsis thaliana* inserted into the CaMV 35S expression cassette of binary vector pCGP2780 (Figure 30), downstream of the CaMV 35S promoter. Abbreviations are as follows: TetR = the tetracycline resistance gene; LB = left border; RB = right border; *SuRB* = the coding region and terminator sequence from the acetolactate synthase gene from tobacco; p35S = a promoter region from the cauliflower mosaic virus (CaMV) 35S gene; t35S = a terminator fragment from the CaMV 35S gene; pVS1 = a broad host range origin of replication from a plasmid from *Pseuodomonas aeruginosa;* pACYC ori = modified replicon from pACYC184 from *E. coli*; ERT = ER transit peptide signal sequence from *Arabidopsis* basic chitinase gene. Selected restriction endonuclease recognition sites are also marked. Refer to Example 11 for further details.

Figure 36 is a diagrammatic representation of the binary plasmid pCGP3259. The T1 cDNA from *Tubastrea* sp. (SEQ ID NO:201)with an in-frame HDEL peptide sequence at the 3' end was cloned into the CaMV 35S expression cassette of binary vector pCGP3257 (Figure 35), downstream of the ER transit-peptide signal sequence from *Arabidopsis thaliana*. Abbreviations are as follows: TetR = the tetracycline resistance gene; LB = left border; RB = right border; *SuRB* = the coding region and terminator sequence from the acetolactate synthase gene from tobacco; p35S = a promoter region from the cauliflower mosaic virus (CaMV) 35S gene; t35S = a terminator fragment from the CaMV 35S gene;

pVS1 = a broad host range origin of replication from a plasmid from *Pseudomonas aeruginosa;* pACYC ori = modified replicon from pACYC184 from *E. coli*; ERT:T1:HDEL = T1 cDNA clone from *Tubastrea* (SEQ ID NO:201) with an in-frame ER transit peptide sequence from *Arabidopsis* basic chitinase gene at the 5' end and an HDEL ER retention sequence at the 3' end. Selected restriction endonuclease recognition sites are also marked. Refer to Example 11 for further details.

Figure 37 is a diagrammatic representation of the binary plasmid pCGP3262 which is comprised of the basic chitinase N-terminal endoplasmic reticulum (ER) transit peptide signal sequence from *Arabidopsis thaliana* inserted into the Rose CHS expression cassette of binary vector pCGP3255 (Figure 26), downstream of the Rose CHS promoter. Abbreviations are as follows: TetR = the tetracycline resistance gene; LB = left border; RB = right border; *SuRB* = the coding region and terminator sequence from the acetolactate synthase gene from tobacco; p35S = a promoter region from the cauliflower mosaic virus (CaMV) 35S gene; t35S = a terminator fragment from the CaMV 35S gene; rCHS rose chalcone synthase promoter fragment; pVS1 = a broad host range origin of replication from a plasmid from *Pseuodomonas aeruginosa;* pACYC ori = modified replicon from pACYC184 from *E. coli*; ERT = ER transit peptide signal sequence from *Arabidopsis* basic chitinase gene. Selected restriction endonuclease recognition sites are also marked. Refer to Example 11 for further details.

Figure 38 is a diagrammatic representation of the binary plasmid pCGP3263. The T1 cDNA from *Tubastrea* sp. (SEQ ID NO:201) with an in-frame HDEL peptide sequence at the 3' end was cloned into the Rose CHS expression cassette of binary vector pCGP3262 (Figure 37), downstream of the ER transit-peptide signal sequence from *Arabidopsis thaliana*. Abbreviations are as follows: TetR = the tetracycline resistance gene; LB = left border; RB = right border; *SuRB* = the coding region and terminator sequence from the acetolactate synthase gene from tobacco; p35S = a promoter region from the cauliflower mosaic virus (CaMV) 35S gene; t35S = a terminator fragment from the CaMV 35S gene; pVS1 = a broad host range origin of replication from a plasmid from *Pseuodomonas*

aeruginosa; pACYC ori = modified replicon from pACYC184 from *E. coli*; ERT:T1:HDEL = T1 cDNA clone from *Tubastrea* (SEQ ID NO:201) with an in-frame ER transit peptide sequence from *Arabidopsis* basic chitinase gene at the 5' end and an HDEL ER retention sequence at the 3' end; rCHS = Rose chalcone synthase promoter fragment. Selected restriction endonuclease recognition sites are also marked. Refer to Example 11 for further details.

Figure 39 is a diagrammatic representation of the binary plasmid pCGP3258. An in-frame fusion of the T1 coding sequence (SEQ ID NO:201) and the mgfp4 sequence was cloned into the CaMV 35S expression cassette of pCGP3257 (Figure 35). Abbreviations are as follows: TetR = the tetracycline resistance gene; LB = left border; RB = right border; *SuRB* = the coding region and terminator sequence from the acetolactate synthase gene from tobacco; p35S = a promoter region from the cauliflower mosaic virus (CaMV) 35S gene; t35S = a terminator fragment from the CaMV 35S gene; pVS1 = a broad host range origin of replication from a plasmid from *Pseuodomonas aeruginosa;* pACYC ori = modified replicon from pACYC184 from *E. coli*; T1:mgfp4 = T1 cDNA clone from *Tubastrea* (SEQ ID NO:201) with an in-frame fusion of the mgfp4 coding sequence. Selected restriction endonuclease recognition sites are also marked. Refer to Example 12 for further details.

Figure 40 is a representation of an autoradiograph of an RNA blot probed with ^{32}P-labelled fragments of (A) a 0.7 kb *Bam*HI/*Hin*dIII fragment of the T1 clone contained in pCGP2921 (Figure 10) and (B) 0.8 kb *Hin*dIII fragment of *SuRB* contained in pCGP1651. Each lane contained a 5 to 10 µg sample of total RNA isolated from the leaves and petals of transgenic*P. hybrida* plants. (C) Ethidium bromide staining of the 18S rRNA is shown as an indication of RNA loading levels. Lane numbers are marked 1 to 12. The numbers above the lane numbers refer to construct pCGP numbers used in the transformation experiments. Refer to Example 15 for further details.

Figure 41 is a representation of an autoradiograph of an RNA blot probed with ^{32}P-labelled fragments of (A) a 0.7 kb *Bam*HI/*Hin*dIII fragment of the T1 clone contained in

pCGP2921 (Figure 10) and (B) 0.8 kb *Hin*dIII fragment of *SuRB* contained in pCGP1651. Each lane contained a 5 μg sample of total RNA isolated from the leaves of non-transgenic and transgenic *A. thaliana* plants. (C) Ethidium bromide staining of the 25S rRNA is shown as an indication of RNA loading levels. Lane numbers are marked 1 to 17. The numbers above the lane numbers refer to construct pCGP numbers used in the transformation experiments with the exception of NTG and 35Smgfp4. NTG = non transgenic; 35Smgfp4 = pBIN35Smgfp4. Refer to Example 14 for further details.

Figure 42 is a graphical representation of absorption, excitation and emission spectra for Rtms-5 (SEQ ID NO:166) and its variants. (A) Absorption spectra for Rtms-5 (SEQ ID NO:166); (B) Absorption spectra for variants generated *via* site directed mutagenesis: Rtms5-H142S and Rtms-5v (SEQ ID NO:216); C Excitation (exc) and emission (em) spectra for Rtms5-H142S and Rtms-5v (SEQ ID NO:216) at wavelengths indicated.

Figure 43 is a graphical representation of examples of excitation and emission spectra for two other colored proteins, showing extinction coefficients ($\varepsilon_{\lambda max}$) based on the method of Whitaker and Granum (1980, *supra*) for calculating protein concentration. x-axis = relative absorption; y-axis = wavelength (nm); (A) Aams-4 (SEQ ID NO:90)-H142S, and (B) Rtms-1 (SEQ ID NO:162)-N142S; λmax for each spectrum is shown on the figure.

Figure 44 is a diagrammatic representation of the binary plasmid pCGP2926. A ~0.1kb *AscI/Bam*HI fragment (containing sequences to a prokaryotic ribosome binding site (RBS), translational initiation consensus sequence (TICS) and an RGSHHHHHH epitope) generated by ligating the primers TICS-His-FWD (SEQ ID NO:227) and TICS-His-REV (SEQ ID NO:228) was introduced into the binary plasmid pCGP2781 (Figure 32). Abbreviations are as follows: TetR = the tetracycline resistance gene; LB = left border; RB = right border; *SuRB* = the coding region and terminator sequence from the acetolactate synthase gene from tobacco; p35S = a promoter region from the cauliflower mosaic virus (CaMV) 35S gene; t35S = a terminator fragment from the CaMV 35S gene; pVS1 = a broad host range origin of replication from a plasmid from *Pseuodomonas aeruginosa;* pACYC ori = modified replicon from pACYC184 from *E. coli*. T1 = T1 cDNA from

Tubastrea sp. (SEQ ID NO:201), His = RGSHHHHHH epitope. Selected restriction endonuclease recognition sites are also marked. Refer to Example 9 for further details.

Figure 45 is diagrammatic representation of the binary plasmid pCGP3261. An ER targeted T1:mGFP4 fusion was cloned into CaMV 35S expression cassette of the binary vector pCGP3257. Abbreviations are as follows: TetR = the tetracycline resistance gene; LB = left border; RB = right border; *SuRB* = the coding region and terminator sequence from the acetolactate synthase gene from tobacco; p35S = a promoter region from the cauliflower mosaic virus (CaMV) 35S gene; t35S = a terminator fragment from the CaMV 35S gene; pVS1 = a broad host range origin of replication from a plasmid from *Pseuodomonas aeruginosa;* pACYC ori = modified replicon from pACYC184 from *E. coli*; ERT:T1:mGFP4:HDEL = T1 cDNA clone from *Tubastrea* (SEQ ID NO:201):mGFP4 in-frame fusion with an in-frame ER transit peptide sequence from *Arabidopsis* basic chitinase gene at the 5' end and an HDEL ER retention sequence at the 3' end. Selected restriction endonuclease recognition sites are also marked. Refer to Example 12 for further details.

Figure 46 is diagrammatic representation of the binary plasmid pCGP3260. An ER targeted mGFP4 coding region was cloned into CaMV 35S expression cassette of the binary vector pCGP2780. Abbreviations are as follows: TetR = the tetracycline resistance gene; LB = left border; RB = right border; *SuRB* = the coding region and terminator sequence from the acetolactate synthase gene from tobacco; p35S = a promoter region from the cauliflower mosaic virus (CaMV) 35S gene; t35S = a terminator fragment from the CaMV 35S gene; pVS1 = a broad host range origin of replication from a plasmid from *Pseuodomonas aeruginosa;* pACYC ori = modified replicon from pACYC184 from *E. coli*; ERT:mGFP4:HDEL = mGFP4 coding sequence with an in-frame ER transit peptide sequence from *Arabidopsis* basic chitinase gene at the 5' end and an HDEL ER retention sequence at the 3' end. Selected restriction endonuclease recognition sites are also marked. Refer to Example 12 for further details.

Figure 47 is a photographic representation of clear nature gel electrophoresis showing separation of fluorescently labeled mitochondrial ATP synthase. 1. b-gfp fusion protein; 2. b-Rtms-5v fusion protein; 3. b-dsRed fusion protein; 4. GFP not fused to another protein.

A summary of sequence identifiers used throughout the subject specification is provided in Table 1.

TABLE 1
SUMMARY OF SEQUENCE IDENTIFIERS

SEQ ID NO.	NAME	DESCRIPTION
1	POC FOR	oligonucleotide
2	POC 220	oligonucleotide
3	MSVIAT FOR	oligonucleotide
4	POC 231	oligonucleotide
5	SVIAK	N-terminal amino acid sequence of a CFM
6	(M)SVIAT	N-terminal amino acid sequence of a CFM
7	SGIAT	N-terminal amino acid sequence of a CFM
8	SVIVT	N-terminal amino acid sequence of a CFM
9	SVSAT	N-terminal amino acid sequence of a CFM
10	SVIATQMTYKVYMSGT	N-terminal amino acid sequence of a CFM
11	SVIATQMTYKVYMSPT	N-terminal amino acid sequence of a CFM
12	SVIATQVTYKVYMSGT	N-terminal amino acid sequence of a CFM
13	SGIATQMTYKVYMSGT	N-terminal amino acid sequence of a CFM
14	SVIVTQMTYKVYMSGT	N-terminal amino acid sequence of a CFM
15	SVSATQMTYKVYMSGT	N-terminal amino acid sequence of a CFM
16	SVIAKQMTYKVNMSGT	N-terminal amino acid sequence of a CFM
17	SVIAKQMTYKVYMSDT	N-terminal amino acid sequence of a CFM
18	SVIAKQMTYX_1X_2YX_3SGT	N-terminal amino acid sequence of a CFM
19	Aasv-1	nucleotide sequence of SVIAK-type clone
20	Aasv-1.pep	translated amino acid sequence of SVIAK CFM
21	Aasv-3	nucleotide sequence of SVIAK-type clone
22	Aasv-3.pep	translated amino acid sequence of SVIAK CFM
23	Aasv-P	nucleotide sequence of SVIAK-type clone
24	Aasv-P.pep	translated amino acid sequence of SVIAK CFM
25	Acasv-A	nucleotide sequence of SVIAK-type clone
26	Acasv-A.pep	translated amino acid sequence of SVIAK CFM
27	Acasv-C	nucleotide sequence of SVIAK-type clone
28	Acasv-C.pep	translated amino acid sequence of SVIAK CFM

SEQ ID NO.	NAME	DESCRIPTION
29	Acasv-D	nucleotide sequence of SVIAK-type clone
30	Acasv-D.pep	translated amino acid sequence of SVIAK CFM
31	Ce61-3sv	nucleotide sequence of SVIAK-type clone
32	Ce61-3sv.pep	translated amino acid sequence of SVIAK CFM
33	Ce61-4sv	nucleotide sequence of SVIAK-type clone
34	Ce61-4sv.pep	translated amino acid sequence of SVIAK CFM
35	Ce61-5sv	nucleotide sequence of SVIAK-type clone
36	Ce61-5sv.pep	translated amino acid sequence of SVIAK CFM
37	Ce61-7sv	nucleotide sequence of SVIAK-type clone
38	Ce61-7sv.pep	translated amino acid sequence of SVIAK CFM
39	GPd58-2sv	nucleotide sequence of SVIAK-type clone
40	GPd58-2sv.pep	translated amino acid sequence of SVIAK CFM
41	LGAsv-A	nucleotide sequence of SVIAK-type clone
42	LGAsv-A.pep	translated amino acid sequence of SVIAK CFM
43	LGAsv-C	nucleotide sequence of SVIAK-type clone
44	LGAsv-C.pep	translated amino acid sequence of SVIAK CFM
45	LGAsv-D	nucleotide sequence of SVIAK-type clone
46	LGAsv-D.pep	translated amino acid sequence of SVIAK CFM
47	LGAsv-E	nucleotide sequence of SVIAK-type clone
48	LGAsv-E.pep	translated amino acid sequence of SVIAK CFM
49	Misv-A	nucleotide sequence of SVIAK-type clone
50	Misv-A.pep	translated amino acid sequence of SVIAK CFM
51	Misv-B	nucleotide sequence of SVIAK-type clone
52	Misv-B.pep	translated amino acid sequence of SVIAK CFM
53	Misv-F	nucleotide sequence of SVIAK-type clone
54	Misv-F.pep	translated amino acid sequence of SVIAK CFM
55	PM1Asv-rep	nucleotide sequence of SVIAK-type clone
56	PM1Asv-rep.pep	translated amino acid sequence of SVIAK CFM
57	PM1Csv-rep	nucleotide sequence of SVIAK-type clone
58	PM1Csv-rep.pep	translated amino acid sequence of SVIAK CFM
59	PMsv-4	nucleotide sequence of SVIAK-type clone
60	PMsv-4.pep	translated amino acid sequence of SVIAK CFM
61	PMsv-5	nucleotide sequence of SVIAK-type clone
62	PMsv-5.pep	translated amino acid sequence of SVIAK CFM
63	PPsv-1	nucleotide sequence of SVIAK-type clone
64	PPsv-1.pep	translated amino acid sequence of SVIAK CFM
65	PPsv-2	nucleotide sequence of SVIAK-type clone
66	PPsv-2.pep	translated amino acid sequence of SVIAK CFM
67	PPsv-3	nucleotide sequence of SVIAK-type clone
68	PPsv-3.pep	translated amino acid sequence of SVIAK CFM
69	PPsv-4	nucleotide sequence of SVIAK-type clone
70	PPsv-4.pep	translated amino acid sequence of SVIAK CFM

SEQ ID NO.	NAME	DESCRIPTION
71	PPsv-5	nucleotide sequence of SVIAK-type clone
72	PPsv-5.pep	translated amino acid sequence of SVIAK CFM
73	PPsv-6	nucleotide sequence of SVIAK-type clone
74	PPsv-6.pep	translated amino acid sequence of SVIAK CFM
75	Pavsv-A	nucleotide sequence of SVIAK-type clone
76	Pavsv-A.pep	translated amino acid sequence of SVIAK CFM
77	Pavsv-B	nucleotide sequence of SVIAK-type clone
78	Pavsv-B.pep	translated amino acid sequence of SVIAK CFM
79	Pavsv-C	nucleotide sequence of SVIAK-type clone
80	Pavsv-C.pep	translated amino acid sequence of SVIAK CFM
81	RTsv-1	nucleotide sequence of SVIAK-type clone
82	RTsv-1.pep	translated amino acid sequence of SVIAK CFM
83	RTsv-2	nucleotide sequence of SVIAK-type clone
84	RTsv-2.pep	translated amino acid sequence of SVIAK CFM
85	RTsv-3	nucleotide sequence of SVIAK-type clone
86	RTsv-3.pep	translated amino acid sequence of SVIAK CFM
87	Aams-2	nucleotide sequence of (M)SVIAT-type clone
88	Aams-2.pep	translated amino acid sequence of (M)SVIAT CFM
89	Aams-4	nucleotide sequence of (M)SVIAT-type clone
90	Aams-4.pep	translated amino acid sequence of (M)SVIAT CFM
91	Aams-5	nucleotide sequence of SGIAT-type clone
92	Aams-5.pep	translated amino acid sequence of SGIAT CFM
93	Aams-6	nucleotide sequence of (M)SVIAT-type clone
94	Aams-6.pep	translated amino acid sequence of (M)SVIAT CFM
95	Aams-A	nucleotide sequence of (M)SVIAT-type clone
96	Aams-A.pep	translated amino acid sequence of (M)SVIAT CFM
97	Aams-B	nucleotide sequence of (M)SVIAT-type clone
98	Aams-B.pep	translated amino acid sequence of (M)SVIA5 CFM
99	Acams-2	nucleotide sequence of (M)SVIAT-type clone
100	Acams-2.pep	translated amino acid sequence of (M)SVIAT CFM
101	Acams-3	nucleotide sequence of (M)SVIAT-type clone
102	Acams-3.pep	translated amino acid sequence of (M)SVIAT CFM
103	Acams-4	nucleotide sequence of (M)SVIAT-type clone
104	Acams-4.pep	translated amino acid sequence of (M)SVIAT CFM
105	Acams-5	nucleotide sequence of (M)SVIAT-type clone
106	Acams-5.pep	translated amino acid sequence of (M)SVIAT CFM
107	Cems-F	nucleotide sequence of (M)SVIAT-type clone
108	Cems-F.pep	translated amino acid sequence of (M)SVIAT CFM
109	Cems-G	nucleotide sequence of (M)SVIAT-type clone
110	Cems-G.pep	translated amino acid sequence of (M)SVIAT CFM
111	Cems-H	nucleotide sequence of (M)SVIAT-type clone
112	Cems-H.pep	translated amino acid sequence of (M)SVIAT CFM

SEQ ID NO.	NAME	DESCRIPTION
113	Cems-I	nucleotide sequence of (M)SVIAT-type clone
114	Cems-I.pep	translated amino acid sequence of (M)SVIAT CFM
115	LGAms-5	nucleotide sequence of (M)SVIAT-type clone
116	LGAms-5.pep	translated amino acid sequence of (M)SVIAT CFM
117	LGAms-6	nucleotide sequence of (M)SVIAT-type clone
118	LGAms-6.pep	translated amino acid sequence of (M)SVIAT CFM
119	Mi68Dms	nucleotide sequence of (M)SVIAT-type clone
120	Mi68Dms.pep	translated amino acid sequence of (M)SVIAT CFM
121	Mims-A	nucleotide sequence of (M)SVIAT-type clone
122	Mims-A.pep	translated amino acid sequence of (M)SVIAT CFM
123	Mims-B	nucleotide sequence of (M)SVIAT-type clone
124	Mims-B.pep	translated amino acid sequence of (M)SVIAT CFM
125	Mims-C	nucleotide sequence of (M)SVIAT-type clone
126	Mims-C.pep	translated amino acid sequence of (M)SVIAT CFM
127	PMms-A	nucleotide sequence of (M)SVIAT-type clone
128	PMms-A.pep	translated amino acid sequence of (M)SVIAT CFM
129	PMms-B	nucleotide sequence of (M)SVIAT-type clone
130	PMms-B.pep	translated amino acid sequence of (M)SVIAT CFM
131	PMms-C	nucleotide sequence of (M)SVIAT-type clone
132	PMms-C.pep	translated amino acid sequence of (M)SVIAT CFM
133	PMms-D	nucleotide sequence of (M)SVIAT-type clone
134	PMms-D.pep	translated amino acid sequence of (M)SVIAT CFM
135	PMms-E	nucleotide sequence of (M)SVIAT-type clone
136	PMms-E.pep	translated amino acid sequence of (M)SVIAT CFM
137	PPd57-1ms	nucleotide sequence of (M)SVIAT-type clone
138	PPd57-1ms.pep	translated amino acid sequence of (M)SVIAT CFM
139	PPd57-2ms	nucleotide sequence of (M)SVIAT-type clone
140	PPd57-2ms.pep	translated amino acid sequence of (M)SVIAT CFM
141	PPd57-3	nucleotide sequence of (M)SVIAT-type clone
142	PPd57-3.pep	translated amino acid sequence of (M)SVIAT CFM
143	PPd57-4ms	nucleotide sequence of (M)SVIAT-type clone
144	PPd57-4ms.pep	translated amino acid sequence of (M)SVIAT CFM
145	PPms-1	nucleotide sequence of (M)SVIAT-type clone
146	PPms-1.pep	translated amino acid sequence of (M)SVIAT CFM
147	PPms-2	nucleotide sequence of (M)SVIAT-type clone
148	PPms-2.pep	translated amino acid sequence of (M)SVIAT CFM
149	PPms-E	nucleotide sequence of (M)SVIAT-type clone
150	PPms-E.pep	translated amino acid sequence of (M)SVIAT CFM
151	PPms-G	nucleotide sequence of (M)SVIAT-type clone
152	PPms-G.pep	translated amino acid sequence of (M)SVIAT CFM
153	Pav5ms	nucleotide sequence of (M)SVIAT-type clone
154	Pav5ms.pep	translated amino acid sequence of (M)SVIAT CFM

SEQ ID NO.	NAME	DESCRIPTION
155	Pavms-2	nucleotide sequence of (M)SVIAT-type clone
156	Pavms-2.pep	translated amino acid sequence of (M)SVIAT CFM
157	Pavms-3	nucleotide sequence of (M)SVIAT-type clone
158	Pavms-3.pep	translated amino acid sequence of (M)SVIAT CFM
159	Pavms-4	nucleotide sequence of (M)SVIAT-type clone
160	Pavms-4.pep	translated amino acid sequence of (M)SVIAT CFM
161	RTms-1	nucleotide sequence of (M)SVIAT-type clone
162	RTms-1.pep	translated amino acid sequence of (M)SVIAT CFM
163	RTms-2	nucleotide sequence of SVSAT-type clone
164	RTms-2.pep	translated amino acid sequence of SVSAT CFM
165	RTms-5	nucleotide sequence of (M)SVIAT-type clone
166	RTms-5.pep	translated amino acid sequence of (M)SVIAT CFM
167	RTms-6	nucleotide sequence of SVIVT-type clone
168	RTms-6.pep	translated amino acid sequence of SVIVT CFM
169	Acasv-B	nucleotide sequence of SVIAK-type clone with a stop codon at amino acid position 14
170	Acasv-B.pep	translated amino acid sequence of SVIAK CFM
171	GPd58-1sv	nucleotide sequence of SVIAK-type clone with a stop codon at amino acid position 14
172	GPd58-1sv.pep	translated amino acid sequence of SVIAK CFM
173	GPd58-3sv	nucleotide sequence of SVIAK-type clone with a stop codon at amino acid position 14
174	GPd58-3sv.pep	translated amino acid sequence of SVIAK CFM
175	GPd58-4sv	nucleotide sequence of SVIAK-type clone with a stop codon at amino acid position 14
176	GPd58-4sv.pep	translated amino acid sequence of SVIAK CFM
177	Misv-D	nucleotide sequence of SVIAK-type clone with a stop codon at amino acid position 14
178	Misv-D.pep	translated amino acid sequence of SVIAK CFM
179	Pavsv-D	nucleotide sequence of SVIAK-type clone with a stop codon at amino acid position 14
180	Pavsv-D.pep	translated amino acid sequence of SVIAK CFM
181	Aapat-1	amino acid sequence of coral protein disclosed in WO00/46233
182	Aapat-2	amino acid sequence of coral protein disclosed in WO00/46233
183	dT(17)Ad2Ad1	oligonucleotide
184	vispro-F1	oligonucleotide
185	vispro-R1	oligonucleotide
186	pQEprom	oligonucleotide
187	pQErev	oligonucleotide
188	Coral-R1	oligonucleotide

SEQ ID NO.	NAME	DESCRIPTION
189	A8 (pCGP2918)	nucleotide sequence of full-length cDNA clone
190	A8.aa	translated amino acid sequence of full-length cDNA clone
191	D10 (pCGP2920)	nucleotide sequence of full-length cDNA clone
192	D10.aa	translated amino acid sequence of full-length cDNA clone
193	S3 (pCGP2924)	nucleotide sequence of full-length cDNA clone
194	S3.aa	translated amino acid sequence of full-length cDNA clone
195	T3 (pCGP2922)	nucleotide sequence of full-length cDNA clone
196	T3.aa	translated amino acid sequence of full-length cDNA clone
197	D1 (pCGP2919)	nucleotide sequence of full-length cDNA clone
198	D1.aa	translated amino acid sequence of full-length cDNA clone
199	S1 (pCGP2923)	nucleotide sequence of full-length cDNA clone
200	S1.aa	translated amino acid sequence of full-length cDNA clone
201	T1 (pCGP2921)	nucleotide sequence of full-length cDNA clone
202	T1.aa	translated amino acid sequence of full-length cDNA clone
203	Kpn.6His.F	oligonucleotide
204	T1/A8.Sal.R	oligonucleotide
205	TSSU-Fnew	oligonucleotide
206	TSSU-R	oligonucleotide
207	AscI-ER.F	oligonucleotide
208	ER-BamHI.R	oligonucleotide
209	CP-HDEL-PacI.R	oligonucleotide
210	Pst-mGFP4F	oligonucleotide
211	mGFP4-PacIR	oligonucleotide
212	visproF1-new	oligonucleotide
213	MSV-RBS	oligonucleotide
214	SVIAK-RBS	oligonucleotide
215	POC 220 H6	oligonucleotide
216	Rtms-5v	mutated variant amino acid sequence from Rtms-5 (SEQ ID NO:166)
217	gtCP	translated amino acid sequence of SVIAK CFM
218	poc4	translated amino acid sequence of SVIAK CFM
219	baspoc3	translated amino acid sequence of SVIAK CFM
220	dsFP593	translated amino acid sequence of a CFM
221	drFP583, also known as dsRed583	translated amino acid sequence of a CFM

SEQ ID NO.	NAME	DESCRIPTION
222	gfp	translated amino acid sequence of a CFM
223	MGFP-4	nucleotide sequence from GFP-4 from *Aequorea victoria* (jelly fish), mutated for plants
224	MGFP-4.pep	translated amino acid sequence of GFP-4 CFM
225	BASPOC4	translated amino acid sequence of a CFM
226	AsFP595	translated amino acid sequence of a CFM
227	TICS-His-FWD	oligonucleotide
228	TICS-His-REV	oligonucleotide
229	mGFP4-HDEL-PacR	oligonucleotide
230	T1.N-QN(AAT)SQ(CAG)	oligonucleotide
231	T1.S-IS(TCC)>I(ATC)	oligonucleotide
232	YGFP3UP	oligonucleotide
233	YGFP3DO	oligonucleotide
234	RFPUP1	oligonucleotide
235	RFPDO1	oligonucleotide
236	MSVIATUP	oligonucleotide
237	COFPDO	oligonucleotide
238	ATP4PROMUP2	oligonucleotide
239	ATP4DO2	oligonucleotide
240	ATP7TUP	oligonucleotide
241	ATP7TDO	oligonucleotide
242	SPPDYTLEFP	N-terminal amino acid sequence of a CFM
243	SPPDYTLERP	N-terminal amino acid sequence of a CFM
244	(D)SS(P)E	N-terminal amino acid sequence of a CFM
245	SYLPN	N-terminal amino acid sequence of a CFM
246	SYLQN	N-terminal amino acid sequence of a CFM
247	MEGIVNG-A	oligonucleotide
248	MEGIVNG-T	oligonucleotide
249	MEGIVNG-C	oligonucleotide
250	REV-MEG-T	oligonucleotide
251	REV-MEG-C	oligonucleotide

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

The present invention is predicated on the identification of peptides, polypeptides and proteins having one or more amino acid sequences or one or more amino acid sequences which exhibit color-facilitating properties, either on their own or following interaction with one or more other amino acids and nucleic acid moleclues encoding same. Such peptides, polypeptides and proteins are referred to herein as "color-facilitating molecules" or "CFMs". The present invention contemplates a range of uses of CFMs, including their use as color expression markers and as color intensifiers, as well as in gel-like formulations for use as photon traps and in light-filtering formulations such as topically-applied sun creens.

The present invention further contemplates the use of genetic material encoding CFMs to generate eukaryotic or prokaryotic cells or eukaryotic or prokaryotic cell tissue which, in the presence of the CFMs, exhibit altered visual characteristics to the human eye in the absence of excitation of the CFMs by extraneous non-white light or particle emission.

Such altered visual characteristics are also referred to as being altered to the naked, unaided eye. Reference to "naked" or "unaided" is not to imply that the eye may not require magnification aids such as in the form of spectacles or glasses or a magnifying glass. Reference to extraneous light or particle emission includes ultraviolet (UV) light, blue laser light, plasma irradiation, γ-irradiation, particle irradiation, single wavelength light such as 340 nm, 382 nm, 396 nm, 405 nm, 475 nm, 490 nm, 575 nm or other forms of emission or particle bombardment. It does not include white light.

Accordingly, one aspect of the present invention provides an isolated nucleic acid molecule comprising a nucleotide sequence encoding a color-facilitating molecule (CFM) which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to said cell when visualized by a human eye in the absence of excitation by extraneous non-white light or particle emission.

Preferably, the nucleic acid molecule is derived from *Anemonia majano, Anemonia sulcata, Clavularia* sp, *Zoanthus* sp, *Discosoma* sp (e.g. *Discosoma striata*), *Aequorea* sp (e.g. *Aequorea victoria*), *Anthozoa* sp, *Cassiopea* sp, (e.g. *Cassiopea xamachana*), *Millepora* sp, *Acropora* sp (e.g. *Acropora aspera* and *Acropora nobilis)*, *Montipora* sp, *Porites murrayensis*, *Pocillopora damicormis*, *Pavona descussaca*, *Acanthastrea* sp, *Platygyra* sp or *Caulastrea* sp.

In a preferred embodiment, the nucleic acid molecule encodes a CFM with an amino acid at its N-terminal region selected from SVIAK (SEQ ID NO:5), (M)SVIAT (SEQ ID NO:6), SGIAT (SEQ ID NO:7), SVIVT (SEQ ID NO:8) or SVSAT (SEQ ID NO:9). Even more particularly, the CFM comprises an amino acid sequence selected from SVIAT QMTY KVYM SGT (SEQ ID NO:10), SVIAT QMTY KVYM PGT (SEQ ID NO:11), SVIAT QVTY KVYM SGT (SEQ ID NO:12), SGIAT QMTY KVYM SGT (SEQ ID NO:13), SVIVT QMTY KVYM SGT (SEQ ID NO:14), SVSAT QMTY KVYM SGT (SEQ ID NO:15), SVIAK QMTY KVNM SGT (SEQ ID NO:16), SVIAK QMTY KVYM SDT (SEQ ID NO:17) and SVIAK QMTY $X_1X_2YX_3$ SGT (SEQ ID NO:18) wherein X_1, X_2 and X_3 may be any amino acid provided that X_1 is not K; X_2 is not V; X_3 is not M.

In a particular embodiment, the present invention provides an isolated nucleic acid molecule comprising a nucleotide sequence encoding a CFM or a fragment, variant or derivative thereof, wherein said isolated nucleic acid molecule comprises a nucleotide sequence selected from the group consisting of SEQ ID NOs:19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 189, 191, 193, 195, 197, 199 and 201, or a biologically active fragment or derivative of these.

Particular preferred nucleic acid molecules comprise the nucleotide sequences set forth in SEQ ID NOs:189, 191, 193, 195, 197, 199 and 201.

The nucleic acid molecule is regarded as genetic material and generally comprises a coding region encoding a CFM optionally operably linked to a single or multiple promoters. In one embodiment, the nucleic acid molecule is a genetic construct under the control of (i.e. operably linked to) a single promoter. In another embodiment, the genetic construct is a bicistronic, tricistronic or multicistronic construct carrying the gene encoding the CFM and optionally other genes such as encoding a reporter molecule.

As used herein, the terms "nucleic acid molecule" including "genetic material" refers to any single-stranded or double-stranded nucleic acid molecule which at least comprises deoxyribonucleotides and/or ribonucleotides, including DNA (cDNA or genomic DNA), RNA, mRNA, or tRNA, amongst others. The combination of such molecules with non-nucleotide substituents derived from synthetic means or naturally-occurring sources is also contemplated by the present invention. Genetic material may also include sequences optimized for expression of codons in a particular host cell.

The present invention extends to derivatives of the nucleic acid molecules and such derivatives includes any isolated nucleic acid molecule which comprises at least 10 and preferably at least 20 contiguous nucleotides derived from the genetic sequence as described herein according to any embodiment. A derivative includes a part, fragment, portion or analog. A derivative also includes a fusion molecule between two or more genetic sequences encoding CFMs.

The present invention also comprises analogs of the nucleic acid molecules. An "analog" means any isolated nucleic acid molecule which is substantially the same as a nucleic acid molecule of the present invention or its complementary nucleotide sequence as described herein according to any embodiment, notwithstanding the occurrence of any non-nucleotide constituents not normally present in said isolated nucleic acid molecule, for example carbohydrates, radiochemicals including radionucleotides, reporter molecules such as, but not limited to, alkaline phosphatase or horseradish peroxidase, amongst others. A "homolog" is a functionally similar molecule from a different species or strain.

Generally, analogs or derivatives of the nucleic acid molecule of the invention are produced by synthetic means or alternatively, derived from naturally-occurring sources. For example, the nucleotide sequence of the present invention may be subjected to mutagenesis to produce single or multiple nucleotide substitutions, deletions and/or insertions. A derivative encompasses a nucleotide sequence modified for optimized or enhanced codon usage in a particular cell.

The genetic sequence of the present invention may comprise a sequence of nucleotides or be complementary to a sequence of nucleotides which comprise one or more of the following: a promoter sequence, a 5' non-coding region, a *cis*-regulatory region such as a functional binding site for transcriptional regulatory protein or translational regulatory protein, an upstream activator sequence, an enhancer element, a silencer element, a TATA box motif, a CCAAT box motif, or an upstream open reading frame, transcriptional start site, translational start site, and/or nucleotide sequence which encodes a leader sequence. The genetic sequence also encodes the CFM.

The term "5' non-coding region" is used herein in its broadest context to include all nucleotide sequences which are derived from the upstream region of an expressible gene, other than those sequences which encode amino acid residues which comprise the polypeptide product of said gene, wherein 5' non-coding region confers or activates or otherwise facilitates, at least in part, expression of the gene.

The nucleic acid molecule may also be regarded as a gene. The term "gene" is used in its broadest context to include both a genomic DNA region corresponding to the gene as well as a cDNA sequence corresponding to exons or a recombinant molecule engineered to encode a functional form of a product. The term "gene" is used in its broadest sense and includes cDNA corresponding to the exons of a gene. Accordingly, reference herein to a "gene" is to be taken to include:-

(i) a classical genomic gene consisting of transcriptional and/or translational regulatory sequences and/or a coding region and/or non-translated sequences (i.e. introns, 5'- and 3'- untranslated sequences); or

(ii) mRNA or cDNA corresponding to the coding regions (i.e. exons) and 5'- and 3'- untranslated sequences of the gene.

The term "gene" is also used to describe synthetic or fusion molecules encoding all or part of a functional product.

As used herein, the term "*cis*-acting sequence" or "*cis*-regulatory region" or similar term shall be taken to mean any sequence of nucleotides which is derived from an expressible genetic sequence wherein the expression of the first genetic sequence is regulated, at least in part, by said sequence of nucleotides. Those skilled in the art will be aware that a *cis*-regulatory region may be capable of activating, silencing, enhancing, repressing or otherwise altering the level of expression and/or cell-type-specificity and/or developmental specificity of any structural gene sequence.

Reference herein to a "promoter" is to be taken in its broadest context and includes the transcriptional regulatory sequences of a classical genomic gene, including the TATA box which is required for accurate transcription initiation, with or without a CCAAT box sequence and additional regulatory elements (i.e. upstream activating sequences, enhancers and silencers) which alter gene expression in response to developmental and/or environmental stimuli, or in a tissue-specific or cell-type-specific manner. A promoter is usually, but not necessarily, positioned upstream or 5', of a structural gene, the expression of which it regulates. Furthermore, the regulatory elements comprising a promoter are usually positioned within 2 kb of the start site of transcription of the gene.

In the present context, the term "promoter" is also used to describe a synthetic or fusion molecule, or derivative which confers, activates or enhances expression of a structural gene or other nucleic acid molecule, in a plant cell. Preferred promoters according to the

subject invention may contain additional copies of one or more specific regulatory elements to further enhance expression in a cell, and/or to alter the timing of expression of a structural gene to which it is operably connected.

In a preferred embodiment, the nucleic acid molecules are expressed in a cell. The cell may be a eukaryotic or prokaryotic cell. Reference to a eukaryotic cell includes a mammalian animal cell, a non-mammalian animal cell or a plant cell. Insofar as the eukaryotic cell is a plant cell, the plant cell may be part of a plant callus or a whole plant. Reference to a "plant" includes ornamental or flowering plants or parts thereof such as flowers, roots, leaves, stems, seeds, fruit or fibers. Particularly preferred plant cells are those selected from rose, carnation, lisianthus, petunia, lily, tulip, pansy, gerbera or chrysanthemum.

The CFM is preferably a GFP or a derivative or homolog thereof such as a non-fluorescent GFP homolog.

Another aspect of the present invention provides an isolated color-facilitating molecule (CFM) comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to said cell when visualized by a human eye in the absence of excitation by extraneous non-white light or particle emission.

The CFM of the present invention is preferably a protein comprising a sequence of amino acids such that upon folding, the sequence alone or following interaction with one or more other amino acids which may be within the same molecule or in another molecule such as in a dimer, trimer or oligomer exhibits chromophore or fluorophore properties. Particularly useful proteins comprise the contiguous amino acid sequence Gln-Tyr-Gly (QYG). Even more preferably, the protein is a GFP or a homolog or derivative thereof. An example of a homolog of a GFP is a non-fluorescent GFP homolog. An example of a derivative of a GFP or non-fluorescent GFP homolog is a GFP modified to cause a shift in the ratio of excitation or emission peaks. Such modifications may result in a more intense fluorescence or may exhibit altered or weaker fluorescence.

Any number of GFP or non-fluorescent GFP homologs or other derivatives may be employed as CFMs in accordance with the present invention. Examples of such molecules are from *Anemonia majano*, *Anemonia sulcata*, *Clavularia* sp, *Zoanthus* sp, *Discosoma* sp (e.g. *Discosoma striata*), *Aequorea* sp (e.g. *Aequorea victoria*), *Anthozoa* sp, *Cassiopea* sp, (e.g. *Cassiopea xamachana*), *Millepora* sp, *Acropora* sp (e.g. *Acropora aspera* and *Acropora nobilis)*, *Montipora* sp, *Porites murrayensis*, *Pocillopora damicormis*, *Pavona descussaca*, *Acanthastrea* sp, *Platygyra* sp and *Caulastrea* sp.

Particularly preferred protein sequences which constitute CFMs of the present invention comprise one of the following sequences of amino acids towards the amino-terminal end of the polypeptide: "SVIAK" (SEQ ID NO:5), "(M)SVIAT" (SEQ ID NO:6), "SGIAT" (SEQ ID NO:7), "SVIVT" (SEQ ID NO:8), or "SVSAT" (SEQ ID NO:9).

Examples of such preferred protein sequences may be selected from the group consisting of:

SVIAT QMTY KVYM SGT (SEQ ID NO:10);
SVIAT QMTY KVYM PGT (SEQ ID NO:11);
SVIAT QVTY KVYM SGT (SEQ ID NO:12);
SGIAT QMTY KVYM SGT (SEQ ID NO:13);
SVIVT QMTY KVYM SGT (SEQ ID NO:14);
SVSAT QMTY KVYM SGT (SEQ ID NO:15);
SVIAK QMTY KVNM SGT (SEQ ID NO:16);
SVIAK QMTY KVYM SDT (SEQ ID NO:17); and
SVIAK QMTY $X_1X_2YX_3$ SGT (SEQ ID NO:18),

wherein X_1, X_2 and X_3 may be any amino acid provided that X_1 is not K; X_2 is not V; X_3 is not M.

Accordingly, in another aspect of the present invention there is provided an isolated polypeptide, or a biologically active fragment thereof, or a variant or derivative of these,

said polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs:10, 11, 12, 13, 14, 15, 16, 17 and 18, with the proviso that, in said isolated polypeptide or biologically active fragment or variant or derivative of SEQ ID NO:18, X_1 is not lysine, X_2 is not valine, and X_3 is not methionine.

Particularly suitable molecules comprise an amino acid sequence selected from the group consisting of SEQ ID NOs:20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 190, 192, 194, 196, 198, 200 and 202.

Accordingly, a preferred embodiment of the present invention provides an isolated polypeptide, or a biologically active fragment thereof, or a variant or derivative of these, said polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs:20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 190, 192, 194, 196, 198, 200 and 202 provided that, where the said biologically active fragment or variant or derivative comprises the sequence SVIAK QMTY $X_1X_2YX_3$ SGT, X_1 is not lysine, X_2 is not valine, and X_3 is not methionine.

Such isolated polypeptides, when present in a prokaryotic or eukaryotic cell or group of prokaryotic or eukaryotic cells such as in plant cells in the form of plant tissue or plant callus, may alone or in combination with one or more other molecules impart an altered visual characteristic to said cell or group of cells when visualized by a human eye in the absence of excitation by extraneous non-white light or particle emission.

Accordingly, another aspect of the present invention provides a prokaryotic or eukaryotic cell or group of prokaryotic or eukaryotic cells in the form of tissue wherein said cell or

group of cells or their parent cells are genetically modified to enable the production of a color-facilitating molecule (CFM) which alone or together with one or more other molecules imparts an altered visual characteristic to said cell or group of cells when visualized by a human eye in the absence of excitation by extraneous non-white light or particle emission.

The CFM is as herein defined and in a preferred embodiment includes polypeptides having amino acid sequence selected from the list comprising SEQ ID NOs:20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 190, 192, 194, 196, 198, 200 and 202 provided that, where the said amino acid sequence comprises the sequence SVIAK QMTY $X_1X_2YX_3$ SGT, X_1 is not lysine, X_2 is not valine, and X_3 is not methionine.

A "eukaryotic" cell is regarded as any cell which is not characterized as being a "prokaryotic" cell. Particularly useful eukaryotic cells are plant cells as well as fungi and yeast. Other eukaryotic cells, however, are also contemplated such as mammalian cells, non-mammalian animal cells including insect cells as well as plant cells. A "plant" may be regarded as a monocotyledonous or dicotyledonous plant and includes ornamental and crop plants. Reference to "tissue" includes plant callus. A "prokaryotic cell" is generally a cell comprising a nucleus not surrounded by a nuclear membrane and includes bacteria and microbial cells. Such prokaryotic cells include *Pseudomonas* sp., *E. coli*, *Enterobacter* sp., *Salmonella* sp., *Klebsiella* sp., *Acetobacter* sp., *Staphylocous* sp., *Streptococcus* sp. or *Bacillus* sp., amongst many others.

In a preferred embodiment, the present invention provides a plant cell or group of plant cells such as in the form of plant tissue or plant callus wherein said plant cells or group of plant cells or their parent cells are genetically modified to enable production of a CFM which alone or in combination with one or more other molecules imparts an altered visual

characteristic to said cell or group of cells when visualized by a human eye in the absence of excitation by extraneous non-white light or particle emission.

Particularly preferred plants are ornamental and flowering plants. Particularly useful plants contemplated by the present invention include but are not limited to rose, carnation, lisianthus, petunia, lily, tulip, pansy, gerbera and chrysanthemum.

Reference herein to a "plant" includes parts of plants. Similarly, reference herein to "plant tissue" includes parts of plants. Examples of such plant parts, include but are not limited to, flowers, roots, leaves, stems, seeds, fruit and fibres. The term "flowers" includes parts of flowers such as petals, petioles, flower heads and flower buds. Plant tissue may also include callus material as well as embryogenic or non-embryogenic material. The term "fibre" includes cotton and hemp fibres.

Accordingly, another aspect of the present invention is directed to a plant or part of a plant including a flower, root, leaf, stem, seed, fruit or fibre or reproductive portion of said plant or cells of said plant wherein said plant or plant part comprises cells genetically modified to enable production of a CFM which alone or in combination with one or other molecules imparts an altered visual characteristic to said cells when visualized by a human eye in the absence of excitation by extraneous non-white light or particle emission.

The term "genetically modified" is used in its broadest sense and includes introducing gene(s) into cells, mutating gene(s) in cells and altering or modulating the regulation of gene(s) in cells.

A "part" of a plant includes flowers (e.g. cut or severed flowers), petals, stems, leaves and fibrous material such as cotton and vegetative, propagative and reproductive material such as cuttings, pollen, seeds and callus.

The altered visual characteristic may be exhibited by all cells in the plant or in selected tissue or plant parts such as flowers, roots, leaves, stems, seeds, fruit or fibres. The

production of the CFM may, therefore, be tissue specific or tissue preferential. Furthermore, CFM production may be developmentally dependent, determined, influenced or otherwise regulated.

The CFM may be produced in the whole plant with the use of a constitutive promoter such as cauliflower mosaic virus (CaMV) 35S promoter, operably connected or operably linked to a gene or other nucleic acid molecule encoding the CFM. Alternatively, the molecule may be confined to, for example, petal tissue, epidermal cell layers of petals or to different organelles within cells. For example, a floral specific promoter such as a chalcone synthase promoter substantially limits a colored protein expression to flower petals.

The use of some gene promoters (e.g. 35S) may produce CFM accumulation in the cytoplasm of transformed cells and confer a visible color to the plant tissue. The CFM may be targeted to different organelles within the plant cell to confer a color change in the tissue visible to the naked unaided eye under white light illumination. The CFM can be targeted to plastids using a chloroplast transit peptide fused in-frame with the colored protein cDNA sequence. An example of a plastid transit peptide that can be used is the transit peptide of the small subunit of ribulose-1, 5-bisphosphate-carboxylase (e.g. InCheol *et al., Molecular Breeding 5:* 453-461, 1999). The targeting of a CFM to plastids can dramatically increase the total amount of protein accumulated (InCheol *et al.*, 1999, *supra*) and thereby increase color intensity.

Chromoplasts are numerous in the petals of some flowers, leaves and fruit. A chromoplast specific transit peptide fused in-frame with the protein cDNA sequence may be used to modify flower or other tissue color with a much reduced potential for interfering with total plant photosynthetic activity, as may occur if an constitutive promoter and a chloroplast transit peptide were used to target the CFM. The use of a chromoplast transit peptide and a floral specific promoter may be optimal for the modification of flower color.

It may be beneficial to target all CFMs to the vacuole or endoplasmic reticulum to avoid any detrimental effects to the transformed cells or plants. An example of an endoplasmic

reticulum targeting peptide sequence that can be used is the amino acid sequence HDEL (Haseloff *et al.*, 1997, *supra*). The CFM may also be targeted to the cell wall.

The term "operably connected" or "operably linked" in the present context means placing a structural gene (e.g. a nucleic acid molecule encoding a CFM) under the regulatory control of a promoter which then controls expression of the gene. Promoters and the like are generally positioned 5' (upstream) to the genes which they control. In the construction of heterologous promoter/structural gene combinations, it is generally preferred to position the genetic sequence or promoter at a distance from the gene transcription start site that is approximately the same as the distance between that genetic sequence or promoter and the gene it controls in its natural setting, i.e., the gene from which the genetic sequence or promoter is derived. As is known in the art, some variation in this distance can be accommodated without loss of function. Similarly, the preferred positioning of a regulatory sequence element with respect to a heterologous gene to be placed under its control is defined by the positioning of the element in its natural setting, i.e., the genes from which it is derived.

The cells genetically modified to enable production of a CFM may be the cells into which genetic material has been introduced or they may represent progeny of genetically modified parent cells.

Accordingly, the present invention contemplates a method for generating a transgenic plant or part of a plant, wherein said plant or plant part comprises cells genetically modified to enable production of a CFM which alone or in combination with one or other molecules imparts an altered visual characteristic to said cells when visualized by a human eye in the absence of excitation by extraneous non-white light or particle emission, said method comprising introducing into said cells an isolated nucleic acid molecule encoding said CFM.

Preferably, the CFM is derived from *Anemonia majano*, *Anemonia sulcata*, *Clavularia* sp, *Zoanthus* sp, *Discosoma* sp (e.g. *Discosoma striata*), *Aequorea* sp (e.g. *Aequorea victoria*),

Anthozoa sp, *Cassiopea* sp, (e.g. *Cassiopea xamachana*), *Millepora* sp, *Acropora* sp (e.g. *Acropora aspera* and *Acropora nobilis*), *Montipora* sp, *Porites murrayensis*, *Pocillopora damicormis*, *Pavona descussaca*, *Acanthastrea* sp, *Platygyra* sp or *Caulastrea* sp.

More preferably, the CFM comprises an amino acid sequence in its N-terminal end selected from SVIAK (SEQ ID NO:5), (M)SVIAT (SEQ ID NO:6), SGIAT (SEQ ID NO:7), SVIVT (SEQ ID NO:8) or SVSAT (SEQ ID NO:9).

Even more preferably, the CFM comprises an amino acid sequence selected from the list comprising SVIAT QMTY KVYM SGT (SEQ ID NO:10), SVIAT QMTY KVYM PGT (SEQ ID NO:11), SVIAT QVTY KVYM SGT (SEQ ID NO:12), SGIAT QMTY KVYM SGT (SEQ ID NO:13), SVIVT QMTY KVYM SGT (SEQ ID NO:14), SVSAT QMTY KVYM SGT (SEQ ID NO:15), SVIAK QMTY KVNM SGT (SEQ ID NO:16), SVIAK QMTY KVYM SDT (SEQ ID NO:17) and SVIAK QMTY $X_1X_2YX_3$ SGT (SEQ ID NO:18) wherein X_1, X_2 and X_3 may be any amino acid provided that X_1 is not K; X_2 is not V; X_3 is not M.

Most preferably, the CFM is encoded by a nucleotide sequence selected from the list comprising SEQ ID NOs:19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 189, 191, 193, 195, 197, 199 and 201.

Another aspect of the present invention provides a transgenic plant wherein said plant or a part thereof such as a flower, leaf, root, stem, seed, fruit or fibre exhibits an altered visual characteristic to a human eye in the absence of extraneous non-white light or particle emission wherein cells of said transgenic plant or of a parent plant have been genetically modified to enable production of a CFM.

As stated above, the present invention extends to genetically modified mammalian cells, non-mammalian animal cells as well as plant cells.

Farmers use conventional breeding techniques to develop new colors in animals and animal products for the market, for example, colored wools and leathers or hides. Presently the main way of coloring these products toobtain novel colors is by using dyes or tints or paints or pigments on natural colored products. However, the use of the CFMs of the present invention can be employed to produce a transgenic animal which exhibits a novel color: for example, sheep with blue or red colored fleece, cows with red colored hide.

Specifically the CFM can be used in a range of agriculturally important animals such as but not limited to sheep, pigs, cattle, horses, goats, llamas, fish, ostriches, emus, ducks and chickens. Accordingly, another aspect of the present invention provides a transgenic mammalian or non-mammalian animal cell or transgenic non-human mammal or non-mammalian animal comprising said cells, said cells exhibiting an altered visual characteristic to a human eye in the absence of extraneous non-white light or particle emission wherein cells of said transgenic plant, mammal or animal or plant cells thereof have been genetically modified to enable production of a CFM.

The CFM is as herein defined. Production of the CFM may be constitutive or developmental or may be inducible in response to internal or external stimulus including stress.

Reference herein to a "color-facilitating molecule", "CFM", "protein", "GFP" or "non-fluorescent GFP-homolog" includes fragments, derivatives, variants and homologs thereto. Examples of derivatives include mutants, parts, fragments and portions of these molecules including single or multiple amino acid substitutions, deletions and/or additions to the molecules. Derivatives also include fusion molecules between two or more CFMs or between a CFM and another molecule such as a leader sequence, targeting sequence, expression-facilitating sequence and/or a reporter molecule capable of providing an identifiable signal.

As stated above a derivative also includes a modified form providing altered ratios of excitation or emission spectra. In addition, or as a consequence of the altered ratios of excitation or emission, the modified GFP or their homologs may have a more intense color-producing capacity relative to an unmodified molecule.

Furthermore, other proteins may be used in conjunction with the CFMs to alter the visual characteristics of the cells. Examples of other proteins include copper containing proteins containing one or more type 1 (CuII) motifs as found in the Fet3 protein from *Saccharomyces cerevisiae* (Hassett *et al.*, *Journal of Biological Chemistry 273:* 23274 - 23282, 1998) and other multinuclear copper ferroxidase enzymes such as laccase, ceruloplasmin and ascorbate oxidase (Messerschmidt and Huber, *Eur. J. Biochem. 187:* 341 - 352, 1990). Similarly, the mononuclear blue or type 1 copper proteins (cupredoxins), such as plastocyanin, azurin, pseudoazurin, plantacyanin, rusticyanin, amicyanin, auracyanin and halocyanin (Nersissian *et al.*, *Protein Sci.ence 5:* 2184 - 2192, 1996). These proteins have not been associated with pigmentation in nature. However, when these proteins are concentrated an intense blue color is evident (Hassett *et al.*, 1998, *supra*; Messerschmidt and Huber, 1990, *supra*). The over-expression of a type 1 (CuII) containing protein in flowers and other plant tissues under conditions that allow correct folding and acquisition of Cu ions can modify or impart a color visible to the naked unaided eye under white light. Reference to "in conjunction" includes reference to a fusion protein between a CFM and another protein such as a cuproprotein and well as the expression of nucleotide sequences in multicistronic form encoding a CFM and at least one other protein.

Another aspect of the present invention provides a eukaryotic or prokaryotic cell or a group of eukaryotic or prokaryotic cells in the form of a tissue wherein said cell or group of cells or their parent cells are genetically modified to produce a GFP or derivative or homolog thereof such as a non-fluorescent GFP homolog which imparts an altered visual characteristic on said cell or group of cells when visualized by a human eye in the absence of excitation by extraneous non-white light or particle emission.

Preferably, the eukaryotic cells are plant cells or plant tissue. The eukaryotic cells may, however, be mammalian cells or non-mammalian animal cells. Reference to "plant tissue" includes "callus".

Accordingly, another aspect of the present invention is directed to a plant or part of a plant including a flower, root, leaf, stem, seed, fruit or fibre or reproductive portion of said plant or cells of said plant wherein said plant or plant part comprises cells genetically modified to enable production of a GFP or a derivative or homolog thereof such as a non-fluorescent GFP homolog which imparts an altered visual characteristic to said cells when visualized by a human eye in the absence of excitation by extraneous non-white light or particle emission.

A particularly preferred embodiment the present invention is directed to a plant or part of a plant including a flower, root, leaf, stem, seed, fruit or fibre or reproductive portion of said plant or cells of said plant wherein said plant or plant part comprises cells genetically modified to comprise a polynucleotide comprising the nucleotide sequence set forth in any one of SEQ ID NOs:19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 189, 191, 193, 195, 197, 199 or 201, or a derivative or homolog of any of these, thereby enabling production of a CFM which alone or in combination with one or more other molecules imparts an altered visual characteristic to said cell or group of cells when visualized by a human eye in the absence of excitation by extraneous non-white light or particle emission.

The present invention particularly provides, in a preferred embodiment, a genetically modified plant carrying flowers having an altered flower color relative to a non-genetically modified plant as well as cut flowers from such a plant. Reference herein to a "genetically modified plant" includes progeny of a genetically modified plant as well as hybrids and derivatives of a genetically modified plant.

The altered coloration of eukaryotic cells such as plant cells is useful not only for the ornamental plant market but also as propriety tags, for example, of seeds, root stock, flowers, crops and whole plants and plant parts. This may be particularly important for distinguishing between transgenic and non-transgenic crops, plants and other horticultural products. Furthermore, the modification of visible color in cotton fibre or hemp is a useful means of reducing the toxicity of dye processes in color fabric manufacture. The modification of visible color in edible and/or ornamental fungal species may also be used to differentiate and enhance marketability.

The modification of visible color in fruit and vegetables may be used to differentiate and enhance their marketability. A suitable gene promoter may be used to control the expression of the CFM to signal optimal time to, for example, harvest crop plants including harvesting plant parts such as flowers or seeds. In addition, a stress-inducible promoter may be utilized to promote an early warning of water or pathogen stress, allowing for early intervention by the grower and subsequent reduction in economic loss.

Other uses for the CFM of the present invention include, for example, the production of novel colored plant extracts wherein the extract includes, for example, a flavouring or food additive or health product or beverage or juice or coloring. Beverages may include but are not limited to wines, spirits, beers, teas, coffee, milk and dairy products.

The CFM may be used to alter the color of many products such as but not limited to foods (e.g. breads and yeast products, confectionery), beverages (see above) or novelty items (e.g. toys).

A further aspect of the present invention provides a transfected or transformed cell, tissue, organ or non-cellular material which contains or is capable of producing a CFM or a functional derivative or homolog thereof. Preferably, the CFM is a protein such as GFP or a non-fluorescent GFP-homolog.

The genetic construct(s) of the present invention may be introduced into a cell by various techniques known to those skilled in the art. The technique used may vary depending on the known successful techniques for that particular organism.

Techniques for introducing recombinant DNA into cells include, but are not limited to, transformation using $CaCl_2$ and variations thereof, direct DNA uptake into protoplasts, PEG-mediated uptake to protoplasts, microparticle bombardment, electroporation, microinjection of DNA, microparticle bombardment of tissue explants or cells, vacuum-infiltration of tissue with nucleic acid, and T-DNA-mediated transfer from *Agrobacterium* to the plant tissue.

For microparticle bombardment of cells, a microparticle is propelled into a cell to produce a transformed cell. Any suitable ballistic cell transformation methodology and apparatus can be used in performing the present invention. Exemplary apparatus and procedures are disclosed by Stomp *et al.* (U.S. Patent No. 5,122,466) and Sanford and Wolf (U.S. Patent No. 4,945,050). When using ballistic transformation procedures, the genetic construct may incorporate a plasmid capable of replicating in the cell to be transformed.

Examples of microparticles suitable for use in such systems include 0.1 to 10 μm and more particularly 10.5 to 5 μm tungsten or gold spheres. The DNA construct may be deposited on the microparticle by any suitable technique, such as by precipitation.

Once introduced into cells such as plant tissue, the expression of a CFM may be assayed in a transient expression system or it may be determined after selection for stable integration within for example, the plant genome. Hence, a CFM of the present invention may be useful as an expression marker. For example, genetic material encoding a CFM of the present invention, optionally operably linked to a single or multiple promoters, may be introduced into cells as a fluorescent "tag", optionally fused with one or more other nucleic acid sequences that may encode a polypeptide or a regulatory nucleotide sequence. In this manner, a CFM fused with another polypeptide may be useful in assessing subcellular

localisation of the fusion or, alternatively, as an expression marker for assessing possible activity of the regulatory nucleotide sequence in a given host cell.

Host cells may be prokaryotic cells, for example bacterial, or eukaryotic cells, for example yeast, plant, and animal cells, including human. Preferred host cells are bacterial or plant.

Plant tissue capable of subsequent clonal propagation, whether by organogenesis or embryogenesis, may be transformed with a genetic construct of the present invention and a whole plant generated therefrom. The particular tissue chosen will vary depending on the clonal propagation systems available for, and best suited to, the particular species being transformed. Exemplary tissue targets include leaf disks, pollen, embryos, cotyledons, hypocotyls, megagametophytes, callus tissue, existing meristematic tissue (e.g. apical meristem, axillary buds, and root meristems), and induced meristem tissue (e.g. cotyledon meristem and hypocotyl meristem).

The regenerated transformed plants may be propagated by a variety of means, such as by clonal propagation or classical breeding techniques. For example, a first generation (or T1) transformed plant may be selfed to give homozygous second generation (or T2) transformant, and the T2 plants further propagated through classical breeding techniques.

Any number of GFP or non-fluorescent GFP-homologs may be employed provided that the GFP or its homolog or other CFM imparts on a cell or group of cells an altered visual characteristic to the human eye in the absence of extraneous non-white light or particle emission. Examples of CFMs contemplated herein include but are not limited to non-fluorescent GFP-homologs such as that encoded by asFP595 (Lukyanov *et al.*, 2000, *supra*) and t7SP6BASPOC3 and T7SP6BASPOC4 (Hoegh-Guldberg and Dove, 2000, *supra*) and fluorescent GFP variants and homologs such as described in Davis and Vierstra, 1996, *supra*; Haseloff *et al.*, 1997, *supra*; Lukyanoy *et al.*, 1999, *supra*; Matz *et al.*, 1999, *supra*; Fradkov *et al.*, *FEBS Letters 479:* 127-130, 2000).

Accordingly, another aspect of the present invention provides a eukaryotic or prokaryotic cell or group of eukaryotic or prokaryotic cells genetically modified to comprise:

(i) a nucleotide sequence set forth in SEQ ID NO:19 or SEQ ID NO:21 or SEQ ID NO:23 or SEQ ID NO:25 or SEQ ID NO:27 or SEQ ID NO:29 or SEQ ID NO:31 or SEQ ID NO:33 or SEQ ID NO:35 or SEQ ID NO:37 or SEQ ID NO:39 or SEQ ID NO:41 or SEQ ID NO:43 or SEQ ID NO:45 or SEQ ID NO:47 or SEQ ID NO:49 or SEQ ID NO:51 or SEQ ID NO:53 or SEQ ID NO:55 or SEQ ID NO:57 or SEQ ID NO:59 or SEQ ID NO:61 or SEQ ID NO:63 or SEQ ID NO:65 or SEQ ID NO:67 or SEQ ID NO:69 or SEQ ID NO:71 or SEQ ID NO:73 or SEQ ID NO:75 or SEQ ID NO:77 or SEQ ID NO:79 or SEQ ID NO:81 or SEQ ID NO:83 or SEQ ID NO:85 or SEQ ID NO:87 or SEQ ID NO:89 or SEQ ID NO:91 or SEQ ID NO:93 or SEQ ID NO:95 or SEQ ID NO:97 or SEQ ID NO:99 or SEQ ID NO:101 or SEQ ID NO:103 or SEQ ID NO:105 or SEQ ID NO:107 or SEQ ID NO:109 or SEQ ID NO:111 or SEQ ID NO:113 or SEQ ID NO:115 or SEQ ID NO:117 or SEQ ID NO:119 or SEQ ID NO:121 or SEQ ID NO:123 or SEQ ID NO:125 or SEQ ID NO:127 or SEQ ID NO:129 or SEQ ID NO:131 or SEQ ID NO:133 or SEQ ID NO:135 or SEQ ID NO:137 or SEQ ID NO:139 or SEQ ID NO:141 or SEQ ID NO:143 or SEQ ID NO:145 or SEQ ID NO:147 or SEQ ID NO:149 or SEQ ID NO:151 or SEQ ID NO:153 or SEQ ID NO:155 or SEQ ID NO:157 or SEQ ID NO:159 or SEQ ID NO:161 or SEQ ID NO:163 or SEQ ID NO:165 or SEQ ID NO:167 or SEQ ID NO:169 or SEQ ID NO:171 or SEQ ID NO:173 or SEQ ID NO:175 or SEQ ID NO:177 or SEQ ID NO:179 or SEQ ID NO:189 or SEQ ID NO:191 or SEQ ID NO:193 or SEQ ID NO:195 or SEQ ID NO:197 or SEQ ID NO:199 or 201;

(ii) a nucleotide sequence having at least about 60% similarity after optimal alignment to SEQ ID NO:19 or SEQ ID NO:21 or SEQ ID NO:23 or SEQ ID NO:25 or SEQ ID NO:27 or SEQ ID NO:29 or SEQ ID NO:31 or SEQ ID NO:33 or SEQ ID NO:35 or SEQ ID NO:37 or SEQ ID NO:39 or SEQ ID NO:41 or SEQ ID NO:43 or SEQ ID NO:45 or SEQ ID NO:47 or SEQ ID NO:49 or SEQ ID NO:51 or SEQ

ID NO:53 or SEQ ID NO:55 or SEQ ID NO:57 or SEQ ID NO:59 or SEQ ID NO:61 or SEQ ID NO:63 or SEQ ID NO:65 or SEQ ID NO:67 or SEQ ID NO:69 or SEQ ID NO:71 or SEQ ID NO:73 or SEQ ID NO:75 or SEQ ID NO:77 or SEQ ID NO:79 or SEQ ID NO:81 or SEQ ID NO:83 or SEQ ID NO:85 or SEQ ID NO:87 or SEQ ID NO:89 or SEQ ID NO:91 or SEQ ID NO:93 or SEQ ID NO:95 or SEQ ID NO:97 or SEQ ID NO:99 or SEQ ID NO:101 or SEQ ID NO:103 or SEQ ID NO:105 or SEQ ID NO:107 or SEQ ID NO:109 or SEQ ID NO:111 or SEQ ID NO:113 or SEQ ID NO:115 or SEQ ID NO:117 or SEQ ID NO:119 or SEQ ID NO:121 or SEQ ID NO:123 or SEQ ID NO:125 or SEQ ID NO:127 or SEQ ID NO:129 or SEQ ID NO:131 or SEQ ID NO:133 or SEQ ID NO:135 or SEQ ID NO:137 or SEQ ID NO:139 or SEQ ID NO:141 or SEQ ID NO:143 or SEQ ID NO:145 or SEQ ID NO:147 or SEQ ID NO:149 or SEQ ID NO:151 or SEQ ID NO:153 or SEQ ID NO:155 or SEQ ID NO:157 or SEQ ID NO:159 or SEQ ID NO:161 or SEQ ID NO:163 or SEQ ID NO:165 or SEQ ID NO:167 or SEQ ID NO:169 or SEQ ID NO:171 or SEQ ID NO:173 or SEQ ID NO:175 or SEQ ID NO:177 or SEQ ID NO:179 or SEQ ID NO:189 or SEQ ID NO:191 or SEQ ID NO:193 or SEQ ID NO:195 or SEQ ID NO:197 or SEQ ID NO:199 or 201;

(iii) a nucleotide sequence capable of hybridizing under low stringency conditions to SEQ ID NO:19 or SEQ ID NO:21 or SEQ ID NO:23 or SEQ ID NO:25 or SEQ ID NO:27 or SEQ ID NO:29 or SEQ ID NO:31 or SEQ ID NO:33 or SEQ ID NO:35 or SEQ ID NO:37 or SEQ ID NO:39 or SEQ ID NO:41 or SEQ ID NO:43 or SEQ ID NO:45 or SEQ ID NO:47 or SEQ ID NO:49 or SEQ ID NO:51 or SEQ ID NO:53 or SEQ ID NO:55 or SEQ ID NO:57 or SEQ ID NO:59 or SEQ ID NO:61 or SEQ ID NO:63 or SEQ ID NO:65 or SEQ ID NO:67 or SEQ ID NO:69 or SEQ ID NO:71 or SEQ ID NO:73 or SEQ ID NO:75 or SEQ ID NO:77 or SEQ ID NO:79 or SEQ ID NO:81 or SEQ ID NO:83 or SEQ ID NO:85 or SEQ ID NO:87 or SEQ ID NO:89 or SEQ ID NO:91 or SEQ ID NO:93 or SEQ ID NO:95 or SEQ ID NO:97 or SEQ ID NO:99 or SEQ ID NO:101 or SEQ ID NO:103 or SEQ ID NO:105 or SEQ ID NO:107 or SEQ ID NO:109 or SEQ ID NO:111 or SEQ ID

NO:113 or SEQ ID NO:115 or SEQ ID NO:117 or SEQ ID NO:119 or SEQ ID NO:121 or SEQ ID NO:123 or SEQ ID NO:125 or SEQ ID NO:127 or SEQ ID NO:129 or SEQ ID NO:131 or SEQ ID NO:133 or SEQ ID NO:135 or SEQ ID NO:137 or SEQ ID NO:139 or SEQ ID NO:141 or SEQ ID NO:143 or SEQ ID NO:145 or SEQ ID NO:147 or SEQ ID NO:149 or SEQ ID NO:151 or SEQ ID NO:153 or SEQ ID NO:155 or SEQ ID NO:157 or SEQ ID NO:159 or SEQ ID NO:161 or SEQ ID NO:163 or SEQ ID NO:165 or SEQ ID NO:167 or SEQ ID NO:169 or SEQ ID NO:171 or SEQ ID NO:173 or SEQ ID NO:175 or SEQ ID NO:177 or SEQ ID NO:179 or SEQ ID NO:189 or SEQ ID NO:191 or SEQ ID NO:193 or SEQ ID NO:195 or SEQ ID NO:197 or SEQ ID NO:199 or 201;

(iv) a nucleotide sequence capable of encoding the amino acid sequence set forth in SEQ ID NO:19 or SEQ ID NO:21 or SEQ ID NO:23 or SEQ ID NO:25 or SEQ ID NO:27 or SEQ ID NO:29 or SEQ ID NO:31 or SEQ ID NO:33 or SEQ ID NO:35 or SEQ ID NO:37 or SEQ ID NO:39 or SEQ ID NO:41 or SEQ ID NO:43 or SEQ ID NO:45 or SEQ ID NO:47 or SEQ ID NO:49 or SEQ ID NO:51 or SEQ ID NO:53 or SEQ ID NO:55 or SEQ ID NO:57 or SEQ ID NO:59 or SEQ ID NO:61 or SEQ ID NO:63 or SEQ ID NO:65 or SEQ ID NO:67 or SEQ ID NO:69 or SEQ ID NO:71 or SEQ ID NO:73 or SEQ ID NO:75 or SEQ ID NO:77 or SEQ ID NO:79 or SEQ ID NO:81 or SEQ ID NO:83 or SEQ ID NO:85 or SEQ ID NO:87 or SEQ ID NO:89 or SEQ ID NO:91 or SEQ ID NO:93 or SEQ ID NO:95 or SEQ ID NO:97 or SEQ ID NO:99 or SEQ ID NO:101 or SEQ ID NO:103 or SEQ ID NO:105 or SEQ ID NO:107 or SEQ ID NO:109 or SEQ ID NO:111 or SEQ ID NO:113 or SEQ ID NO:115 or SEQ ID NO:117 or SEQ ID NO:119 or SEQ ID NO:121 or SEQ ID NO:123 or SEQ ID NO:125 or SEQ ID NO:127 or SEQ ID NO:129 or SEQ ID NO:131 or SEQ ID NO:133 or SEQ ID NO:135 or SEQ ID NO:137 or SEQ ID NO:139 or SEQ ID NO:141 or SEQ ID NO:143 or SEQ ID NO:145 or SEQ ID NO:147 or SEQ ID NO:149 or SEQ ID NO:151 or SEQ ID NO:153 or SEQ ID NO:155 or SEQ ID NO:157 or SEQ ID NO:159 or SEQ ID NO:161 or SEQ ID NO:163 or SEQ ID NO:165 or SEQ ID NO:167 or SEQ ID NO:169 or SEQ ID NO:171 or SEQ ID NO:173 or SEQ ID NO:175 or SEQ ID

NO:177 or SEQ ID NO:179 or SEQ ID NO:189 or SEQ ID NO:191 or SEQ ID NO:193 or SEQ ID NO:195 or SEQ ID NO:197 or SEQ ID NO:199 or 201;

(v) a nucleotide sequence capable of encoding an amino acid sequence having at least about 60% similarity after optimal alignment to SEQ ID NO:19 or SEQ ID NO:21 or SEQ ID NO:23 or SEQ ID NO:25 or SEQ ID NO:27 or SEQ ID NO:29 or SEQ ID NO:31 or SEQ ID NO:33 or SEQ ID NO:35 or SEQ ID NO:37 or SEQ ID NO:39 or SEQ ID NO:41 or SEQ ID NO:43 or SEQ ID NO:45 or SEQ ID NO:47 or SEQ ID NO:49 or SEQ ID NO:51 or SEQ ID NO:53 or SEQ ID NO:55 or SEQ ID NO:57 or SEQ ID NO:59 or SEQ ID NO:61 or SEQ ID NO:63 or SEQ ID NO:65 or SEQ ID NO:67 or SEQ ID NO:69 or SEQ ID NO:71 or SEQ ID NO:73 or SEQ ID NO:75 or SEQ ID NO:77 or SEQ ID NO:79 or SEQ ID NO:81 or SEQ ID NO:83 or SEQ ID NO:85 or SEQ ID NO:87 or SEQ ID NO:89 or SEQ ID NO:91 or SEQ ID NO:93 or SEQ ID NO:95 or SEQ ID NO:97 or SEQ ID NO:99 or SEQ ID NO:101 or SEQ ID NO:103 or SEQ ID NO:105 or SEQ ID NO:107 or SEQ ID NO:109 or SEQ ID NO:111 or SEQ ID NO:113 or SEQ ID NO:115 or SEQ ID NO:117 or SEQ ID NO:119 or SEQ ID NO:121 or SEQ ID NO:123 or SEQ ID NO:125 or SEQ ID NO:127 or SEQ ID NO:129 or SEQ ID NO:131 or SEQ ID NO:133 or SEQ ID NO:135 or SEQ ID NO:137 or SEQ ID NO:139 or SEQ ID NO:141 or SEQ ID NO:143 or SEQ ID NO:145 or SEQ ID NO:147 or SEQ ID NO:149 or SEQ ID NO:151 or SEQ ID NO:153 or SEQ ID NO:155 or SEQ ID NO:157 or SEQ ID NO:159 or SEQ ID NO:161 or SEQ ID NO:163 or SEQ ID NO:165 or SEQ ID NO:167 or SEQ ID NO:169 or SEQ ID NO:171 or SEQ ID NO:173 or SEQ ID NO:175 or SEQ ID NO:177 or SEQ ID NO:179 or SEQ ID NO:189 or SEQ ID NO:191 or SEQ ID NO:193 or SEQ ID NO:195 or SEQ ID NO:197 or SEQ ID NO:199 or 201;

(vi) a nucleotide sequence capable of hybriding under low stringency conditions to the nucleotide sequence in (iv) or (v) or its complementary form;

wherein said nucleotide sequences encode a CFM which imparts an altered visual characterization to said cell or group of cells to a human eye in the absence of extraneous non-white light or particle emission.

More particularly, the present invention provides a eukaryotic or prokaryotic cell or group of eukaryotic or prokaryotic cells genetically modified to comprise:

(i) a nucleotide sequence set forth in SEQ ID NO:189 or SEQ ID NO:191 or SEQ ID NO:193 or SEQ ID NO:195 or SEQ ID NO:197 or SEQ ID NO:199 or SEQ ID NO:201;

(ii) a nucleotide sequence having at least about 60% similarity after optimal alignment to SEQ ID NO:189 or SEQ ID NO:191 or SEQ ID NO:193 or SEQ ID NO:195 or SEQ ID NO:197 or SEQ ID NO:199 or SEQ ID NO:201;

(iii) a nucleotide sequence capable of hybridizing under low stringency conditions to SEQ ID NO:189 or SEQ ID NO:191 or SEQ ID NO:193 or SEQ ID NO:195 or SEQ ID NO:197 or SEQ ID NO:199 or SEQ ID NO:201 or its complementary form;

(iv) a nucleotide sequence capable of encoding the amino acid sequence set forth in SEQ ID NO:190 or SEQ ID NO:192 or SEQ ID NO:194 or SEQ ID NO:196 or SEQ ID NO:198 or SEQ ID NO:200 or SEQ ID NO:202;

(v) a nucleotide sequence capable of encoding an amino acid sequence having at least about 60% similarity after optimal alignment to SEQ ID NO:190 or SEQ ID NO:192 or SEQ ID NO:194 or SEQ ID NO:196 or SEQ ID NO:198 or SEQ ID NO:200 or SEQ ID NO:202;

(vi) a nucleotide sequence capable of hybridizing under low stringency conditions to the nucleotide sequence in (iv) or (v) or its complementary form;

wherein said nucleotide sequences encode a CFM which imparts an altered visual characterization to said cell or group of cells to a human eye in the absence of extraneous non-white light or particle emission.

Preferably, the eukaryotic cells are plant cells.

Accordingly, in another aspect of the present invention, there is provided a plant or cells of a plant or parts of a plant or progeny of a plant wherein said plant comprises cells comprising:

(i) a nucleotide sequence set forth in SEQ ID NO:19 or SEQ ID NO:21 or SEQ ID NO:23 or SEQ ID NO:25 or SEQ ID NO:27 or SEQ ID NO:29 or SEQ ID NO:31 or SEQ ID NO:33 or SEQ ID NO:35 or SEQ ID NO:37 or SEQ ID NO:39 or SEQ ID NO:41 or SEQ ID NO:43 or SEQ ID NO:45 or SEQ ID NO:47 or SEQ ID NO:49 or SEQ ID NO:51 or SEQ ID NO:53 or SEQ ID NO:55 or SEQ ID NO:57 or SEQ ID NO:59 or SEQ ID NO:61 or SEQ ID NO:63 or SEQ ID NO:65 or SEQ ID NO:67 or SEQ ID NO:69 or SEQ ID NO:71 or SEQ ID NO:73 or SEQ ID NO:75 or SEQ ID NO:77 or SEQ ID NO:79 or SEQ ID NO:81 or SEQ ID NO:83 or SEQ ID NO:85 or SEQ ID NO:87 or SEQ ID NO:89 or SEQ ID NO:91 or SEQ ID NO:93 or SEQ ID NO:95 or SEQ ID NO:97 or SEQ ID NO:99 or SEQ ID NO:101 or SEQ ID NO:103 or SEQ ID NO:105 or SEQ ID NO:107 or SEQ ID NO:109 or SEQ ID NO:111 or SEQ ID NO:113 or SEQ ID NO:115 or SEQ ID NO:117 or SEQ ID NO:119 or SEQ ID NO:121 or SEQ ID NO:123 or SEQ ID NO:125 or SEQ ID NO:127 or SEQ ID NO:129 or SEQ ID NO:131 or SEQ ID NO:133 or SEQ ID NO:135 or SEQ ID NO:137 or SEQ ID NO:139 or SEQ ID NO:141 or SEQ ID NO:143 or SEQ ID NO:145 or SEQ ID NO:147 or SEQ ID NO:149 or SEQ ID NO:151 or SEQ ID NO:153 or SEQ ID NO:155 or SEQ ID NO:157 or SEQ ID NO:159 or SEQ ID NO:161 or SEQ ID NO:163 or SEQ ID NO:165 or SEQ ID NO:167 or SEQ ID NO:169 or SEQ ID NO:171 or SEQ ID NO:173 or SEQ ID NO:175 or SEQ ID NO:177 or SEQ ID NO:179 or SEQ ID

NO:189 or SEQ ID NO:191 or SEQ ID NO:193 or SEQ ID NO:195 or SEQ ID NO:197 or SEQ ID NO:199 or 201;

(ii) a nucleotide sequence having at least about 60% similarity after optimal alignment to SEQ ID NO:19 or SEQ ID NO:21 or SEQ ID NO:23 or SEQ ID NO:25 or SEQ ID NO:27 or SEQ ID NO:29 or SEQ ID NO:31 or SEQ ID NO:33 or SEQ ID NO:35 or SEQ ID NO:37 or SEQ ID NO:39 or SEQ ID NO:41 or SEQ ID NO:43 or SEQ ID NO:45 or SEQ ID NO:47 or SEQ ID NO:49 or SEQ ID NO:51 or SEQ ID NO:53 or SEQ ID NO:55 or SEQ ID NO:57 or SEQ ID NO:59 or SEQ ID NO:61 or SEQ ID NO:63 or SEQ ID NO:65 or SEQ ID NO:67 or SEQ ID NO:69 or SEQ ID NO:71 or SEQ ID NO:73 or SEQ ID NO:75 or SEQ ID NO:77 or SEQ ID NO:79 or SEQ ID NO:81 or SEQ ID NO:83 or SEQ ID NO:85 or SEQ ID NO:87 or SEQ ID NO:89 or SEQ ID NO:91 or SEQ ID NO:93 or SEQ ID NO:95 or SEQ ID NO:97 or SEQ ID NO:99 or SEQ ID NO:101 or SEQ ID NO:103 or SEQ ID NO:105 or SEQ ID NO:107 or SEQ ID NO:109 or SEQ ID NO:111 or SEQ ID NO:113 or SEQ ID NO:115 or SEQ ID NO:117 or SEQ ID NO:119 or SEQ ID NO:121 or SEQ ID NO:123 or SEQ ID NO:125 or SEQ ID NO:127 or SEQ ID NO:129 or SEQ ID NO:131 or SEQ ID NO:133 or SEQ ID NO:135 or SEQ ID NO:137 or SEQ ID NO:139 or SEQ ID NO:141 or SEQ ID NO:143 or SEQ ID NO:145 or SEQ ID NO:147 or SEQ ID NO:149 or SEQ ID NO:151 or SEQ ID NO:153 or SEQ ID NO:155 or SEQ ID NO:157 or SEQ ID NO:159 or SEQ ID NO:161 or SEQ ID NO:163 or SEQ ID NO:165 or SEQ ID NO:167 or SEQ ID NO:169 or SEQ ID NO:171 or SEQ ID NO:173 or SEQ ID NO:175 or SEQ ID NO:177 or SEQ ID NO:179 or SEQ ID NO:189 or SEQ ID NO:191 or SEQ ID NO:193 or SEQ ID NO:195 or SEQ ID NO:197 or SEQ ID NO:199 or 201;

(iii) a nucleotide sequence capable of hybridizing under low stringency conditions to SEQ ID NO:19 or SEQ ID NO:21 or SEQ ID NO:23 or SEQ ID NO:25 or SEQ ID NO:27 or SEQ ID NO:29 or SEQ ID NO:31 or SEQ ID NO:33 or SEQ ID NO:35 or SEQ ID NO:37 or SEQ ID NO:39 or SEQ ID NO:41 or SEQ ID NO:43 or SEQ

ID NO:45 or SEQ ID NO:47 or SEQ ID NO:49 or SEQ ID NO:51 or SEQ ID NO:53 or SEQ ID NO:55 or SEQ ID NO:57 or SEQ ID NO:59 or SEQ ID NO:61 or SEQ ID NO:63 or SEQ ID NO:65 or SEQ ID NO:67 or SEQ ID NO:69 or SEQ ID NO:71 or SEQ ID NO:73 or SEQ ID NO:75 or SEQ ID NO:77 or SEQ ID NO:79 or SEQ ID NO:81 or SEQ ID NO:83 or SEQ ID NO:85 or SEQ ID NO:87 or SEQ ID NO:89 or SEQ ID NO:91 or SEQ ID NO:93 or SEQ ID NO:95 or SEQ ID NO:97 or SEQ ID NO:99 or SEQ ID NO:101 or SEQ ID NO:103 or SEQ ID NO:105 or SEQ ID NO:107 or SEQ ID NO:109 or SEQ ID NO:111 or SEQ ID NO:113 or SEQ ID NO:115 or SEQ ID NO:117 or SEQ ID NO:119 or SEQ ID NO:121 or SEQ ID NO:123 or SEQ ID NO:125 or SEQ ID NO:127 or SEQ ID NO:129 or SEQ ID NO:131 or SEQ ID NO:133 or SEQ ID NO:135 or SEQ ID NO:137 or SEQ ID NO:139 or SEQ ID NO:141 or SEQ ID NO:143 or SEQ ID NO:145 or SEQ ID NO:147 or SEQ ID NO:149 or SEQ ID NO:151 or SEQ ID NO:153 or SEQ ID NO:155 or SEQ ID NO:157 or SEQ ID NO:159 or SEQ ID NO:161 or SEQ ID NO:163 or SEQ ID NO:165 or SEQ ID NO:167 or SEQ ID NO:169 or SEQ ID NO:171 or SEQ ID NO:173 or SEQ ID NO:175 or SEQ ID NO:177 or SEQ ID NO:179 or SEQ ID NO:189 or SEQ ID NO:191 or SEQ ID NO:193 or SEQ ID NO:195 or SEQ ID NO:197 or SEQ ID NO:199 or 201;

(iv) a nucleotide sequence capable of encoding the amino acid sequence set forth in SEQ ID NO:19 or SEQ ID NO:21 or SEQ ID NO:23 or SEQ ID NO:25 or SEQ ID NO:27 or SEQ ID NO:29 or SEQ ID NO:31 or SEQ ID NO:33 or SEQ ID NO:35 or SEQ ID NO:37 or SEQ ID NO:39 or SEQ ID NO:41 or SEQ ID NO:43 or SEQ ID NO:45 or SEQ ID NO:47 or SEQ ID NO:49 or SEQ ID NO:51 or SEQ ID NO:53 or SEQ ID NO:55 or SEQ ID NO:57 or SEQ ID NO:59 or SEQ ID NO:61 or SEQ ID NO:63 or SEQ ID NO:65 or SEQ ID NO:67 or SEQ ID NO:69 or SEQ ID NO:71 or SEQ ID NO:73 or SEQ ID NO:75 or SEQ ID NO:77 or SEQ ID NO:79 or SEQ ID NO:81 or SEQ ID NO:83 or SEQ ID NO:85 or SEQ ID NO:87 or SEQ ID NO:89 or SEQ ID NO:91 or SEQ ID NO:93 or SEQ ID NO:95 or SEQ ID NO:97 or SEQ ID NO:99 or SEQ ID NO:101 or SEQ ID NO:103 or SEQ ID NO:105 or SEQ ID NO:107 or SEQ ID NO:109 or SEQ ID NO:111 or SEQ ID

NO:113 or SEQ ID NO:115 or SEQ ID NO:117 or SEQ ID NO:119 or SEQ ID NO:121 or SEQ ID NO:123 or SEQ ID NO:125 or SEQ ID NO:127 or SEQ ID NO:129 or SEQ ID NO:131 or SEQ ID NO:133 or SEQ ID NO:135 or SEQ ID NO:137 or SEQ ID NO:139 or SEQ ID NO:141 or SEQ ID NO:143 or SEQ ID NO:145 or SEQ ID NO:147 or SEQ ID NO:149 or SEQ ID NO:151 or SEQ ID NO:153 or SEQ ID NO:155 or SEQ ID NO:157 or SEQ ID NO:159 or SEQ ID NO:161 or SEQ ID NO:163 or SEQ ID NO:165 or SEQ ID NO:167 or SEQ ID NO:169 or SEQ ID NO:171 or SEQ ID NO:173 or SEQ ID NO:175 or SEQ ID NO:177 or SEQ ID NO:179 or SEQ ID NO:189 or SEQ ID NO:191 or SEQ ID NO:193 or SEQ ID NO:195 or SEQ ID NO:197 or SEQ ID NO:199 or 201;

(v) a nucleotide sequence capable of encoding an amino acid sequence having at least about 60% similarity after optimal alignment to SEQ ID NO:19 or SEQ ID NO:21 or SEQ ID NO:23 or SEQ ID NO:25 or SEQ ID NO:27 or SEQ ID NO:29 or SEQ ID NO:31 or SEQ ID NO:33 or SEQ ID NO:35 or SEQ ID NO:37 or SEQ ID NO:39 or SEQ ID NO:41 or SEQ ID NO:43 or SEQ ID NO:45 or SEQ ID NO:47 or SEQ ID NO:49 or SEQ ID NO:51 or SEQ ID NO:53 or SEQ ID NO:55 or SEQ ID NO:57 or SEQ ID NO:59 or SEQ ID NO:61 or SEQ ID NO:63 or SEQ ID NO:65 or SEQ ID NO:67 or SEQ ID NO:69 or SEQ ID NO:71 or SEQ ID NO:73 or SEQ ID NO:75 or SEQ ID NO:77 or SEQ ID NO:79 or SEQ ID NO:81 or SEQ ID NO:83 or SEQ ID NO:85 or SEQ ID NO:87 or SEQ ID NO:89 or SEQ ID NO:91 or SEQ ID NO:93 or SEQ ID NO:95 or SEQ ID NO:97 or SEQ ID NO:99 or SEQ ID NO:101 or SEQ ID NO:103 or SEQ ID NO:105 or SEQ ID NO:107 or SEQ ID NO:109 or SEQ ID NO:111 or SEQ ID NO:113 or SEQ ID NO:115 or SEQ ID NO:117 or SEQ ID NO:119 or SEQ ID NO:121 or SEQ ID NO:123 or SEQ ID NO:125 or SEQ ID NO:127 or SEQ ID NO:129 or SEQ ID NO:131 or SEQ ID NO:133 or SEQ ID NO:135 or SEQ ID NO:137 or SEQ ID NO:139 or SEQ ID NO:141 or SEQ ID NO:143 or SEQ ID NO:145 or SEQ ID NO:147 or SEQ ID NO:149 or SEQ ID NO:151 or SEQ ID NO:153 or SEQ ID NO:155 or SEQ ID NO:157 or SEQ ID NO:159 or SEQ ID NO:161 or SEQ ID NO:163 or SEQ ID NO:165 or SEQ ID NO:167 or SEQ ID NO:169 or SEQ ID NO:171 or

SEQ ID NO:173 or SEQ ID NO:175 or SEQ ID NO:177 or SEQ ID NO:179 or SEQ ID NO:189 or SEQ ID NO:191 or SEQ ID NO:193 or SEQ ID NO:195 or SEQ ID NO:197 or SEQ ID NO:199 or 201;

(vi) a nucleotide sequence capable of hybriding under low stringency conditions to the nucleotide sequence in (iv) or (v) or its complementary form;

wherein said nucleotide sequences encode a CFM which imparts an altered visual characterization to said cell or group of cells to a human eye in the absence of extraneous non-white light or particle emission.

More particularly, there is provided a plant or cells of a plant or parts of a plant or progeny of a plant wherein said plant comprises cells comprising:

(i) a nucleotide sequence set forth in SEQ ID NO:189 or SEQ ID NO:191 or SEQ ID NO:193 or SEQ ID NO:195 or SEQ ID NO:197 or SEQ ID NO:199 or SEQ ID NO:201;

(ii) a nucleotide sequence having at least about 60% similarity after optimal alignment to SEQ ID NO:189 or SEQ ID NO:191 or SEQ ID NO:193 or SEQ ID NO:195 or SEQ ID NO:197 or SEQ ID NO:199 or SEQ ID NO:201;

(iii) a nucleotide sequence capable of hybridizing under low stringency conditions to SEQ ID NO:189 or SEQ ID NO:191 or SEQ ID NO:193 or SEQ ID NO:195 or SEQ ID NO:197 or SEQ ID NO:199 or SEQ ID NO:201 or its complementary form;

(iv) a nucleotide sequence capable of encoding the amino acid sequence set forth in SEQ ID NO:190 or SEQ ID NO:192 or SEQ ID NO:194 or SEQ ID NO:196 or SEQ ID NO:198 or SEQ ID NO:200 or SEQ ID NO:202;

(v) a nucleotide sequence capable of encoding an amino acid sequence having at least about 60% similarity after optimal alignment SEQ ID NO:190 or SEQ ID NO:192 or SEQ ID NO:194 or SEQ ID NO:196 or SEQ ID NO:198 or SEQ ID NO:200 or SEQ ID NO:202;

(vi) a nucleotide sequence capable of hybridizing under low stringency conditions to the nucleotide sequence in (iv) or (v) or its complementary form;

wherein said nucleotide sequences encode a CFM which imparts an altered visual characterization to said plant or cells of a plant to a human eye in the absence of extraneous non-white light or particle emission.

In a particularly preferred embodiment, there is provided a use of a CFM such as but not limited to GFP or a non-fluorescent GFP-homolog in the manufacture of a plant exhibiting altered visual characteristics to all or a part of said plant or to cells of said plant to a human eye in the absence of extraneous non-white light or particle emission.

Reference herein to extraneous light is not to be read as encompassing white light or background irradiation. The altered visual characteristics are visualized in the presence of white light, for example the light as generated by an 60 W electric bulb or daylight. White light includes light that contains all the wavelengths of the visible spectrum, such as sunlight.

The term "similarity" as used herein includes exact identity between compared sequences at the nucleotide or amino acid level. Where there is non-identity at the nucleotide level, "similarity" includes differences between sequences which result in different amino acids that are nevertheless related to each other at the structural, functional, biochemical and/or conformational levels. Where there is non-identity at the amino acid level, "similarity" includes amino acids that are nevertheless related to each other at the structural, functional, biochemical and/or conformational levels. In a particularly preferred embodiment,

nucleotide and sequence comparisons are made at the level of identity rather than similarity.

Terms used to describe sequence relationships between two or more polynucleotides or polypeptides include "reference sequence", "comparison window", "sequence similarity", "sequence identity", "percentage of sequence similarity", "percentage of sequence identity", "substantially similar" and "substantial identity". A "reference sequence" is at least 12 but frequently 15 to 18 and often at least 25 or above, such as 30 monomer units, inclusive of nucleotides and amino acid residues, in length. Because two polynucleotides may each comprise (1) a sequence (i.e. only a portion of the complete polynucleotide sequence) that is similar between the two polynucleotides, and (2) a sequence that is divergent between the two polynucleotides, sequence comparisons between two (or more) polynucleotides are typically performed by comparing sequences of the two polynucleotides over a "comparison window" to identify and compare local regions of sequence similarity. A "comparison window" refers to a conceptual segment of typically 12 contiguous residues that is compared to a reference sequence. The comparison window may comprise additions or deletions (i.e. gaps) of about 20% or less as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. Optimal alignment of sequences for aligning a comparison window may be conducted by computerized implementations of algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package Release 7.0, Genetics Computer Group, 575 Science Drive Madison, WI, USA) or by inspection and the best alignment (i.e. resulting in the highest percentage homology over the comparison window) generated by any of the various methods selected. Reference also may be made to the BLAST family of programs as for example disclosed by Altschul *et al.* (*Nucl. Acids Res. 25:* 3389, 1997). A detailed discussion of sequence analysis can be found in Unit 19.3 of Ausubel *et al.* (Current Protocols in Molecular Biology, John Wiley & Sons Inc, 1994-1998, Chapter 15).

The terms "sequence similarity" and "sequence identity" as used herein refers to the extent that sequences are identical or functionally or structurally similar on a nucleotide-by-

nucleotide basis or an amino acid-by-amino acid basis over a window of comparison. Thus, a "percentage of sequence identity", for example, is calculated by comparing two optimally aligned sequences over the window of comparison, determining the number of positions at which the identical nucleic acid base (e.g. A, T, C, G, I) or the identical amino acid residue (e.g. Ala, Pro, Ser, Thr, Gly, Val, Leu, Ile, Phe, Tyr, Trp, Lys, Arg, His, Asp, Glu, Asn, Gln, Cys and Met) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison (i.e., the window size), and multiplying the result by 100 to yield the percentage of sequence identity. For the purposes of the present invention, "sequence identity" will be understood to mean the "match percentage" calculated by the DNASIS computer program (Version 2.5 for windows; available from Hitachi Software engineering Co., Ltd., South San Francisco, California, USA) using standard defaults as used in the reference manual accompanying the software. Similar comments apply in relation to sequence similarity.

Reference herein to a low stringency includes and encompasses from at least about 0 to at least about 15% v/v formamide and from at least about 1 M to at least about 2 M salt for hybridization, and at least about 1 M to at least about 2 M salt for washing conditions. Generally, low stringency is at from about 25-30°C to about 42°C. The temperature may be altered and higher temperatures used to replace formamide and/or to give alternative stringency conditions. Alternative stringency conditions may be applied where necessary, such as medium stringency, which includes and encompasses from at least about 16% v/v to at least about 30% v/v formamide and from at least about 0.5 M to at least about 0.9 M salt for hybridization, and at least about 0.5 M to at least about 0.9 M salt for washing conditions, or high stringency, which includes and encompasses from at least about 31% v/v to at least about 50% v/v formamide and from at least about 0.01 M to at least about 0.15 M salt for hybridization, and at least about 0.01 M to at least about 0.15 M salt for washing conditions. In general, washing is carried out $T_m = 69.3 + 0.41 (G+C)\%$ (Marmur and Doty, *J. Mol. Biol. 5:* 109, 1962). However, the T_m of a duplex DNA decreases by 1°C with every increase of 1% in the number of mismatch base pairs (Bonner and Laskey, *Eur. J. Biochem. 46:* 83, 1974). Formamide is optional in these hybridization conditions.

Accordingly, particularly preferred levels of stringency are defined as follows: low stringency is 6 x SSC buffer, 0.1% w/v SDS at 25°-42°C; a moderate stringency is 2 x SSC buffer, 0.1% w/v SDS at a temperature in the range 20°C to 65°C; high stringency is 0.1 x SSC buffer, 0.1% w/v SDS at a temperature of at least 65°C.

The tobacco ribosomal DNA spacer element may be used to increase the expression of CFMs or colored proteins in transgenic *Arabidopsis*, carnation, rose or other plant species. The tobacco ribosomal DNA spacer element can be used to increase copy number and expression levels of transgenes in plants (Borisjuk *et al.*, *Nat. Biotechnol. 18:* 1303-1306, 2000). The tobacco ribosomal DNA spacer element may be inserted into pCGP2772, pCGP2785, pCGP3259 or other construct used to express CFMs or colored proteins in plants.

There is a clear correlation between codon usage and gene expression levels in *Arabidopsis*, *Caenorhabditis* and *Drosophila* (Duret and Mouchiroud, *Proc. Natl. Acad. Sci. USA 96:* 4482-4487, 1999).

Codon usage within the open reading frames of CFM or colored proteins may be modified to increase levels of CFMs or colored protein in transgenic *Arabidopsis*, carnation, rose or other plant species.

A recent study by Stevens *et al.* (*Plant Physiology* 173-182, 2000) has highlighted the possibility of increasing the stability of recombinant proteins in transgenic plants by modifying protein glycosylation patterns.

Plant virus gene vectors may be used for high level gene expression of foreign genes in plants (Scholthof and Scholthof, *Annu. Rev. of Phytopathol. 34:* 299-323, 1996; Chapman *et al.*, *Plant Journal 2:* 549-557, 1992).

The use of a plant virus expression system may increase levels of CFMs or colored protein in transgenic *Arabidopsis*, carnation, rose or other plant species. Selection of an

appropriate virus type or strain may allow the expression of CFMs or colored protein in specific tissues or patterns to produce novel phenotypes. For example a CFM or colored protein gene may be incorporated into the genome of tulip breaking virus or tulip chlorotic blotch potyvirus to induce colored sector production in tulip or other flowers.

The availability of the isolated CFMs of the present invention further provides the possibility for generating antibodies, whether monoclonal or polyclonal, against any or all of these isolated sequences or derivatives or homologs thereof.

Well-known protocols applicable to antibody production, purification and use may be found, for example, in Chapter 2 of Coligan *et al.* (*Current Protocols in Immunology*, John Wiley & Sons, N.Y., 1991-94) and Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor, Cold Spring Harbor Laboratory, 1988, which are both herein incorporated by reference.

Generally, antibodies of the invention bind to or conjugate with a polypeptide, fragment, variant or derivative thereof. For example, the antibodies may comprise polyclonal antibodies. Such antibodies may be prepared, for example, by injecting a polypeptide, fragment, variant or derivative thereof into a production species, which may include mice or rabbits, to obtain polyclonal antisera. Methods for the production of polyclonal antibodies are well known to those skilled in the art. Exemplary protocols are described in Coligan *et al.*, 1991-1994, *supra* and Harlow and Lane, 1988, *supra*.

In lieu of polyclonal antisera obtained in a production species, monoclonal antibodies may be produced using the standard method as described by Köhler & Milstein (*European Journal of Immunology 6:* 511-519, 1976) or by more recent modifications thereof as, for example, described in Coligan *et al.* (1991-1994, *supra*) by immortalizing spleen or other antibody-producing cells derived from a production species which has been inoculated with one or more of the polypeptides, fragments, variants or derivatives of the present invention.

The present invention also contemplates antibodies that comprise Fc or Fab fragments of the polyclonal or monoclonal antibodies referred to above. Alternatively, the antibodies may comprise single chain Fv antibodies (scFvs) against the peptides of the present invention. Such scFvs may be prepared, for example, in accordance with the methods described respectively in U.S. Patent No. 5,091,513, European Patent No 239,400 or Winter and Milstein (*Nature 349:* 293, 1991).

Antibodies produced in accordance with the present invention may be used for affinity chromatography in isolating natural or recombinant pigment polypeptides. For appropriate protocols, reference may be made to immunoaffinity chromatographic procedures described in Chapter 9.5 of Coligan *et al.* (1991-1994, *supra*).

Accordingly, the present invention provides an antibody specific for a CFM, said CFM comprising an amino acid sequence in its N-terminal end selected from SVIAK (SEQ ID NO:5), (M)SVIAT (SEQ ID NO:6), SGIAT (SEQ ID NO:7), SVIVT (SEQ ID NO:8) or SVSAT (SEQ ID NO:9).

Preferably, the isolated antibody is specific for a CFM comprising an amino acid sequence selected from the list comprising SVIAT QMTY KVYM SGT (SEQ ID NO:10), SVIAT QMTY KVYM PGT (SEQ ID NO:11), SVIAT QVTY KVYM SGT (SEQ ID NO:12), SGIAT QMTY KVYM SGT (SEQ ID NO:13), SVIVT QMTY KVYM SGT (SEQ ID NO:14), SVSAT QMTY KVYM SGT (SEQ ID NO:15), SVIAK QMTY KVNM SGT (SEQ ID NO:16), SVIAK QMTY KVYM SDT (SEQ ID NO:17) and/or SVIAK QMTY $X_1X_2YX_3$ SGT (SEQ ID NO:18) wherein X_1, X_2 and X_3 may be any amino acid provided that X_1 is not K; X_2 is not V; X_3 is not M.

Most preferably, the antibody is specific for a CFM comprising an amino acid sequence selected from the listing comprising SEQ ID NOs:20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126,

128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 190, 192, 194, 196, 198, 200 and 202.

Once antibodies have been produced, one or more polypeptides of the present invention may be conjugated thereto, preferably to a secondary antibody as part of an antibody staining complex, and thereby become useful as a fluorescent marker in microscopy and related procedures. Alternatively, or in addition, one or more nucleic acid sequence encoding a polypeptide of the present invention may be expressed as a recombinant polypeptide fused with a secondary antibody. These antibodies may be useful for *in situ* labelling procedures or in other related procedures such as fluorescence *in situ* hybridization (FISH).

As already described above, a fusion partner well known in the art is GFP. This fusion partner may serve as a fluorescent "tag" which facilitates the identification and/or localization, by fluorescence microscopy or by flow cytometry, of a polypeptide fused thereto. Flow cytometric methods such as fluorescence activated cell sorting (FACS) are particularly useful in this regard.

There is perpetual interest in developing high-sensitivity biochemical assays, which employ luminescence, fluorescence or visible color rather than radioisotopes, for use in research and in medicine. Interest in developing assays with visible detection systems is increasing as these often obviate the need for expensive luminescence, fluorescence or isotopic detection equipment.

Accordingly, the present invention further comprises a diagnostic assay comprising screening for the presence of CFM wherein the nucleic acid molecule encoding said CFM is expressed in a cell.

The capability of the CFMs to absorb incident light which encompasses the UV range (320-700 nm) makes them useful candidates for inclusion as components in topically-applicable sun screen formulations. The purpose of a sun screen is to block the excessive

UV radiation from affecting the skin. Sun screen formulations act by deflecting and scattering the incident light that produces burning and tanning of the skin or by absorbing this light. It is known that careful selection of sun screens can offer this protection to the skin and reduce the darkening and damaging effects of the radiation.

Such a formulation would include, for example, an effective amount of one or more CFMs of the present invention, optionally admixed with a pharmaceutically acceptable vehicle such as a carrier or excipient that will not harm the skin. By "carrier" is meant a solid or liquid filler, diluent or substance that may be safely used in topical administration. These carriers may be selected from a group including powder absorbants, creams, oils, synthetic oils, phosphate buffered solutions, emulsifiers, and liquids such as emollients, propellants, solvents, humectants, thickners, isotonic saline, and pyrogen-free water. The sun screen formulation may also include other screening agents, well known in the art, such as propyl hydroxybenzoate, dimethylaminobenzoate (PABA), phenyl salicylates and/or octyl methoxycinnamate. These formulations may be prepared for topical application to the skin in the form of conventional products such as lotions, creams, ointments and aerosol products. A useful sun screen formulation and method of preparing an emulsion therefor are provided in International Patent Publication No. WO 00/46233 in Example 4.

Accordingly, the present invention provides a biomatrix comprising a CFM, said CFM comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to said cell when visualized by a human eye in the absence of excitation by extraneous non-white light or particle emission.

Reference to a "biomatrix" includes any composition comprising a CFM such as a cell, sun screen, a purified preparation of a CFM or any solid support onto or into which a CFM is immobilized. Reference to a biomatrix also includes a bioinstrument.

Yet another aspect of the present invention contemplates the use of a CFM in a cosmetic or light filtering composition. Cosmetics include many products that can be applied to the face or body in order to alter appearance or color. New combinations of ingredients may

result in cosmetic compositions that protect against environmental stresses such as exposure to the sun. The use of a CFM in a cosmetic may provide a visible coloration that is aesthetically desirable and/or it may provide light filtering capability such as may be afforded, for example, by a sun screen.

Light filtering compositions may also be used to screen out or block UV light or different wavelengths of light within the entire spectrum. A cosmetic or light filtering composition according to the invention may also include cosmetically or pharmaceutically compatible carriers, preservatives, emusifiers, thickners, perfume, color, as well as other materials having properties which are beneficial for skin, such as moisturizers, emollients anti-ageing compounds *inter alia*.

Other applications of the CFMs of the present invention may also be contemplated. Since they are active in affecting the manner in which, and degree to which, various kinds of impinging light/radiation are processed and detected, the CFMs may find application in, for example, transducing or intensifying an image. For example, converting less visible wavelengths of light such as UV radiation to wavelengths that are more visible might be beneficial. A gel or similar material comprising a CFM may be located behind a membrane or selective barrier and combined with an optic fiber probe, such as an optode or micro-electrode. Changes in physical and chemical environments into which the probe is inserted may be calibrated to changes in fluorescent intensity and/or fluorescence half-life, to provide micro-scale measurements of parameters such as oxygen concentration and pH. Similar applications involving fluorescence intensity and/or half-life fluorescent imaging techniques may also incorporate a CFM of the present invention.

As stated above, each of the CFMs of the present invention and homologs thereof, has distinct excitation and emission characteristics. These may be fluorescently coupled such that captured photons can be passed successively between a plurality of CFMs, for example as many as six. This lengthens the pathway and the amount of time that a photon spends within any material comprising the CFMs and may thereby increase light intensity within these environments considerably. Such a light enhancement effect may be useful for

providing additional light for growing phototrophic organisms, for example plants, algae and/or corals, by increasing the likelihood of a photon's interaction with constituent photosystems.

This embodiment of the present invention may also be useful for creating light enhancer fluids that may be used to increase light intensity within a medium above that of incident light.

Furthermore, a CFM embedded in a gel matrix or other useful material may improve image quality in situations of distorted light spectra such as, for example, under water where light is shifted to the blue end of the spectrum. A CFM rendered water-soluble may prove useful in a range of different types of liquids. Alternatively, or in addition, a derivative or homolog of polypeptide of the present invention may be synthesised by substituting amino acids or adding N- or C-terminal tags to increase their insolubility and hence make them more useful in less polar environments. In this embodiment, a CFM, or a CFM modified such as through amino acid inclusion or substitution to make it more hydrophobic, combined with a water-soluble or non-water soluble emulsion, may be used to coat materials that experience UV damage such as, for example, plastics and car upholstery.

The present invention is further described by the following non-limiting Examples.

EXAMPLE 1

General methods

In general, the methods followed were as described in Sambrook *et al.* (*Molecular Cloning: A Laboratory Manual.* (2nd edition), Cold Spring Harbor Laboratory Press, USA, 1989).

The cloning vectors pBluescript and PCR script were obtained from Stratagene. pCR7 2.1 was obtained from Invitrogen.

The bacterial expression vector pQE-30 was obtained from Qiagen.

E. coli transformation

The *Escherichia coli* strains used were:-

DH5α
supE44, Δ (lacZYA-ArgF)U169, (ø80lacZΔM15), hsdR17(r_k^-, m_k^+),
recA1, endA1, gyrA96, thi-1, relA1, deoR. (Hanahan, *J. Mol. Biol. 166:* 557 1983

XL1-Blue
supE44, hsdR17(r_k^-, m_k^+), recA1, endA1, gyrA96, thi-1, relA1,
lac$^-$,[F'proAB, lacI^q, lacZΔM15, Tn10(tet^R)] (Bullock *et al., Biotechniques 5:* 376, 1987).

BL21-CodonPlus-RIL strain
ompT hsdS(rB– mB–) *dcm*+ Tet^r *gal endA* Hte [*argU ileY leuW* Cam^r]
M15 *E. coli* is derived from *E.coli* K12 and has the phenotype Nal^s, Str^s, Rif^s, Thi$^-$, Ara$^+$, Gal$^+$, Mtl$^-$, F$^-$, RecA$^+$, Uvr$^+$, Lon$^+$.

Transformation of the *E. coli* strains was performed according to the method of Inoue *et al.*, (*Gene 96:* 23-28, 1990).

Agrobacterium tumefaciens strains and transformations

The disarmed *Agrobacterium tumefaciens* strain used was AGL0 (Lazo *et al. Bio/technology 9:* 963-967, 1991).

Plasmid DNA was introduced into the *Agrobacterium tumefaciens* strain AGL0 by adding 5 µg of plasmid DNA to 100 µL of competent AGL0 cells prepared by inoculating a 50 mL LB culture and growing for 16 hours with shaking at 28°C. The cells were then pelleted and resuspended in 0.5mL of 85% v/v 100mM $CaCl_2$/15% v/v) glycerol. The DNA-*Agrobacterium* mixture was frozen by incubation in liquid N_2 for 2 minutes and then allowed to thaw by incubation at 37°C for 5 minutes. The DNA/bacterial mix was then placed on ice for a further 10 minutes. The cells were then mixed with 1mL of LB (Sambrook *et al.*, 1989 *supra*) media and incubated with shaking for 16 hours at 28°C. Cells of *A. tumefaciens* carrying the plasmid were selected on LB agar plates containing 50 µg/mL tetracycline. The confirmation of the plasmid in *A. tumefaciens* was done by restriction enzyme analysis of DNA isolated from the tetracycline-resistant transformants.

Saccharomyces cerevisiae strains and transformations

The yeast expression vector used was pYE22m (Tanaka *et al., J. Biochem. 103:* 954-961, 1988).

The yeast strain G-1315 (Mat α, trpl) (Ashikari *et al., Appl. Microbiol. Biotechnol. 30:* 515-520, 1989) was transformed with plasmid DNA according to Ito *et al.*, (*J. Bacteriol. 153:* 163-168, 1983). The transformants were selected by their ability to restore G-1315 to tryptophan prototrophy.

DNA ligations

DNA ligations were carried out using the Amersham Ligation Kit according to procedures recommended by the manufacturer.

Isolation and purification of DNA fragments

Fragments were generally isolated on a 1% w/v agarose gel and purified using the QIAEX II Gel Extraction kit (Qiagen).

Reparation of overhanging ends after restriction digestion

Overhanging 5' ends were repaired using DNA polymerase (Klenow fragment) according to standard protocols (Sambrook *et al.*, 1989 *supra*). Overhanging 3' ends were repaired using T4 DNA polymerase according to standard protocols (Sambrook *et al.*, 1989 *supra*).

Removal of phosphoryl groups from nucleic acids

Shrimp alkaline phosphatase (SAP) (USB) was typically used to remove phosphoryl groups from cloning vectors to prevent re-circularization according to the manufacturer's recommendations.

Polymerase Chain Reaction (PCR)

Unless otherwise specified, PCR conditions using plasmid DNA as template included using 2ng plasmid, 100ng each of primers, 2 µL 10 mM dNTP mix, 5 µL 10 x PfuTurbo (registered trademark) DNA polymerase buffer (Stratageme), 0.5 µL PfuTurbo (registered trademark) DNA polymerase (2.5 units/µL) (Stratagene) in a total volume of 50 µL. Cycling conditions were an initial denaturation step of 5 min at 94°C, followed by 35 cycles of 94°C for 20 sec, 50°C for 30 sec and 72°C for 1 min with a last treatment of 72°C for 10 min and then finally storage at 4°C.

PCRs were performed in a Perkin Elmer GeneAmp PCR System 9600.

^{32}P-Labelling of DNA Probes

DNA fragments (50 to 100 ng) were radioactively labelled with 50 µCi of [α-^{32}P]-dCTP using a Gigaprime kit (Geneworks). Unincorporated [α-^{32}P]-dCTP was removed by chromatography on a Sephadex G-50 (Fine) column.

Plasmid Isolation

Single colonies were analyzed for inserts by growing in LB broth (Sambrook *et al.*, 1989, *supra*) with appropriate antibiotic selection (e.g. 100 µg/mL ampicillin or 10 to 50 µg/mL tetracycline for binary vector constructs). Plasmid DNA was purified using the alkali-lysis procedure (Sambrook *et al.*, 1989, *supra*) or using The WizardPlus SV minipreps DNA purification system (Promega) or Qiagen Plasmid Mini Kit (Qiagen). Once the presence of an insert had been determined, larger amounts of plasmid DNA were prepared from 50 mL overnight cultures using a QIAfilter Plasmid Midi kit (Qiagen).

DNA Sequence Analysis

DNA sequencing was performed using the PRISM (trademark) Ready Reaction Dye Primer Cycle Sequencing Kits from Applied Biosystems. The protocols supplied by the manufacturer were followed. The cycle sequencing reactions were performed using a Perkin Elmer PCR machine (GeneAmp PCR System 9600). Sequencing runs were performed by the Australian Genome Research Facility at The Walter and Eliza Hall Institute of Medical Research (Melbourne, Australia).

Homology searches against Genbank, SWISS-PROT and EMBL databases were performed using the FASTA and TFASTA programs (Pearson and Lipman, 1988) or BLAST programs (Altschul *et al., J. Mol. Biol. 215(3):* 403-410, 1990). Percentage sequence

similarities were obtained using LALIGN program (Huang and Miller, *Adv. Appl. Math. 12:* 373-381, 1991) using default settings.

Multiple sequence alignments were produced using ClustalW (Thompson *et al., Nucleic Acids Research 22:* 4673-4680, 1994).

Petunia transformations

(a) Plant Material

Leaf tissue from mature plants of *P. hybrida* cv Mitchell (or Ba20 or Br140w) was treated in 1.88% w/v sodium hypochlorite for 2 minutes and then rinsed three times in sterile water. The leaf tissue was then cut into 25-50 mm^2 squares and precultured on MS media (Murashige and Skoog, *Physiol. Plant 15:* 73-97, 1962) supplemented with 1.0 mg/L α-benzylaminopurine (BAP) and 0.1 mg/L α-naphthalene acetic acid (NAA) for 24 hours under white fluorescent lights.

(b) Co-cultivation of Agrobacterium and Petunia Tissue

A. tumefaciens strain AGL0 containing a binary vector were maintained at 4°C on LB agar plates with 50 µg/mL tetracycline. A single colony was grown overnight in liquid LB medium containing 40 µg/mL tetracycline. The following morning 1-2 mL of the overnight culture was added to a fresh batch of 25 mL liquid LB medium and the culture was grown at 37°C with shaking until an absorbance reading at 650nm (A_{650}) of 0.4 to 0.8 was reached. A final concentration of 5×10^8 cells/mL was prepared by dilution in liquid MS medium containing 50 µM acetosyringone and 3% w/v sucrose B5 vitamins (Gamborg *et al., Exp. Cell Res. 50:* 151-158, 1968). The leaf discs were dipped for 2 minutes into the inoculum and then blotted dry and placed on co-cultivation media for 5 days. The co-cultivation medium consisted of SH medium (Schenk and Hildebrandt, *Can. J. Bot. 50:* 199-204, 1972) supplemented with 0.05 mg/L kinetin and 1.0 mg/L 2,4-D.

(c) Recovery of transgenic petunia plants

After co-cultivation, the leaf discs were transferred to selection medium (MS medium supplemented with 3% w/v sucrose, 3 mg/L BAP, 0.2 mg/L IAA, 1 µg/L chlorsulfuron, 300 mg/L timentin and 0.3% w/v Gelrite Gellan Gum (Schweizerhall). Regenerating explants were transferred to fresh selection medium after 2 weeks.

Adventitious shoots which survive the chlorsulfuron selection are isolated and transferred to BPM containing 1 µg/L chlorsulfuron and 300 mg/L timentin for root induction. All cultures are maintained under a 16 hour photoperiod (60 µmol. m^{-2}, s^{-1} cool white fluorescent light) at 23 ± 2°C. When roots reach 2-3 cm in length the transgenic petunia plantlets are transferred to autoclaved Debco 51410/2 potting mix in 8 cm tubes. After 4 weeks, plants are be replanted into 15 cm pots, using the same potting mix, and maintained at 23°C under a 14 hour photoperiod (300 µmol. m^{-2}, s^{-1} mercury halide light).

Arabidopsis transformations

Arabisopsis thaliana ecotype WS-2 seeds were obtained from The University of Melbourne, Parkville, Melbourne, Australia.

Plant growth conditions and transformation of *A. thaliana* were as essentially as described by Clough and Bent, (*Plant J., 16:* 735-743, 1998) except that seeds from the transformed plants were selected on 100 µg/mL chlorsulfuron when binary vectors containing the *SuRB* selectable marker gene were used for the transformation process.

EXAMPLE 2

Isolation of new colored-protein sequences from Heron Island coral

Coral samples were collected from Heron Island Reef flat, Queensland, Australia. These samples were viewed as whole tissue under a fluorescent microscope, as described herein.

Assessment of fluorescence properties

Table 2 shows taxonomic relationships of GFP isolated from the phylum Cnidaria and comparison with one amino acid sequence of the invention (Aams2-pep; SEQ ID NO:88). Fluorescent properties were analysed using an Olympus fluorescent microscope (BH2 - RFL) with filter combinations, as shown in Table 3. Tables 4 and 5 show fluorescent properties of colors for different species of organisms from Anthozoa and Hydrozoa.

Total RNA isolation

Plating corals were ground with a mortar and pestle and branching corals were scrubbed with a toothbrush directly into cold solution D, as described in Chomczynski and Sacchi, 1987, *supra*. Solution D-comprising tissue was homogenized using a glass homogenizer and transferred to 1.5 ml eppendorf microcentrifuge tubes. A 10% w/v 2 M sodium acetate (pH 4) solution was added prior to phenol chloroform extraction and extracted material was precipitated overnight in isopropanol at -20°C. Pellets were resuspended in solution D, and precipitated again in isopropanol. Resulting pellets were dissolved in 3 mM EDTA and 50 mM sodium acetate (pH 5) to be finally precipitated and stored at -20°C in ethanol.

cDNA construction

RNA isolated from collected coral tissue was used to prepare cDNA. cDNA were constructed using a directional cDNA synthesis kit from Clontech Laboratories (Palo Alto, CA, USA) herein incorporated by reference.

5' Forward primers for PCR amplification

SEQ ID NO:1 **POC FOR**

TCC GTT ATC GCT AAA CAG ATG ACC TAC AAA

SEQ ID NO:2 **POC 220**

GGC GAC CAC AGG TTT GCG TGT

SEQ ID NO:3 MSVIAT(FOR)

ATG AGT GTG ATC GCT ACA CAA

SEQ ID NO:1 was previously designed as a 5' (or forward primer) for PCR amplification of nucleic acids encoding coral pigment proteins. SEQ ID NO:1 was shown to anneal to nucleic acids encoding a polypeptide comprising amino acids, SVIAK (SEQ ID NO:5): Refer to Dove *et al.* (2001; *supra*) and International Patent Publication No. WO 00/46233.

SEQ ID NO:2 was originally designed as a 3' (or reverse primer) for PCR amplification of nucleic acids encoding coral pigment polypeptides as disclosed in WO 00/46233. In addition to annealing to a 3' region of the nucleic acid as intended, SEQ ID NO:2 also anneals to a 5' UTR region of pocilloporin from *Acropora aspera* as disclosed herein.

SEQ ID NO:3 is newly designed and synthesized based on sequence information from PCR amplification products using SEQ ID NO:1 and SEQ ID NO:2. The amplified products comprise 5' UTR nucleotide sequence that includes sequence encoding a novel amino terminal end for a polypeptide similar to, but distinct from, the polypeptide disclosed in International Patent Publication No. WO 00/46233. This novel polypeptide has an amino terminal end comprising amino acids (M)SVIAT (SEQ ID NO:6; Figure 3). Accordingly, SEQ ID NO:3 anneals to nucleic acids encoding a peptide comprising (M)SVIAT (SEQ ID NO:6). Although peptide sequences SVIAK (SEQ ID NO:5) and (M)SVIAT (SEQ ID NO:6) differ by only one amino acid, the corresponding nucleic acids only share 67% identity (12 nucleic acids of 18). Notably, SEQ ID NO:1 cannot be used to amplify sequences starting with the N-terminal peptide (M)SVIAT (SEQ ID NO:6), and SEQ ID NO:3 cannot be used to amplify sequences beginning with the SVIAK (SEQ ID NO:5) peptide.

3' Reverse primers for PCR amplification

SEQ ID NO:4 **POC 231**

TTT GTG CCT TGA TTT GAC TCT

SEQ ID NO:2 was also used as a 3' reverse primier and is described above. SEQ ID NO:4 was designed to anneal to a 3' end of previously isolated pocilloporin from *Acropora aspera* (Dove *et al.* [2001; *supra*] and International Patent Publication No. WO 00/46233).

PCR amplification

PCR amplification was performed using a combination of the abovementioned SEQ ID NOs as described in more detail hereinafter. Hybaid PCR express (Hybaid PCR Express, Integrated Sciences, Australia) was used according to instructions provided therein. Amplification products were separated by gel electrophoresis on a 1.5% w/v agarose gel and nucleic acid bands comprising desired nucleic acids were visualized using standard methods. Agarose gel comprising the desired nucleic acids were gel purified and the gel purified nucleic acids were inserted by ligation into pGemT-vector (Promega, Madison, WI, USA) producing a recombinant vector.

The inserted nucleic acids were sequenced using T7 and SP6 primers, which flank the inserted nucleic acid (sequencing service provided by AGRF; University of Queensland, Australia). Sequencing of the insert was performed at least twice in both forward and reverse directions until ambiguities were resolved. The following sequences were sequenced in a single direction: Ce61-7sv-rep (SEQ ID NO:37); Ce61-5sv-rep (SEQ ID NO:35); PM1Csv-rep (SEQ ID NO:57); PM1Asv-rep (SEQ ID NO:55); Mi68Dms (SEQ ID NO:119); Acams-3 (SEQ ID NO:101).

Table 6 shows amino acid sequences within 5 Angstroms of the fluorphore which encode possible spectral variants of the polypeptides of the invention comprising an amino acid sequence SGIAT (SEQ ID NO:7), SVIVT (SEQ ID NO:8), SVSAT (SEQ ID NO:9) or

(M)SVIAT (SEQ ID NO:6) at the amino terminal end. These amino acid sequences were translated from nucleic acid sequences derived by PCR using 5' primers: SEQ ID NO:2 (5' UTR) and SEQ ID NO:3 [(M)SVIAT]; and 3' primers: SEQ ID NO:2 and SEQ ID NO:4.

Table 7 shows amino acid sequences within 5 Angstroms of the fluorphore which encode possible spectral variants of the polypeptides of the invention comprising an amino acid sequence SVIAK (SEQ ID NO:5) at the amino terminal end. These amino acid sequences were translated from nucleic acid sequences derived by PCR using 5' primer SEQ ID NO:1 and 3' primer SEQ ID NO:2, and 3' SEQ ID NO:3.

Polypeptide modelling

A 3-dimensional model of the polypeptides was used to predict those amino acids within 5 Angstroms of the fluorophore "QYG". These amino acids have potential to influence spectral properties (Tsien, 1998, *supra* and Dove *et al.*, 2001, *supra*) and are shown in Tables 6 and 7. The amino acids which are predicted to be located within 5 Angstroms of the fluorophore correspond to amino acid residues 37, 39, 56-65 (which comprises the fluorophore QYG), 86, 88, 90, 104, 106, 115, 139, 141, 143, 156, 158, 171, 192, 194, 208, 209 and 210. Amino acid residue numbers refer to numbering beginning with amino terminal amino acids S-V-I as residues 1, 2 and 3, respectively.

Information in relation to amino acid residues within 5 Angstroms of the fluorophore and details of atomic contacts for the polypeptide disclosed in Table 4 of International Patent Publication No. WO 00/46233, may be useful with the polypeptides of the present invention. In Tables 6 and 7, "Type" refers to a grouping or class of common amino acids within 5 Angstroms of the fluorophore, and "*" indicates an internal stop codon. "Name" refers to consensus sequence name from multiple repeat sequences.

Figure 9 lists many of the pigment polypeptides of the invention and indicates the amino acid residues that are located within 5 Angstroms of a fluorophore region of the polypeptide. In addition, those amino acids residue positions where variation is found

throughout the different polypeptides are shown. Variable amino acids indicated throughout the polypeptide may be significant, as they may interfere with polypeptide folding.

Amino acid and nucleotide sequence comparisons

Figures 1 and 3 show amino acid sequences for polypeptides comprising amino terminal SVIAK (SEQ ID NO:5; Figure 1) and comprising (M)SVIAT (SEQ ID NO:6), SGIAT (SEQ ID NO:7), SVIVT (SEQ ID NO:8) and SVSAT (SEQ ID NO:9) at or near the terminal amino end (Figure 3). Aams-2.pep (SEQ ID NO:88) and Aams-4.pep (SEQ ID NO:90) are shown comprising additional amino acids at the amino terminal end. Alignments of the corresponding nucleotide sequences of the amino acid sequences shown in Figures 1 and 3 are set forth in Figures 2 and 4, respectively.

Polypeptides comprising five shared amino acid sequences SVIAK (SEQ ID NO:5), (M)SVIAT (SEQ ID NO:6), SGIAT (SEQ ID NO:7), SVIVT (SEQ ID NO:8) and SVSAT (SEQ ID NO:9) may be grouped accordingly. Additional common amino acids immediately adjacent to the abovementioned amino acids are shown below:

SVIAT QMTY KVYM SGT (SEQ ID NO:10);
SVIAT QMTY KVYM PGT (SEQ ID NO:11);
SVIAT QVTY KVYM SGT (SEQ ID NO:12);
SGIAT QMTY KVYM SGT (SEQ ID NO:13);
SVIVT QMTY KVYM SGT (SEQ ID NO:14);
SVSAT QMTY KVYM SGT (SEQ ID NO:15);
SVIAK QMTY KVNM SGT (SEQ ID NO:16);
SVIAK QMTY KVYM SDT (SEQ ID NO:17); and
SVIAK QMTY $X_1X_2YX_3$ SGT (SEQ ID NO:18),

wherein X_1, X_2 and X_3 may be any amino acid provided that X_1 is not K; X_2 is not V; X_3 is not M.

Figure 5 shows an alignment of amino acid sequences comprising SVIAK (SEQ ID NO:5) at the amino terminus and a stop or termination codon at corresponding amino acid residue 14. The termination codon results from the addition of two nucleic acid residues. The resulting polypeptide is much different when compared with polypeptides lacking this termination codon. An alignment of the corresponding nucleic acid sequences is shown in Figure 6. These nucleic acids are approximately 40 nucleotide bases longer than those lacking the termination codon (Figure 6). The differences can be more redily seen by referring to Figure 7, which shows an alignment of one nucleic acid sequence comprising the termination codon (SEQ ID NO:169) and a nucleic acid sequence lacking the termination codon (SEQ ID NO:19).

Previously-disclosed SVIAK (SEQ ID NO:5)-containing proteins Aapat-1 (SEQ ID NO:181) and Aapat-2 (SEQ ID NO:182) are also included on an amino acid sequence alignment with many of the SVIAK (SEQ ID NO:5)-containing polypeptides of the present invention, in Figure 8. Shaded amino acid residues indicate amino acids unique to SEQ ID NO:181 and/or SEQ ID NO:182.

EXAMPLE 3

Isolation of new colored-protein sequences from Melbourne coral

Extraction and visualization of colored proteins from coral

Samples of various coral and algae were purchased from Water World Aquarium (Melbourne, Australia) and Coburg Aquarium (Melbourne, Australia). These included *Goniopora* sp. ("flower pot coral") [brownish tentacles with an iridescent green centre underwater], green *Acropora* sp. coral ("staghorn coral"), brown/light blue *Porites* sp. coral ("finger"), *Sinularia* sp. and *Tubastrea* sp. corals as well as deep blue and bright orange Corallimorphs *(Discosoma* sp.).

Small samples of each coral were incubated in 1 M sodium phosphate buffer pH 7.5 at 4°C. A sample of "purple algae" that was growing on dead coral (normally sold as "living rock") was also collected in buffer. After 48 h the *Acropora* sp. extract appeared yellow-brown in color, the *Porites* sp. extract appeared orange in color and the purple algae extract was a clear pink color.

When the extracts were exposed to UV light the *Acropora* sp. extract contained orange and blue fractions, the *Porites* sp. extract contained pink fractions and the "purple algae" extract was a bright orange color.

Goniopora sp. coral tips were extracted in 1 M Na phosphate buffer pH 7.5. After an overnight incubation at 4°C the extract was orange-pink under natural light and appeared orange under UV light. Fluorescent green fractions were also observed in the solid phase under UV light.

A 10 μL sample of the crude extracts described above was electrophoresed through precast SDS PAGE gels (12% w/v resolving, 4% w/v stacking gel) (Ready Gels, Biorad) in a running buffer made of 25 mM Tris-HCl, pH 8.3, 192 mM glycine, 0.1% w/v SDS at 100V for 75 min. The crude protein extracts were either denatured by boiling in 10% v/v glycerol, 3% w/v SDS, 3% β-mercaptoethanol, 0.025% w/v bromophenol blue or loaded in their native state in 5% v/v glycerol, 0.04% w/v bromophenol blue. Standards included pre-stained Low Range markers (Biorad) which contained standard protein samples of 116 kDa, 80 kDa, 51.8 kDa and 34.7 kDa.

Prior to staining with Coomassie blue (0.25% (w/v) Coomassie Brilliant Blue, 45% (v/v) methanol, 10% (v/v) acetic acid), PAGE gels were examined under a hand-held UV transilluminator (BLAK-RAY, longwave UV lamp, model B100 AP, UVP Inc). The non-denatured crude protein extract from *Goniopora* sp. contained orange bands (running higher than 116 kD marker protein) and blue-green bands (running between 51.8 kD and 80 kD protein markers). The non-denatured crude protein extract from *Porites* sp. contained two orange bands under UV light at approximately the same position as that

from *Goniopora* sp (i.e. running higher than 116 kD marker protein). The non-denatured crude protein extract from *Acropora* sp. contained a single orange band under UV light at approximately the same position as that from *Goniopora* sp. (i.e. running higher than 116 kD marker protein) as well as a green band (running between 80 kD and 116 kD marker proteins).

These fluorescent bands were not observed in any of the denatured crude protein extracts. No protein bands were visible under natural light before Coomasie blue staining.

Isolation of RNA and synthesis of cDNA from coral

Total RNA was isolated from the anthozoans *Acropora* sp., *Discosoma* sp., *Sinularia* sp. and *Tubastrea* sp. using RNeasy Plant mini kit (Qiagen) or the method of Turpen and Griffith (*Biotechniques 4:* 11-15, 1986).

Complementary DNA was synthesized using 1 µg total RNA, 1 µL DNase RQ1 RNase free (Promega), 1 µL 10 x buffer (final concentration: 40 mM Tris-HCl pH 8, 10 mM NaCl, 6 mM $MgCl_2$, 10 mM $CaCl_2$). The reactions were incubated at 37°C for 10 min then 65°C for 10 min. One microlitre (1 µg) of primer dT(17)Ad2Ad1 (SEQ ID NO:183) was then added and the reaction was boiled for 5 min and then incubated on ice for 5 min. 4 µL 5 x RT buffer, 2 µL 0.1 M DTT, 1 µL 10 mM dNTPS and 1 µL RNasin (Promega) were then added and the reaction was incubated at 50°C for 2 min. 1 µL (200 U) Superscript II reverse tranciptase (Gibco BRL) was then added and the reaction was incubated at 50°C for 1.5 h. The cDNA was purified using QIAquick PCR purification kit (Qiagen).

PCR of colored protein sequences

Oligonucleotide primers "vispro-F1" (SEQ ID NO:184) and "vispro-R1" (SEQ ID NO:185) were designed to hybridize to the 5' and 3' ends of T7SP6BASPOC3 and T7SP6BASPOC4 sequences, respectively (International Patent Application No. PCT/AU00/00056). The primer "vispro-F1" (SEQ ID NO:184) contained a *Bam*HI site for

cloning into the bacterial expression vector pQE-30 (Qiagen) and an *Asc*I site with a translation initiating codon for cloning into binary vectors. The primer "vispro-R1" (SEQ ID NO:185) contains a *Pst*I site for cloning into the bacterial expression vector pQE-30 and a *Pac*I site with translation termination codon for cloning into binary vectors.

SEQ ID NO: 184 vispro-F1 (5' to 3')

```
     AscI         BamHI

CAG GGCGCGCC ATG GGA TCC GTT ATC GCT AAA CAG ATG ACC
              M   G   S   V   I   A   K   Q   M   T
```

SEQ ID NO:185 vispro-R1 (5' to 3')

```
       PacI       PstI
GGG TTA ATT AAG CTG CAG GGC GAC CAC AGG TTT GCG TG
    stop N   L   Q   L   A   V   V   P   K   R
```

Polymerase chain reactions were set up using 20 pmole vispro-F1 (SEQ ID NO:184) and 20 pmole vispro-R1 (SEQ ID NO:185) primers and 5 µL cDNA synthesized from coral RNA as template, 2.5 units HotStarTaq (trademark) DNA polymerase (Qiagen), 200 µM dNTP mix and 1 X PCR buffer (Qiagen) in a 50 µL reaction.

PCR conditions included a denaturation step at 95°C for 15 min, followed by 35 cycles of 94°C for 30 sec, 50°C for 30 sec and 72°C for 1 min with a final treatment at 72°C for 10 min followed by storage at 4°C.

PCR products were electrophoresed through a 1% w/v agarose gel. Products of ~700 bp were excised from the gel and purified using QIAEX II Gel Extraction Kit (Qiagen). Purified DNA was digested with *Bam*HI and *Pst*I restriction enzymes and re-purified using a QIAquick PCR purification Kit (Qiagen). The purified DNA was ligated with *Bam*HI/*Pst*I ends of the bacterial expression vector pQE-30 (Qiagen). Ligated DNA was transformed into *Eschericia coli* BL21-RIL, M15 (containing pREP4 (Qiagen)) or XL1-blue competent cells and plated onto Luria Broth (LB) agar plates containing 100 µg/mL

ampicillin. After overnight incubation at 37°C a colony lift on nylon membrane (DuPont/NEN) was taken and placed colony side up onto LB agar containing 100 μg/mL ampicillin and 1 mM IPTG. The plates were incubated overnight at 37°C or alternatively at room temperature for 2 nights. Blue and purple colored colonies that were visible under natural light were obtained from products originating from *Acropora* sp., *Discosoma* sp., *Sinularia* sp. and *Tubastrea* sp.

Cultures of the purple and blue colonies were initiated and incubated overnight at 37°C. Plasmid DNA was isolated and analyzed by restriction endonuclease digestion. Plasmid DNA isolated from purple colonies included pCGP2915 (A10 clone from *Acropora* sp.), pCGP2916 (A11 clone from *Acropora* sp.), pCGP2917 (A12 clone from *Acropora* sp.), pCGP2918 (A8 clone from *Acropora* sp.), pCGP2920 (D10 clone from *Discosoma* sp.), pCGP2922 (T3 clone from *Tubastrea* sp.), pCGP2924 (S3 clone from *Sinularia* sp.).

Plasmid DNA isolated from blue colonies included pCGP2919 (D1 clone from *Discosoma* sp.), pCGP2921 (T1 clone from *Tubastrea* sp.), pCGP2923 (S1 clone from *Sinularia* sp.).

See Figure 10 for all schematics of above mentioned plasmids.

Sequence analysis of cDNA clones

Complete sequence analysis of the cDNA clones contained in the pQE-30 vectors was generated using pQEprom (Qiagen) (SEQ ID NO:186), pQErev (Qiagen) (SEQ ID NO:187), Coral-R1 (SEQ ID NO:188), vispro-F1 (SEQ ID NO:184) and vispro-R1 (SEQ ID NO:185) as sequencing primers.

SEQ ID NO:186 pQEprom

CCC GAA AAG TGC CAC CTG

SEQ ID NO:187 pQErev

GTT CTG AGG TCA TTA CTG G

SEQ ID NO:188 Coral-R1

TCA GGG TAC TTG GTG AAT GG

Complete nucleotide sequences were generated from the:-

A8 cDNA clone from *Acropora* sp. contained in pCGP2918 (SEQ ID NO:189);
D10 cDNA clone from *Discosoma* sp contained in pCGP2920 (SEQ ID NO:191);
S3 cDNA clone from *Sinularia* sp contained in pCGP2924 (SEQ ID NO:193);
T3 cDNA clone from *Tubastrea* sp. contained in pCGP2922 (SEQ ID NO:195);
D1 cDNA clone from *Discosoma* sp. contained in pCGP2919 (SEQ ID NO:197);
S1 cDNA clone from *Sinularia* sp. contained in pCGP2923 (SEQ ID NO:199); and
T1 cDNA clone from *Tubastrea* sp. contained in pCGP2921 (SEQ ID NO:201).

The A8 nucleotide sequence contained a putative open reading frame of 669 bases which encodes a putative polypeptide of 223 amino acids (SEQ ID NO:190).

The D10 nucleotide sequence contained a putative open reading frame of 669 bases which encodes a putative polypeptide of 223 amino acids (SEQ ID NO:192).

The S3 nucleotide sequence contained a putative open reading frame of 669 bases which encodes a putative polypeptide of 223 amino acids (SEQ ID NO:194).

The T3 nucleotide sequence contained a putative open reading frame of 669 bases which encodes a putative polypeptide of 223 amino acids (SEQ ID NO:196).

The D1 nucleotide sequence contained a putative open reading frame of 669 bases which encodes a putative polypeptide of 223 amino acids (SEQ ID NO:198).

The S1 nucleotide sequence contained a putative open reading frame of 669 bases which encodes a putative polypeptide of 223 amino acids (SEQ ID NO:200).

The T1 nucleotide sequence contained a putative open reading frame of 669 bases which encodes a putative polypeptide of 223 amino acids (SEQ ID NO:202).

Nucleotide and amino acid sequence similarities were determined using LALIGN (Huang and Miller, 1991, *supra*). The sequences isolated from the four species of coral share high nucleic acid and amino acid sequence similarities (Table 8 and Table 9).

EXAMPLE 4

Colored protein expression from Heron Island coral cDNAs

For expression in bacteria, nucleotide sequences encoding CFMs were retrieved from pGEM-T cloning vector using a forward oligonucleotide primer consisting of the Not*I* restriction binding site, a ribosomal binding site, a spacer and 15 bases encoding the N-terminus of the protein and a reverse oligonucleotide primer encoding H6-tag (POC220-H6; POC220 is SEQ ID NO:2). PCR product was gel purified and diluted (x10) prior to cloning into PCRII-TOPO and transformed into Top 10 cells (Invitogen). Cells were induced with 0.5 mM IPTG, and protein was purified on Ni-columns (Pro-Bond, Invitrogen) eluting with 50 mM, 200 mM, 350 mM and 500 mM Imidazole in PBS pH 6.0, prior to overnight dialysis against 50 mM Potassium Phosphate pH 6.65.

Expression of examples of Type 1 peptides

Results of expressing sequences of type 1 (as defined in Tables 6 and 7 and in Figure 9) in bacteria are set forth in Table 10. Only non-identical sequences are shown. Several additional sequences, which are identical to those shown in the Table, are indicated at the top of the Table (i.e.: Acasv-D = PavsvB, etc.). Sequence alignment is taken from International Patent Publication No. WO 00/46233 and Dove *et al.* (2001; *supra*). Horizontal bars above the amino acid sequence indicate β-strands from GFP structure. The

chromophore "QYG" is shown in white type on black background. Amino acid differences in the sequences are grey-shaded.

The majority of type 1 sequences are deep blue with λ_{max} ranging from 589 nm to 593 nm. Naturally-occurring amino acid substitution L161P, as seen in RTms5 (SEQ ID NO:166) compared with Acasv-D (SEQ ID NO:30) leads to clear bacteria that no longer absorb within 520-600 nm range. Reverse substitution of P161L re-establishes the ability to absorb in this range. The alignment shows amino acids that appear to affect colour of protein and those that do not.

Absorption scans for examples of expressed type 1 sequences are shown in Figure 11. Extinction coefficients at λ_{max}, as shown in this and in subsequent Figures 12 and 13, are based on the method of Whitaker and Granum (1980, *supra*) for protein detection. Extinction coefficient variability is partly due to the state of protein maturation; similar variability has been demonstrated for DsRed (Baird *et al., Proc. Natl. Acad. Sci. USA 97:* 11984-11989, 2000).

Expression of examples of Types 2 and 14 peptides

Results of expressing sequences of type 2 in bacteria are shown in Table 11. Again, only non-identical sequences are shown. Additional sequences, identical to those shown in the Table, are indicated at the top of the Table (i.e.: PMms-B = PMms-E = PPd57-4ms, etc.). The majority of type 2 sequences are pinky-purple with λ_{max} ranging from 579 nm to 580 nm. Naturally-occurring amino acid substitution P15S leads to clear bacteria that no longer absorb within 520-600 nm range. Alignment shows amino acids that do not affect the colour of protein, although it was noted that some of these proteins had a greater tendency to aggregate and precipitate than did others.

Analogous results, following expressing of type 14 sequences in bacteria, are shown in Table 12. Only non-identical sequences are shown. Table formatting is the same as in Tables 10 and 11. The majority of type 14 sequences are pinky-purple, with λ_{max} ranging

from 579 nm to 579.5 nm. Alignment shows amino acids that do not affect the colour of protein. It was noted, however, that MisvF and MisvA, with AA147 = F, was more soluble at higher concentrations than at others.

The spectral properties of Type 2 and Type 14 sequences are similar. This may be driven by AA61, which is Ser in both of these cases as opposed to Cys in type 1 and Thr in type 6 sequences. Figures 12A and B show absorption scans for examples of expressed type 2 and type 14 sequences. As described above for type 1 sequences, observed extinction coefficient variability is partly due to the state of protein maturation.

Expression of examples of Type 6 peptides

Examples of Type 6 sequences were similarly expressed in bacteria. Again, only non-identical sequences are shown. In this case, the majority of sequences are blue-purple, with λ_{max} ranging from 583.5 nm to 585.5 nm. Alignment shows that naturally occurring amino acid substitutions V8M and/or T182P lead to colourless bacteria, as does G238E, and that substitutions at AA101 and AA147 have slight effect on λ_{max}. Results are shown in Table 13 (see over). The format is the same as for Tables 10, 11 and 12.

Figure 13 shows absorption scans for examples of expressed type 6 sequences. As already stated above, extinction coefficient variability is partly due to the state of protein maturation and similar variability has been demonstrated for DsRed (Baird et al. 2000).

Expression of examples of peptides of other Types

Results of bacterial expression of sequence types other than the major types 1, 2, 6 and 14, are shown in Table 14 (see over). Many of the sequences that failed to express blue-purple or pink proteins were isolated from cDNA in which this was not the predominant GFP homolog present.

EXAMPLE 5

Estimation of amount of total soluble protein for colored proteins

Raw phosphate buffer extracts of two colour morphs of *Acropora aspera* (a dark blue pigmented morph and a cream morph) were used in the determination of the colored protein proportion of total soluble protein. Two separate estimations were made - by absorption spectroscopy and by gel filtration (n=5; 95% confidence intervals, in each case). Results are set forth in Figures 14A/B.

Figure 14A shows an absorption scan of the two *Acropora aspera* morphs. Estimation of blue-purple pocilloporin concentration (Dove *et al.*, 1995, *supra*; Dove *et al.*, 2001, *supra*) per surface area of coral tissue is based on an extinction coefficient range of 50,000 - 100,000 $M^{-1}cm^{-1}$. Figure 14B shows the results for chromatograms of gel filtrated protein elution, determined from 235 nm and 280 nm chromatograms, applying the equation (235 nm -280 nm)/2.51 (Whitaker and Granum, 1980, *supra*). The total area under the graph provides a measure of the total soluble protein. Blue-purple pocilloporin concentration is based on the difference between areas under the blue and cream graphs in the range of pocilloporin elution (24 - 26.5 min). Notably the independent methods for blue-purple pocilloporin concentration give similar results.

EXAMPLE 6

Colored protein expression from Melbourne coral cDNAs

Colonies of coral cDNA clones isolated from *Discosoma* sp. (D2 (pCGP2925 (blue in color)), *Sinularia* sp. (S1, pCGP2923) and *Tubastrea* sp. (T1, pCGP2921, T3, pCGP2922) were grown overnight with shaking at 37°C in 2mL LB media containing 100 μg/mL ampicillin. One mL of the overnight culture was then used to inoculate 25 mL LB media containing 100 μg/mL ampicillin. This culture was then incubated at 37°C with shaking until the OD_{600} was around 0.5. IPTG was added to a final concentration of 1 mM and the cultures were grown overnight with shaking at 37°C. Cells (10 mL) of the incubated cultures were pelleted by centrifugation at 2000 rpm for10 min. The bacterial pellets and

supernatant of the D2 (pCGP2925), S1 (pCGP2923) and T1 (pCGP2921) were blue those of T3 (pCGP2922) were purple under natural light. Bacterial pellets were stored at -20°C.

Proteins contained in the supernatant of the cultures were concentrated using Centricon 30 spin columns (Amicon) according to the manufacturer's instructions. The final volume of each of the concentrated protein extract was ~200 μL.

Aliquots (8 μL) of the concentrated proteins derived from the supernatants of the cultures were electrophoresced through precast SDS PAGE gels (12% w/v resolving, 4% w/v stacking gel) (Ready Gels, BIORAD) in a running buffer made of 25 mM Tris-HCl, Ph 8.3, 192 mM glycine, 0.1% w/v SDS at 100V for 75 min. Standards included Biorad Pre-stained Broad Range markers which contained standard protein samples of 206 kDa, 119 kDa, 91 kDa, 51.4 kDa, 34.7 kDa, 28.1 kDa, 20.4 kDa and 7.2k Da.

Samples were either denatured by boiling in 10% v/v glycerol, 3% w/v SDS, 3% β-mercaptoethanol (ßME), 0.025% w/v bromophenol blue or denatured by boiling in 10% v/v glycerol, 3% w/v SDS, 0.025% w/v bromophenol blue or loaded in their native state in 5% v/v glycerol, 0.04% w/v bromophenol blue.

Prior to staining with Coomassie blue, protein bands were examined under a hand-held UV transilluminator. No fluorescent bands were visible under UV light in any of the samples. However, under natural light a blue band running at the same position as the 28 kDa protein standard was visible in the concentrated protein sample from the D2 supernatant. Blue smears that extended between the 28 kDa and 51 kDa protein standards were visible under natural light in the non-denatured concentrated protein samples from T1 and S1 supernatants. A purple smear which extended between the 28 kDa and 51 kDa protein standards was visible under natural light in the non-denatured concentrated protein samples from the S3 supernatant. There were no bands observed under natural light in samples that were denatured by boiling. Staining the gel with Coomassie blue showed that the proteins produced co-migrated with a 25 kDa protein marker (Biorad Precision Broadrange Prestained Marker).

Cultures of (*E. coli* XL1-blue) coral cDNA clones from *Discosoma* sp. (D1 in pCGP2919), *Sinularia* sp. (S1 in pCGP2923) and *Tubastrea* sp. (T1 in pCGP2921 and T3 in pCGP2922) that had grown at 37°C overnight with shaking were used to inoculate 100 mL LB media containing 100 μg/mL ampicillin and further incubated with shaking at 37°C until the OD_{600} was ~ 0.5. IPTG was added to a final concentration of 1 mM and the cultures were grown overnight with shaking at 37°C. Proteins expressed by *Tubastrea* sp. clones (T1 and T3) were purified under native conditions using Ni-NTA Superflow resin (Qiagen; QIAexpressionist 03/97) as recommended by the manufacturer. The elution buffer was exchanged with 20 mM Tris-HCl pH 8.0 using Sephadex G-25 columns (NAP10; Pharmacia) as per the manufacturer's instructions. Proteins expressed by the *Discosoma* sp. clone D1 and the *Sinularia* sp. clone S1 were purified under native conditions using the Ni-NTA method (Qiagen; QIAexpressionist 03/97) except that protein was precipitated from cleared bacterial lysate using 65% isopropanol and centrifuged at 10,000 rpm, 4°C, 10 min. The colored pellet was resuspended in 20mM Tris-HCl pH 8.0.

The proteins encoded by the *Acropora* sp. A8 clone in pCGP2918, the *Discosoma* sp. D10 clone in pCGP2920, the *Sinularia* sp S3 clone in pCGP2924 and the *Tubastrea* sp. T3 clone in pCGP2922 were a purple color (Royal Horticultural Society Color Chart (RHSCC) 88A) when concentrated. The proteins from *Tubastrea* sp. T3 clone and the *Sinularia* sp. S3 clone had absorbance peaks at approximately 580 nm.

The proteins encoded by the *Discosoma* sp. D1 clone in pCGP2919 and the *Tubastrea* sp. T1 clone in pCGP2921 were a blue color (RHSCC 102A) when concentrated and absorbance peaks at approximately 595 nm. The protein encoded by *Sinularia* sp. S1 clone in pCGP2923 was a blue-purple color (RHSCC 90A) when concentrated and had an absorbance peak at approximately 590 nm.

Amino acid sequence alignment

A multiple alignment of the encoded amino acid sequence of T1 (SEQ ID NO:202), D1 (SEQ ID NO:198), S1 (SEQ ID NO:200), A8 (SEQ ID NO:190), T3 (SEQ ID NO:196), D10 (SEQ ID NO:192) and S3 (SEQ ID NO:194) was produced using the Clustal W (1.4) program in MacVector (6.5.3; Oxford Molecular Group Plc, 1999) (Figure 15). The multiple alignment of encoded amino acids showed that there are only 16 amino acid positions that differed between proteins exhibiting blue, blue-purple and purple color. From this alignment there appear to be eight amino acid positions that may influence the color of the protein (Table 15).

The protein encoded by S1 (SEQ ID NO:200) has a color that is intermediate of the blue and purple proteins. The amino acid sequence alignment (Figure 15) showed that the S1 amino acid sequence contained four amino acid identities characteristic of blue proteins towards the amino-terminal end and four amino acid identities characteristic to purple proteins towards the carboxy-terminal end (Table 15). The substitution of one or more amino acids listed in Table 15 may influence the visible color characteristics of the protein.

Alignment of Melbourne and Heron Island coral protein sequences

The amino acid sequences of the above seven polypeptides (SEQ ID NOs 190, 192, 194, 196, 198, 200 and 202) were compared with other SVIAK (SEQ ID NO:5)-containing polypeptides, as set forth in Figure 1. The resulting alignment is shown in Figure 16.

EXAMPLE 7

Expression of colored proteins in an eukaryotic organism Saccharomyces cerevisiae

In order to observe whether the colored protein sequences were able to produce color in a eukaryotic cell, the colored protein cDNA clones T1 (SEQ ID NO:201) and A8 (SEQ ID

NO:189) were introduced into a yeast expression vector (pYE22m) (Tanaka *et al.*, 1988, *supra*) and transformed into *Saccharomyces cerevisiae* strain G1315.

Construction of pCGP3269 and pCGP3270 (T1 or A8 in pYE22m)

The plasmids pCGP3269 (Figure 17) and pCGP3270 (Figure 18) were constructed by cloning the T1 or A8 cDNA clones, respectively, in a sense orientation behind the yeast glyceraldehyde 3-phosphate dehydrogenase promoter of pYE22m (Tanaka *et al.*, 1988, *supra*).

A forward primer (Kpn.6His.F; SEQ ID NO:203) was designed to amplify the colored protein sequences that would result in 6 x Histidine tag fused in-frame with the colored protein at the N-terminus and a *Kpn*I restriction endonuclease recognition site at the 5' end. A reverse primer (T1/A8.Sal.R; SEQ ID NO:204) included a *Sal*I restriction endonuclease recognition site at the 3' end

SEQ ID NO:203 Kpn.6His.F

```
     KpnI
GCAT GGT ACC ATG AGA GGA TCG CAT CAC CAT CAC CAT CAC
              M   R   G   S   H   H   H   H   H   H
```

SEQ ID NO:204 T1/A8.Sal.R

```
     SalI
CTGA GTC GAC TCA CTG CAG GGC GAC CAC AGG TTT
              *   Q   L   A   V   V   P   K
```

The coding regions of T1 (SEQ ID NO:201) and A8 (SEQ ID NO:189) were amplified by PCR using the primers Kpn.6His.F (SEQ ID NO:203) and T1/A8.Sal.R (SEQ ID NO:204) and the plasmid DNA pCGP2921 (T1) (Figure 10) and pCGP2918 (A8) (Figure 10) as template. The ~700bp PCR products were purified using a QIAquick PCR purification kit

(Qiagen) and then digested with the restriction endonucleases *Kpn*I and *Sal*I. The *KpnI/SalI* digested products were finally purified using a QIAquick PCR purification kit (Qiagen) and subsequently ligated with the *KpnI/SalI* ends of the pYE22m yeast expression vector (Tanaka *et al.*, 1988 *supra*) using a DNA Ligation Kit (Amersham) according to the manufacturer's recommendations. Correct insertion of the T1 or A8 cDNA clones into the yeast expression vector was confirmed by visualisation of colour of transformants that were selected by their ability to restore G-1315 to tryptophan prototrophy. The T1 clone in the yeast expression vector pYE22m (designated as pCGP3269) produced blue coloured colonies (RHSCC 101C) when introduced into the yeast strain G1315. The A8 clone in the yeast expression vector pYE22m (designated as pCGP3270) produced purple coloured colonies (RHSCC 82B) when introduced into the yeast strain G1315.

EXAMPLE 8

Estimation of colored protein amounts produced by bacterial and yeast cultures

__Quantitation of colored protein expression in Saccaryomyces cerevisiae__

Pure cultures of yeast cells harbouring pCGP3269 (Figure 17) or pCGP3270 (Figure 18) were grown at 29°C for 48 hours in 100 mL of YEPD liquid broth (1% yeast extract, 2% bacto-peptone, 2% w/v glucose, pH5.0). The cultures were centrifuged at 2000 rpm for 15 min. The resulting pellets were blue (pCGP3270) and purple (pCGP3269). The His-tagged colored proteins were extracted under native conditions by first resuspending the pellets in 4 mL lysis buffer (50 mM NaH_2PO_4, pH 8.0, 300 mM NaCl, 10 mM imidazole, 5 mg/mL Yeast Lytic enzyme (IBN)) and incubated at 30°C for 1 hour. The solutions were sonicated on ice 10 times for 10 sec with 15 sec cooling between treatments. The lysates were then centrifuged at 10 000 rpm for 10 min and the supernatants (crude extract) collected. The His-tagged colored proteins were purified by nickel-nitrilotriacetic acid metal-affinity chromatography (Qiagen) as recommended by the manufacturer.

The protein content of the crude extracts and purified His-tagged colored proteins were measured using a Bio-Rad Protein Assay using 1, 3 and 5 µL aliquots of extracts as per the manufacturer's instructions (Bio-Rad Microassay Procedure). The absorbances at 595 nm were compared with bovine serum albumin (BSA) standard curves (0-10 µg/mL) to obtain estimations of protein concentrations.

Samples of crude extracts and a dilution series of known amounts of purified His-tagged colored protein were electrophoresed through precast SDS PAGE gels (12% w/v resolving, 4% w/v stacking gel) (Ready Gels, Biorad) as described in Example 3. The gels were then stained with Coomasie blue (0.25% (w/v) Coomassie Brilliant Blue, 45% (v/v) methanol, 10% (v/v) acetic acid) and the amounts of colored protein in the crude extracts were estimated by comparing the intensities of the stained bands with those of the purified His-tagged colored protein dilution series. This allowed the estimation of expression of colored protein in yeast as a percentage of total soluble protein (Table 16).

Quantitation of colored protein expression in Escherichia coli

One mL of an overnight *Escherichia coli* XL1blue culuture harbouring the plasmid pCGP2921 (T1) (Figure 10) (Example 3) was used to inoculate 100 mL LB broth (containing 50 µg/mL ampicillin) and incubated 37°C with shaking at 200 rpm until the OD600 was between 0.5 - 0.7. Protein production was induced with the addition of IPTG to 1 mM and incubation overnight at 29°C with shaking at 200 rpm. The cells were pelleted by centrifugation at 2000 rpm for 15 min. The resulting pellet was blue. The pellet was resuspended in 4 mL lysis buffer (50 mM NaH_2PO_4, pH 8.0, 300 mM NaCl, 10 mM imidazole) and sonicated on ice 6 times for 10 sec with 15 sec cooling between treatments. The solution was centrifuged at 10 000 rpm for 10 min and the (crude extract) supernatant collected. The His-tagged colored protein (T1) was extracted under native conditions by nickel-nitrilotriacetic acid metal-affinity chromatography (Qiagen) as recommended by the manufacturer.

The protein content of the crude extract and purified His-tagged colored protein was measured using a Bio-Rad Protein Assay using 1, 3 and 5 µL of extracts as per the manufacturers instructions (Bio-Rad Microassay Procedure). The absorbances at 595 nm were compared with BSA standard curves (0-10 µg/mL) to obtain estimations of protein concentrations.

Samples of crude extract and a dilution series of known amounts of purified His-tagged colored protein were electrophoresed through SDS PAGE gels as per the crude extract from yeast cultures (as described above). The amounts of colored protein in the crude extracts were estimated by comparing the intensites of the stained bands with those of the purified His-tagged colored protein dilution series. This allowed the estimation of expression of colored protein in *E. coli* as a percentage of total soluble protein (Table 16).

EXAMPLE 9

Expression of colored proteins in plants under the control of a constitutive promoter

Construction of pCGP2756 (35S: MCS: 35S expression cassette)

Plasmid pCGP2756 (Figure 19) was constructed by cloning the multicloning site (MCS) (containing the rare restriction endonuclease sites *Pac*I and *Asc*I) from pNEB193 (New England Biolabs) into the CaMV35S expression cassette of pRTppoptcAFP (Wnendt *et al., Curr Genet 25*: 510-523, 1994). The plasmid pRTppoptcAFP was digested with *Eco*RI and *Xba*I to release 300 bp AFP (antifungal protein) insert and the 3.3kb vector containing the CaMV 35S expression cassette. The plasmid pNEB193 was digested with *Eco*RI and *Xba*I to release the 40 bp fragment containing the multicloning site. The 40 bp *Eco*RI/*Xba*I fragment from pNEB193 and the 3.3 kb vector containing the CaMV35 expression cassette from pRTppoptcAFP were isolated and purified using the QIAEX II Gel Extraction kit (Qiagen) and ligated together. The ligation was carried out using the Amersham ligation kit. Correct insertion of the fragment in pCGP2756 was established by restriction enzyme

analysis (*Sal*I, *Kpn*I, *Bam*HI, *Xba*I, *Asc*I, *Pac*I, *Hind*III/*Bam*HI) of DNA isolated from ampicillin-resistant transformants.

Construction of pCGP2757 (35S: MCS: 35S binary vector)

Plasmid pCGP2757 (Figure 20) was constructed by cloning the CaMV35S expression cassette of pCGP2756 (described above) into the binary vector pWTT2132 (DNAP). The plasmid pCGP2756 was digested with *Pst*I to release the 0.7 kb CaMV35S expression cassette containing the multicloning site from pNEB193. The 0.7 kb fragment was isolated and purified using the QIAEX II Gel Extraction kit (Qiagen) and ligated with *Pst*I ends of pWTT2132 binary vector. Correct insertion of the fragment in a tandem orientation to the CaMV35S: *surB* cassette in pWTT2132 was established by restriction enzyme analysis (*Kpn*I, *Pac*I/*Asc*I, *Eco*RI, *Xba*I, *Pst*I) of DNA isolated from tetracycline-resistant transformants.

PCR products of CFMs or colored proteins derived using the primers vispro-F1 (SEQ ID NO:184) and vispro-R1 (SEQ ID NO:185) or using any primers containing *Asc*I and *Pac*I restriction endonuclease recognition sites, can be digested with *Asc*I and *Pac*I and ligated with *Asc*I/*Pac*I ends of pCGP2757.

Construction of pCGP2765 (35S: A8: 35S binary)

Plasmid pCGP2765 (Figure 21) was constructed by cloning the A8 PCR clone amplified from *Acropora sp.* into the CaMV35S expression cassette contained in the binary vector of pCGP2757 (described above). The A8 PCR product generated using the vispro-F1 (SEQ ID NO:184) and vispro-R1 (SEQ ID NO:185) primers and cDNA synthesized from *Acropora sp.* total RNA as template (see Example 1), was digested with *Asc*I and *Pac*I. The ~0.7 kb fragment was isolated and purified using the QIAEX II Gel Extraction kit (Qiagen) and ligated with *Asc*I/*Pac*I ends of pCGP2757 binary vector. Correct insertion of the fragment in a sense orientation behind the CaMV35S promoter was established by restriction enzyme analysis (*Eco*RI, *Pst*I, *Bst*XI) of DNA isolated from tetracycline-resistant transformants.

Construction of pCGP2769 (35S: D1: 35S binary) (Figure 22)

Plasmid pCGP2769 (Figure 22) was constructed by cloning the D1 PCR clone amplified from *Discosoma sp.* into the CaMV35S expression cassette contained in the binary vector of pCGP2757 (described above). The PCR product generated using the primers vispro-F1 (SEQ ID NO:184) and vispro-R1 (SEQ ID NO:185) and the template pCGP2919 (containing the D1 cDNA clone) was digested with *Asc*I and *Pac*I. PCR was carried out in 50 µL reactions with 200 µM dNTPs, 20 pmol vispro-F1 (SEQ ID NO:184), 20 pmol visproR1 (SEQ ID NO:185), 1 x Pfu buffer (Stratagene), 2.5 units Pfu trubo DNA Polymerase (Stratagene) and ~2ng pCGP2919 plasmid DNA as template. The ~0.7kb fragment was isolated and purified using the QIAEX II Gel Extraction kit (Qiagen) and ligated with *AscI/Pac*I ends of pCGP2757 binary vector. Correct insertion of the fragment in a sense orientation behind the CaMV35S promoter was established by restriction enzyme analysis (*Eco*RI, *Pst*I, *Bst*XI, *Bam*HI) of DNA isolated from tetracycline-resistant transformants.

Construction of pCGP2770 (35S: S1: 35S binary) (Figure 23)

Plasmid pCGP2770 (Figure 23) was constructed by cloning the S1 PCR clone amplified from *Sinularia sp.* into the CaMV35S expression cassette contained in the binary vector of pCGP2757 (described above). The PCR product generated using the primers vispro-F1 (SEQ ID NO:184) and vispro-R1 (SEQ ID NO:185) and the template pCGP2923 (containing the S1 cDNA clone) was digested with *Asc*I and *Pac*I. PCR was carried out in 50 µL reactions with 200 µM dNTPs, 20 pmol vispro-F1 (SEQ ID NO:184), 20 pmol vispro-R1 (SEQ ID NO:185), 1 x Pfu buffer (Stratagene), 2.5 units Pfu trubo DNA Polymerase (Stratagene) and ~2 ng pCGP2923 plasmid DNA as template. The ~0.7 kb fragment was isolated and purified using the QIAEX II Gel Extraction kit (Qiagen) and ligated with *AscI/Pac*I ends of pCGP2757 binary vector. Correct insertion of the fragment in a sense orientation behind the CaMV35S promoter was established by restriction enzyme

analysis (*Eco*RI, *Pst*I, *Bst*XI, *Bam*HI) of DNA isolated from tetracycline-resistant transformants.

Construction of pCGP2772 (35S: T1: 35S binary) (Figure 24)

Plasmid pCGP2772 (Figure 24) was constructed by cloning the T1 PCR clone amplified from *Tubastrea sp.* into the CaMV35S expression cassette contained in the binary vector of pCGP2757 (described above). The PCR product generated using the primers vispro-F1 (SEQ ID NO:184) and vispro-R1 (SEQ ID NO:185) and the template pCGP2921 (containing the T1 cDNA clone) was digested with *Asc*I and *Pac*I. PCR was carried out in 50 µL reactions with 200 µM dNTPs, 20 pmol vispro-F1 (SEQ ID NO:184), 20 pmol vispro-R1 (SEQ ID NO:185), 1 x Pfu buffer (Stratagent), 2.5 units Pfu trubo DNA Polymerase (Stratagene) and ~2 ng pCGP2921 plasmid DNA as template. The ~0.7 kb fragment was isolated and purified using the QIAEX II Gel Extraction kit (Qiagen) and ligated with *AscI*/*PacI* ends of pCGP2757 binary vector. Correct insertion of the fragment in a sense orientation behind the CaMV35S promoter was established by restriction enzyme analysis (*Eco*RI, *Pst*I, *Bst*XI, *Bam*HI) of DNA isolated from tetracycline-resistant transformants.

Construction of pCGP2926 (35S:His T1: 35S binary)

A histidine-tagged version of T1 was also produced for expression in the CaMV 35S gene expression cassette. The expression of this modified version of T1 will allow for a way of easily concentrating the expressed T1 protein to calculate the amount being produced in plants.

The RGS-His epitope was created by ligation of the 2 complementary primers TICS-His-FWD (SEQ ID NO:227) and TICS-His-REV (SEQ ID NO:228). This ligation resulted in a fragment containing the sequences to a prokaryotic ribosome binding site (RBS), a translational initiation consensus sequence (TICS) (for optimal translation in plants), the RGS-His epitope (consisting of sequences that encode the amino acids RGSHHHHHH) and

overhanging *Asc*I (at 5' end) and *Bam*HI (at 3' end). This *Asc*I/*Bam*HI fragment was ligated with *Asc*I/*Bam*HI ends of plasmid pCGP2781 (Figure 32). Correct ligation of the insert into pCGP2781 was established by restriction enzyme analysis of DNA isolated

from tetracycline-resistant transformants. The plasmid was designated as pCGP2926 (Figure 44).

SEQ ID NO:227 TICS-His-FWD (5' to 3')

```
CGCGCC AAGGAGATAT AACA ATG AGA GGA TCG CAT CAC CAT CAC CAT CAC G
             RBS   TICS M   R   G   S   H   H   H   H   H   H
                             RGS-His epitope
```

SEQ ID NO:228 TICS-His-REV (5' to 3')

```
GATCC GTG ATG GTG ATG GTG ATG CGA TCC TCT CAT TGTT ATATCTCCTT GG
                 RGS-His epitope            TICS  RBS
```

A. tumefaciens transformations

The plasmids pCGP2772 and pCGP2765 were introduced into the *Agrobacterium tumefaciens* strain AGL0 by adding 5 µg of plasmid DNA to 100 µL of competent AGL0 cells prepared by inoculating a 50 mL LB culture and growing for 16 hours with shaking at 28°C. The cells were then pelleted and resuspended in 0.5mL of 85% v/v 100 mM $CaCl_2$/15% v/v) glycerol. The DNA-*Agrobacterium* mixture was frozen by incubation in liquid N_2 for 2 minutes and then allowed to thaw by incubation at 37°C for 5 minutes. The DNA/bacterial mix was then placed on ice for a further 10 minutes. The cells were then mixed with 1 mL of LB (Sambrook *et al.*, 1989, *supra*) media and incubated with shaking for 16 hours at 28°C. Cells of *A. tumefaciens* carrying pCGP2772 and pCGP2765 were selected on LB agar plates containing 50 µg/mL tetracycline. The presence of pCGP2772 and pCGP2765 were confirmed by restriction enzyme analysis of DNA isolated from the tetracycline-resistant transformants.

EXAMPLE 10

Spatial and temporal expression of colored proteins in plants

The use of constitutive promoters such as CaMV35S can be used to direct expression of CFM or colored proteins throughout the whole plant and may be useful in cases where a novel phenotype is sought with respect to the whole plant. However in some cases novel color is sought in specific tissues such as floral, seeds, leaves, fibre (e.g. cotton fibre), stems, roots, pollen, etc. In these cases tissue-specific promoters can be used to target expression of CFM or colored proteins to specific tissues. There are many cases in the literature, which describe the use of promoters to direct spatial and temporal expression. These promoters include, but are not limited to, the examples of a seed specific promoters (Song *et al., Journal of Cotton Science 4:* 217-223, 2000), leaf and chlorophyll containing tissue specific promoters (Song *et al.*, 2000, *supra*), and tuber specific promoters (Rocha-Sosa *et al., EMBO J 8:* 23-29, 1989).

Isolation of Rose CHS promoter

A rose genomic DNA library was prepared from *Rosa hybrida* cv. Kardinal.

The rose library was screened with rose CHS cDNA clone.

A 6.6kb fragment upstream from the translational initiation site was cloned into pBluescript KS (-) (Stratagene) and the plasmid designated pCGP1114.

The plasmid pCGP1114 was digested with *Hind*III and *Eco*RV to release a ~2.7-3.0kb fragment which was purified using a Bresaclean kit (Geneworks) and ligated with *Hind*III/*Sma*I ends of pUC19 (New England Biolabs). Correct insertion of the Rose CHS promoter fragment was established by restriction enzyme analysis of DNA isolated from ampicillin-resistant transformants. The resulting plasmid was designated as pCGP1116 (Figure 25).

Construction of pCGP3255 (Rose CHS 5': 35S 3' pre-binary)

The plasmid pCGP3255 (Figure 26) was constructed by replacing the CaMV 35S promoter in the binary vector pCGP2757 with the Rose CHS promoter fragment from pCGP1116. Plasmid pCGP1116 was initially digested with *Hind*III. The overhanging 5' ends were filled-in using DNA polymerase (Klenow fragment) (Promega) according to the manufacturer's recommendation. The linearized vector was then digested with Asp718 to release a ~2.7kb rose CHS promoter fragment. The plasmid pCGP2757 was initially digested with *Sal*I. The overhanging 5' ends were filled-in using DNA polymerase (Klenow fragment) (Promega) according to the manufacturer's recommendation. The *Sal*I digested pCGP2757 was then digested with Asp718 to release the ~19kb binary vector fragment and the CaMV 35S promoter fragment. The *Sal*I (filled-in)/Asp718 ~19kb vector fragment was purified using QIAEX II Gel Extraction kit (Qiagen) and ligated with the *Hind*III (filled-in)/Asp718 ends of the rose CHS promoter fragment. Correct insertion of the rose CHS promoter was established by restriction enzyme analysis (*Bgl*II, *Pst*I, *Eco*RI, *Hind*III, *Xba*I, *Eco*RV) of DNA isolated from tetracycline-resistant transformants.

PCR products of CFMs or colored proteins derived using the primers vispro-F1 (SEQ ID NO:184) and vispro-R1 (SEQ ID NO:185) or using any primers containing *Asc*I and *Pac*I restriction endonuclease recognition sites, can be digested with *Asc*I and *Pac*I and ligated with *AscI/Pac*I ends of pCGP3255.

Construction of pCGP2782 (Rose CHS: T1: 35S 3' binary)

The plasmid pCGP2782 (Figure 27) was constructed by inserting the cDNA of the T1 coral protein contained in pCGP2921 (Example 1) behind the Rose CHS promoter contained in pCGP3255.

The PCR product generated using the primers vispro-F1 (SEQ ID NO:184) and vispro-R1 (SEQ ID NO:185) and the template pCGP2921 (containing the T1 cDNA clone) was digested with *Asc*I and *Pac*I. PCR was carried out in 50 μL reactions with 200 μM dNTPs,

20 pmol vispro-F1 (SEQ ID NO:184), 20 pmol vispro-R1 (SEQ ID NO:185), 1 x Pfu buffer (Stratagene), 2.5 units Pfu trubo DNA Polymerase (Stratagene) and ~2ng pCGP2921 plasmid DNA as template. The resulting product was purified using QIAquick Gel Extraction (Qiagen) and ligated with *AscI/PacI* ends of pCGP3255. Correct insertion of the T1 coding region behind the Rose CHS promoter was established by restriction endonuclease digestion (*Hind*III, *Eco*RI, *Pst*I, *Xba*I, *Bst*X1) of tetracycline-resistant transformants.

Construction of pCGP2773 (Rose CHS: D1: 35S 3' binary)

The plasmid pCGP2773 (Figure 28) was constructed by inserting the cDNA of the D1 coral protein (Example 1) contained in pCGP2919 behind the Rose CHS promoter contained in pCGP3255.

The PCR product generated using the primers vispro-F1 (SEQ ID NO:184) and vispro-R1 (SEQ ID NO:185) and the template pCGP2919 (containing the D1 cDNA clone) was digested with *Asc*I and *Pac*I. The PCR product generated using the primers vispro-F1 (SEQ ID NO:184) and vispro-R1 (SEQ ID NO:185) and the template pCGP2919 (containing the D1 cDNA clone) was digested with *Asc*I and *Pac*I. PCR was carried out in 50 µL reactions with 200 µM dNTPs, 20 pmol vispro-F1 (SEQ ID NO:184), 20 pmol vispro-R1 (SEQ ID NO:185), 1 x Pfu buffer (Stratagene), 2.5 units Pfu trubo DNA Polymerase (Stratagene) and ~2ng pCGP2919 plasmid DNA as template. The resulting fragment was purified using QIAquick Gel Extraction (Qiagen) and ligated with *AscI/PacI* ends of pCGP3255. Correct insertion of the D1 coding region behind the Rose CHS promoter was established by restriction endonuclease digestion (*Hind*III, *Eco*RI, *Pst*I, *Xba*I) of tetracycline-resistant transformants.

Construction of pCGP2774 (Rose CHS: S1: 35S 3' binary)

The plasmid pCGP2774 (Figure 29) was constructed by inserting the cDNA of the S1 coral protein (Example 1) contained in pCGP2923 behind the Rose CHS promoter contained in pCGP3255.

The PCR product generated using the primers vispro-F1 (SEQ ID NO:184) and vispro-R1 (SEQ ID NO:185) and the template pCGP2923 (containing the S1 cDNA clone) was digested with *Asc*I and *Pac*I. The PCR product generated using the primers vispro-F1 (SEQ ID NO:184) and vispro-R1 (SEQ ID NO:185) and the template pCGP2923 (containing the S1 cDNA clone) was digested with *Asc*I and *Pac*I. PCR was carried out in 50 µL reactions with 200 µM dNTPs, 20 pmol vispro-F1 (SEQ ID NO:184), 20 pmol vispro-R1 (SEQ ID NO:185), 1 x Pfu buffer (Stratagene), 2.5 units Pfu trubo DNA Polymerase (Stratagene) and ~2ng pCGP2923 plasmid DNA as template. The resulting fragment was purified using QIAquick Gel Extraction (Qiagen) and ligated with *AscI/Pac*I ends of pCGP3255. Correct insertion of the S1 coding region behind the Rose CHS promoter was established by restriction endonuclease digestion (*Hind*III, *Eco*RI, *Pst*I, *Xba*I) of tetracycline-resistant transformants.

EXAMPLE 11

Targeting of colored proteins to increase expression in plants

The levels of some CFMs or colored proteins produced in the cytosol of cells may have to be elevated in order to impart a visible color or a phenotype with commercial value. It is expected that targeting the CFM or colored proteins to different organelles within transgenic cells will significantly increase CFM or colored protein levels. The increased accumulation of transgene products by targeting to organelles has been demonstrated previously. For example, see Table 17.

It is also expected that plastid transformation of *Arabidopsis*, carnation, rose or other plant species will significantly increase CFM or colored protein levels. Increased accumulation

of transgene products by plastid transformation has been demonstrated previously. For example, see Table 18.

Cloning of the chloroplast/plastid transit peptide sequence from tobacco

CFMs or colored proteins may be targeted to plastids with the inclusion of N-terminal plastid or chloroplast targeting peptides.

The 57 amino acid transit peptide of small subunit (SSU) of ribulose biphosphate carboxylase from *Nicotiana sylvestris* (Pinck *et al., Biochimie 66:* 539-545, 1984) was selected to target coral colored proteins to plastids of transgenic *Arabidopsis*, carnation, rose or other plant species.

The primers TSSU-Fnew (SEQ ID NO:205) and TSSU-R (SEQ ID NO:206) were used to amplify the tobacco chloroplast transit-peptide coding region using the plasmid pCGN5075 (Calgene) as template.

SEQ ID NO:205 TSSU-Fnew

CAG	GGCGCGCC	AAGGAGATAT	AACA	ATG	GCT	TCC	TCA	GTT	CTT	TCC
	AscI	RBS	TICS	M	A	S	S	V	L	S

SEQ ID NO:206 TSSU-R

CACT	GGATCC	GCA	TTG	CAC	TCT	TCC	GCC	GTT	GC
	BamHI	C	Q	V	R	G	G	N	

TSSU-Fnew (SEQ ID NO:205) contains an *Asc*I site for cloning into 35S and Rose CHS expression vectors, a prokaryotic ribosomal binding site (RBS) for bacterial expression and a plant translational initiation context sequence (TICS) for improved translation in plants. TSSU-R (SEQ ID NO:206) contains a *Bam*HI site to allow the cloning of the transit

peptide in frame with coral colored protein sequences produced using vispro-F1 (SEQ ID NO:184) and vispro-R1 (SEQ ID NO:185) primers.

PCR conditions included 1 µL TSSU-Fnew (20 pmol/µL) (SEQ ID NO:205), 1 µL TSSU-R (20 pmol/µL) (SEQ ID NO:206), 5 µL 10 x pfu buffer (Stratagene), ~20ng pCGN5075 plasmid DNA as template, 1 µL 10mM dNTP mix, 0.5 µL Pfu turbo DNA polymerase (2.5 U/µL) (Stratagene) in a 50 µL reaction. The cycling conditions were 94°C for 5 minutes, followed by 35 cycles of 94°C for 30 min, 50°C for 30 min and 72°C for 60 min, and a final incubation at 72°C for 10 min. After completion of the PCR the products were stored at 4°C. PCR products were purified using a QIAquick PCR purification Kit (Qiagen) and cloned into pUC18 *Sma*I vector (Pharmacia/Amersham). The resulting plasmid was designated pCGP2783. The sequence of the transit peptide (TSSU) was confirmed by sequencing across both strands.

Construction of pCGP2780 (35S expression binary with unique BamHI site)

Plasmid pCGP2780 (Figure 30) was constructed by removing a ~290bp *Sal*I fragment from pCGP2757. The plasmid pCGP2757 was digested with *Sal*I to release a ~290bp fragment and ~19kb binary vector. The ~19kb binary vector was isolated and purified using the QIAEX II Gel Extraction kit (Qiagen) and self-ligated using the Amersham Ligation Kit. Correct religation of the *Sal*I ends was established by restriction enzyme analysis (*Pvu*II, *Bam*HI, *Sal*I) of DNA isolated from tetracycline-resistant transformants.

Construction of pCGP2784 (35S expression pre-binary containing plastid transit peptide)

The plasmid pCGP2784 (Figure 31) was constructed by inserting the chloroplast transit peptide from tobacco contained in pCGP2783 into the binary vector pCGP2781.

Plasmid pCGP2783 was digested with *Asc*I and *Bam*HI to release the ~0.2 kb TSSU fragment. The 0.2kb TSSU fragment was isolated and purified using the QIAEX II Gel Extraction kit (Qiagen) and ligated with *AscI/Bam*HI ends of pCGP2781 binary vector.

Correct insertion of the transit peptide in frame and upstream of the T1 coding sequence was established by restriction enzyme analysis (*Eco*RI, *Pst*I, *Xba*I, *Asc*I/*Pac*I) of DNA isolated from tetracycline-resistant transformants.

PCR products of CFMs or colored proteins derived using the primers vispro-F1 (SEQ ID NO:184) and vispro-R1 (SEQ ID NO:185) or using any primers containing *Bam*HI and *Pac*I restriction endonuclease recognition sites, can be digested with *Bam*HI and *Pac*I and ligated with *Bam*HI/*Pac*I ends of pCGP2784. The coding region of the CFMs or colored proteins will then be in-frame with the plastid targeting peptide to allow expression of the proteins in the plastids or chloroplasts.

Construction of pCGP2781 (35S: T1: 35S binary with unique BamHI site)

Plasmid pCGP2781 (Figure 32) was constructed by removing a ~290bp *Sal*I fragment from pCGP2772. The plasmid pCGP2772 was digested with *Sal*I to release a ~290bp fragment and ~19kb binary vector. The ~19kb binary vector was isolated and purified using the QIAEX II Gel Extraction kit (Qiagen) and self-ligated using the Amersham Ligation Kit. Correct religation of the *Sal*I ends was established by restriction enzyme analysis (*Pvu*II, *Bam*HI, *Sal*I, *Xba*I) of DNA isolated from tetracycline-resistant transformants.

Construction of pCGP2785 (35S: TSSU: T1: 35S binary)

The plasmid pCGP2785 (Figure 33) was constructed by inserting the chloroplast transit peptide from tobacco contained in pCGP2783 into the binary vector pCGP2781.

Plasmid pCGP2783 was digested with *Asc*I and *Bam*HI to release the ~0.2 kb TSSU fragment. The 0.2kb TSSU fragment was isolated and purified using the QIAEX II Gel Extraction kit (Qiagen) and ligated with *Asc*I/*Bam*HI ends of pCGP2781 binary vector. Correct insertion of the transit peptide in frame and upstream of the T1 coding sequence was established by restriction enzyme analysis (*Eco*RI, *Pst*I, *Xba*I, *Asc*I/*Pac*I) of DNA isolated from tetracycline-resistant transformants.

Construction of pCGP2787 (Rose CHS: TSSU: T1: 35S binary)

The plasmid pCGP2787 (Figure 34) was constructed by inserting the chloroplast transit peptide from tobacco contained in pCGP2783 (Example 11) into the binary vector pCGP2782 (Figure 27).

Plasmid pCGP2783 was digested with *Asc*I and *Bam*HI to release the ~0.2 kb TSSU fragment. The 0.2kb TSSU fragment was isolated and purified using the QIAEX II Gel Extraction kit (Qiagen) and ligated with *AscI/Bam*HI ends of pCGP2782 binary vector. Correct insertion of the transit peptide in frame and upstream of the T1 coding sequence was established by restriction enzyme analysis of DNA isolated from tetracycline-resistant transformants (Figure 34)

Targeting of CFMs or colored proteins to endoplasmic reticulum

CFMs or colored proteins are targeted to endoplasmic reticulum with the inclusion of N-terminal endoplasmic reticulum (ER) targeting peptides and C-terminal ER retaining signals.

The *Arabidopsis thaliana* basic chitinase N-terminal signal sequence was isolated to target CFMs and colored proteins to the ER (Haseloff *et al.*, 1997, *supra*). To retain the proteins in the ER an HDEL peptide sequence was generated to be cloned in at the 3' end of the coding region (Haseloff *et al.*, 1997, *supra*). These ER-targeting and ER-retention signals are used to increase levels of CFMs and colored protein in transgenic *Arabidopsis,* carnation, rose or other plant species.

The plasmid pBIN35Sm-GFP4-ER (Haseloff *et al.*, 1997, *supra*) (http://www.plantsci.cam.ac.uk/Haseloff/GFP/mgfp4.html) was used as the source of *Arabidopsis thaliana* basic chitinase N-terminal signal sequence and HDEL ER-retention signal.

A PCR based approach was used to generate *Asc*I and *Bam*HI sites flanking the N-terminal ER transit peptide sequence. The primers *Asc*I-ER.F (SEQ ID NO:207) and ER-*Bam*HI.R (SEQ ID NO:208) were used to amplify the N-terminal ER sequence contained in pBIN35Sm-GFP4-ER.

Primer *Asc*I-ER.F (SEQ ID NO:207) contains an *Asc*I site for cloning into 35S and Rose CHS expression binaries (see Examples 9 and 10), a prokaryotic ribosome binding site (RBS) to allow for bacterial expression and a plant translational initiation context sequence (TICS).

SEQ ID NO: 207 ***Asc*I-ER.F** (5' to 3')

```
GCAT GGCGCGCC AAGGAGATAT AACA ATG AAG ACT AAT CTT TTT C
       AscI        RBS      TICS  M   K   T   N   L   F
```

SEQ ID NO: 208 **ER-*Bam*HI.R** (5' to 3')

```
       BamHI       EcoRI
GCAT GGA TCC GAA TTC GGC CGA GGA TAA TGA TAG
      S   G   F   E   A   S   S   L   S   L
```

PCR conditions included using 1ng plasmid pBIN35Sm-GFP4-ER template, 100 ng each of primers *Asc*I-ER.F (SEQ ID NO:207) and ER-*Bam*HI.R (SEQ ID NO:208), 2.5 µL 10 x pfu turbo buffer (Stratagene), 1 µL pfu turbo (Stratagene) in a total volume of 25 µL. Cycling conditions were an initial denaturation step of 5 min at 94°C, followed by 35 cycles of 94°C for 30 sec, 50°C for 30 sec and 72°C for 1 min with a last treatment of 72°C for 5 min and then finally storage at 4°C.

An expected product of ~100bp was amplified and purified using the QIAEX II Gel Extraction kit (Qiagen) according to procedures recommended by the manufacturer. The 100bp fragment was then cloned into pCR2.1 (Invitrogen) and the plasmid was designated

pCGP3256. The sequence of the N-terminal ER transit peptide fragment was confirmed by sequence analysis using the M13 reverse and M13 -20 primers.

Construction of pCGP3257 (35S:ER:MCS:35S pre-binary)

The N-terminal ER transit peptide fragment was cloned downstream of the 35S promoter contained in the pre-binary pCGP2780 (Figure 30) to produce pCGP3257 (Figure 35). Plasmid pCGP3256 was digested with *Asc*I and *Bam*HI to release the ~100bp N-terminal ER transit peptide fragment. The fragment was isolated and purified using QIAEX II Gel Extraction kit (Qiagen) and ligated with *AscI/Bam*HI ends of pCGP2780. Correct insertion of the N-terminal ER transit peptide fragment was established by restriction endonuclease analysis of DNA isolated from tetracycline-resistant transformants.

PCR products of CFMs or colored proteins derived using the primers vispro F1 (SEQ ID NO:185) and CP-HDEL-*Pac*I.R (described in this Example below) can be digested with *Bam*HI and *Pac*I and ligated with *BamHI/Pac*I ends of pCGP3257. The coding region of the CFMs or colored proteins will be under the control of the CaMV 35S promoter and in-frame with the ER transit targeting peptide to allow targeting of the proteins to the ER. The coding region of the CFMs or colored proteins will also contain the HDEL sequence at the C-terminal end to allow retention of the proteins in the ER.

Construction of pCGP3259 (35S: ER: T1.HDEL: 35S binary)

The coding sequence of the colored protein T1 was amplified by PCR using the primers vispro-F1 (SEQ ID NO:184) and CP-HDEL-*Pac*I.R (SEQ ID NO:209) and the plasmid pCGP2779 as template. The primer CP-HDEL-*Pac*I.R was designed to include a *Pac*I site with a translational termination codon for cloning into the binary vectors described in this specification, a HDEL peptide sequence in-frame with the colored protein sequence and a *Pst*I site for cloning into the bacterial expression vector pQE-30 (Qiagen).

SEQ ID NO:209 CP-HDEL-*Pac*I. R (5' to 3')

```
       PacI                             PstI
GATCTTAAT TAA AGC TCA TCA TGC TGC AGG GCG ACC ACA GGT TTG C
           *   L   E   D   H   Q   L   A   V   V   P   K
```

PCR conditions included using 2ng plasmid pCGP2779 as template, 100ng each of primers vispro-F1 (SEQ ID NO:184) and CP-HDEL-*Pac*I.R (SEQ ID NO:209), 2 µL 10 mM dNTP mix, 5 µL 10 x PfuTurbo (registered trademark) DNA polymerase buffer (Stratagene), 0.5 µL PfuTurbo (registered trademark) DNA polymerase (2.5 units/µL) (Stratagene) in a total volume of 50 µL. Cycling conditions were an initial denaturation step of 5 min at 94°C, followed by 35 cycles of 94°C for 20 sec, 50°C for 30 sec and 72°C for 1 min with a last treatment of 72°C for 10 min and then finally storage at 4°C.

The resulting ~700bp product was digested with *Bam*HI and *Pac*I, isolated and purified using QIAEXII Gel Extraction kit (Qiagen) and ligated with *Bam*HI/*Pac*I ends of pCGP3257. Correct insertion of the T1 coding region and HDEL sequence in-frame with the ER transit peptide sequence under the control of the 35S promoter was established by restriction endonuclease analysis (*Bam*HI, *Eco*RI, *Asc*I, *Pac*I) of DNA isolated from tetracycline-resistant transformants. The resulting plasmid was designated pCGP3259 (Figure 36).

Construction of pCGP3262 (RoseCHS:ER:MCS:35S pre-binary)

The N-terminal ER transit peptide fragment was cloned downstream of the Rose CHS promoter contained in the pre-binary pCGP3255 to produce pCGP3262 (Figure 37). Plasmid pCGP3256 was digested with *Asc*I and *Bam*HI to release the ~100bp N-terminal ER transit peptide fragment. The fragment was isolated and purified using QIAEX II Gel Extraction kit (Qiagen) and ligated with *Asc*I/*Bam*HI ends of pCGP3255. Correct insertion of the N-terminal ER transit peptide fragment was established by restriction endonuclease analysis of DNA isolated from tetracycline-resistant transformants.

PCR products of CFMs or colored proteins derived using the primers vispro-F1 (SEQ ID NO:184) and CP-HDEL-*Pac*I.R (SEQ ID NO:209) can be digested with *Bam*HI and *Pac*I and ligated with *Bam*HI/*Pac*I ends of pCGP3262. The coding region of the CFMs or colored proteins will be under the control of the Rose CHS promoter and in-frame with the ER transit targeting peptide to allow targeting of the proteins to the ER. The coding region of the CFMs or colored proteins will also contain the HDEL sequence at the C-terminal to allow retention of the proteins in the ER of floral tissues.

Construction of pCGP3263 (Rose CHS:ER: T1-HDEL:35S binary)

The coding sequence of the colored protein T1 was amplified by PCR using the primers vispro-F1 (SEQ ID NO:184) and CP-HDEL-*Pac*I.R (SEQ ID NO:209) and the plasmid pCGP2779 as template.

PCR conditions were as described above for construction of pCGP3259.

The resulting ~700bp product was digested with *Bam*HI and *Pac*I, isolated and purified using QIAEX II Gel Extraction kit (Qiagen) and ligated with *Bam*HI/*Pac*I ends of pCGP3262. Correct insertion of the T1 coding region and HDEL sequence in-frame with the ER transit peptide sequence under the control of the Rose CHS promoter was established by restriction endonuclease analysis (*Bam*HI, *Eco*RI, *Asc*I, *Pac*I) of DNA isolated from tetracycline-resistant transformants. The resulting plasmid was designated pCGP3263 (Figure 38).

A site predicting N-glycosylation was identified within the coloured protein T1 ('NDS' - surrounding amino acid 107) (SEQ ID NO:202). This site is conserved among the colored protein clones D1, D10, T1, T3, S3 and A8 and these include both purple and blue varieties. Comparison of this region in sequences of other coloured and fluorescent varieties in the GenBank database (e.g., asCP562, asFP499, Clavularia FP484, Discosoma FP483 etc) indicate the presence of two alternative sequences in this position - QDS or NDI. The first converts an asparagine residue (N) to a glutamine (Q) (a conservative

change given both residues are polar) and the second changes the serine (S) to an isoluecine (I) (a non conservative change from a polar to a non polar residue). Both naturally occurring sequence alternatives for this region of the protein were be performed separately. That is, mutation of the T1 sequence from NDS to QDS and a separate mutation from NDS to NDI.

The plasmid pCGP2921 (Figure 10) was used as a source of the coding sequence for T1 blue protein. A *Bam*HI/*Hin*dIII fragment was isolated from pCGP2921 and cloned with *Bam*HI/*Hin*dIII ends of pBluescript to produce pCGP3268. The GeneEditor *in vitro* Site Directed Mutagenesis Kit (Promega) was used following the manufacturer's instructions along with the following oligonucleotides (T1.N-Q N(AAT) > Q(CAG) **SEQ ID NO:230**) and T1.S-I S(TCC) > I(ATC) **SEQ ID NO:231**) to introduce the mutations in pCGP3268.

SEQ ID NO:230 T1.N-Q N(AAT) > Q(CAG)

```
GTG TGT ACT GTC AGC CAG GAT TCC AGC ATC CAA G
 V   C   T   V   S   Q   D   S   S   I   Q
```

SEQ ID NO:231 T1.S-I S(TCC) > I(ATC)

```
CT GTC AGC AAT GAT ATC AGC ATC CAA GGC AAC
```

The resultant plasmids pCGP3271 and pCGP3272 containing the N107Q and S109I mutated forms of T1 blue protein in pBluescript were sequenced thoroughly to confirm the presence of the mutated sequence.

Construction of pCGP3273 (pQE30:T1(N107Q) and pCGP3274 (pQE30:T1(S109I)

E. coli expression of the mutated forms of T1 in pCGP3271 and pCGP3272 was necessary to determine if the mutations had any effect on the colour of the expressed protein. Thus, *Bam*HI/*Hin*dIII fragments pCGP3271 and pCGP3272 were subcloned with *Bam*HI/*Hin*dIII ends of pQE30. The resultant plasmids were designated pCGP3273 (T1- N107Q) and pCGP3274 (T1-S109I) and were expressed in *E. coli* as previously described (Example 3

and 6) to determine the colour of the expressed protein. The protein expressed by the sequence encoded in pCGP3273 was found to retain the original colour of T1 as expressed by pCGP2921, while the protein expressed by pCGP3274 was not coloured. This suggested that the S109I mutation may have had a deleterious effect on the color of the protein. Investigation of this protein will provide information on the amino acids that are critical to color formation of colored proteins.

__Construction of pCGP3275 (35S: ER:T1(N107Q).HDEL:35S binary) and pCGP3276 (35S: ER:T1(S109I).HDEL:35S binary)__

The coding sequence of the coloured protein T1(N107Q) was amplified by PCR using the primers vispro-F1 (SEQ ID NO:184) and CP-HDEL-*Pac*I.R (SEQ ID NO:207) and the plasmids pCGP3271 (described above) and pCGP3272 (described above) as template essentially as described in the construction of pCGP3259 (Example 11).

The resulting ~700bp products were digested with *Bam*HI and *Pac*I, isolated and purified using QIAEXII Gel Extraction kit (Qiagen) and ligated with *Bam*HI/*Pac*I ends of pCGP3257 (Figure 35). Correct insertion of the coding regions of T1(N107Q) and T1(S109I) and HDEL sequence in-frame with the ER transit peptide sequence under the control of the CaMV 35S promoter was established by restriction endonuclease analysis (*Bam*HI, *Eco*RI, *Asc*I, *Pac*I, *Eco*RV) of DNA isolated from tetracycline resistant transformants. The resulting plasmids were designated pCGP3275 and pCGP3276.

__Construction of pCGP3277 (RoseCHS: ER:T1(N107Q).HDEL:35S binary) and pCGP3276 (Rose CHS: ER:T1(S109I).HDEL:35S binary)__

The coding sequence of the coloured protein T1(N107Q) was amplified by PCR using the primers vispro F1 (SEQ ID NO:184) and CP-HDEL-*Pac*I.R (SEQ ID NO:207) and the plasmids pCGP3271 and pCGP3272 as template essentially as described in the construction of pCGP3259 (Example 11).

The resulting ~700bp products were digested with *Bam*HI and *Pac*I, isolated and purified using QIAEXII Gel Extraction kit (Qiagen) and ligated with *Bam*HI/*Pac*I ends of pCGP3262 (Figure 37). Correct insertion of the coding regions of T1(N107Q) and T1(S109I) and HDEL sequence in-frame with the ER transit peptide sequence under the control of the Rose CHS promoter was established by restriction endonuclease analysis (*Bam*HI, *Eco*RI, *Asc*I, *Pac*I, *Eco*RV) of DNA isolated from tetracycline resistant transformants. The resulting plasmids were designated pCGP3277 and pCGP3278.

EXAMPLE 12

Fusion proteins with GFP

Construction of pCGP3258 (35S:T1/mGFP4:35S binary)

As a way of tracking the expression and localisation of the T1 coloured protein the T1 coding region was fused with the N-terminus of mGFP4 (Haseloff *et al., PNAS 94*: 2122-2127, 1997).

The mGFP4 coding sequence was amplified using the primers PstI-mGFP4F (SEQ ID NO:210) and mGFP4-PacIR (SEQ ID NO:211) and pBIN35SmGFP4ER (Haseloff *et al.*, 1997) as template. A ~700bp product was gel purified and then digested with the restriction endonucleases *Pst*I and *Pac*I. The T1 coding sequence was amplified using the primers visproF1-new (SEQ ID NO:212) and visproR1 (SEQ ID NO:185) and pCGP2779 as template.

SEQ ID NO:210 Pst-mGFP4F (5' to 3')

```
       PstI   linker sequences
GCAT CTG CAG GTC GCC ACC AGT AAA GGA GAA GAA CTT TTC AC
      L   Q   V   A   T   S   K   G   E   E   L   F
```

SEQ ID NO:211 mGFP4-PacIR

```
      PacI
CTGA TTAATTAA TTA TTT GTA TAG TTC ATC CAT GCC ATG
               *   K   Y   L   E   D   M   G   H
```

SEQ ID NO:212 visproF1-new

```
      AscI       RBS    TICS          BamHI
CAG GGCGCGCC AAGGAGATAT AACA ATG GGA TCC GTT ATC GCT AAA CAG ATG ACC
                              M   G   S   V   I   A   K   Q   M   T
```

A ~700bp product was gel purified and then digested with the restriction endonucleases *Asc*I and *Pst*I.

The *PstI/Pac*I mGFP4 fragment was ligated with the *AscI/Pst*I T1 fragment. The resulting ligated fragment was then ligated with the *AscI/Pac*I ends of the binary vector pCGP3257 (Figure 35) to produce pCGP3258 (Figure 39). Correct insertion of the T1:mGFP4 fusion was established by restriction endonuclease analysis (*Bst*X1, *Eco*RI, *Nco*I, *Pst*I) of DNA isolated from tetracycline-resistant transformants. The resulting plasmid was designated pCGP3258 (Figure 39).

Construction of pCGP3261 (35S:ER:T1:GFP: 35S binary)

An ER targeted version of the T1:mGFP4 fusion in pCGP3258 under the control of the CaMV 35S promoter was also prepared. This plasmid was designated pCGP3261 (Figure 45).

The T1:mGFP4 fusion was amplified using the primers vispro-F1 (SEQ ID NO:184) and mGFP4-HDEL-PacR (SEQ ID NO:229) and pCGP3258 (Figure 39) as template. A ~1.4kb product was gel purified and then digested with the restriction endonucleases *Bam*HI and *Pac*I. The resulting fragment was then ligated with *Bam*HI/*Pac*I ends of the binary vector

pCGP3257 (Figure 35) to produce pCGP3261 (Figure 45). Correct insertion of the T1:mGFP4 fusion was established by restriction endonuclease analysis (*Bst*X1, *Eco*RI, *Nco*I, *Pst*I, *Asc*I/*Pac*I, *Xba*I) of DNA isolated from tetracycline-resistant transformants. The resulting plasmid was designated pCGP3261 (Figure 45).

SEQ ID NO:229 mGFP4-HDEL-PacR (5' TO 3')

CTG ATT AAT TAA AGC TCA TCA TGT TTG TAT AGT TCA TCC ATG CCA TG

Construction of pCGP3260 (35S:ER:GFP: 35S binary)

An ER targeted version of the mGFP4 in pBIN35SmGFP4ER (Haseloff *et al.*, 1997 *supra*) under the control of the CaMV 35S promoter and CaMV 35S terminator was prepared to use as a control for the binaries pCGP3258 (Figure 39) and pCGP3261 (Figure 45).

The plasmid pBIN35SmGFP4ER (Haseloff *et al.*, 1997 *supra*) was initially digested with the restriction endonuclease *Sac*I. The resulting overhang was repaired and the linearized vector was then digested with *Bam*HI to release a ~0.7kb fragment containing the mGFP4 coding sequence. The resulting *Sac*I(blunt)/*Bam*HI mGFP4 fragment was gel purified and then ligated with *Bam*HI/*Pac*I (blunt) ends of the binary vector pCGP2780 (Figure 30). Correct insertion of the mGFP4 coding sequence was established by restriction endonuclease analysis (*Eco*RI, *Nco*I, *Pst*I, *Bam*HI, *Xba*I) of DNA isolated from tetracycline-resistant transformants. The resulting plasmid was designated pCGP3260 (Figure 46).

EXAMPLE 13

Reconstruction of color

In order to determine whether rose petals or plant material in general conatin proteases that may degrade colored proteins reconstructions of rose petal extracts with the T1 colored protein were set up.

Petals of *Rosa hybrida* cultivar Medeo are generally white to pale apricot. Expression of colored proteins in a white flower should allow visualisation of color when colored proteins are expressed in flowers.

One gram amounts of Medeo rose petals were ground in 500 μL water using a mortar and pestle. The resultant slurries were centrifuged at 14 000 rpm for 5 min in 1.5mL centrifuge tubes. The supernatants were collected and 100 μL of the extracts were aliquoted into the wells of a microtitre tray. Ten microlitres aliquots containing ~30 μg of His-tag purified T1 protein (purified as described in Example 8) were added to the Medeo extracts. In order to determine whether the color of the colored protein is affected by pH, the pH of some of the reconstructions was modified by addition of NaOH so that the final pH was 7.0, 8.5 or 10.0. The pH of Medeo petal extract alone was pH 4.5 and 4.6. The pH of Medeo petal extract mixed with T1 protein was pH 5.2, 5.8 and 6.1. The color of reconstructions of Medeo petal extract mixed with T1 protein at pH 5.2, 5.8 and 6.1 was light blue (RHSCC 101C/ RHSCC 115B). However the color at pH 7.0 and 8.5 was a pale blue-green (RHSCC 122C) and that at pH 10.0 was yellow. The colors were still evident after 5 hours incubation at room temperature as well as 48 hours at room temperature indicating that the colored protein was stable in petal extract.

An interesting and unexpected observation was that the color of the T1 protein changed to yellow when in a high pH solution. Analysis of the conformation of the protein at this high pH provides information that allows for the design of targeted mutations to T1 or other colored protein sequence and thus allows for the production of a yellow color in a low to neutral pH environment such is found in plant cells. Alternatively random shuffling (US Patent No. 6, 132 970) using selections of the vast number of colored protein sequences isolated and then expressing these mutated versions in *E. coli* or yeast as described in Examples 3, 4, 6 and 7 will provide a means of selecting for altered or improved colors and/or brightness of the proteins expressed.

Incubation of petunia petals with T1 protein

The flowers of *Petunia hybrida* cultivar Mitchell are white. Mitchell petal sections were incubated with the T1 protein to determine the color that would be produced in white petals upon production of the colored proteins. Petal sections (including part of the tube and limb) were incubated in 200 µL His-tag purified T1 protein (from *E. coli* cultures as described in Example 8) (6 mg/mL in 20 mM Tris HCl pH 8.0) and His-tag purified A8 protein (from yeast cultures as described in Example 8) (1 mg/mL in 20 mM Tris HCl pH 8.0). In both cases the colored proteins were taking up by the petal fragments within a few minutes as visualised by coloration of the cut surface of the petal. Incubation of white petals in the T1 protein solution resulted in petals of a pale blue (RHSCC 112D) color whereas incubation of white petals in the A8 protein solution resulted in a pale purple color in the petal tissue. This experiment showed that the protein is stable in petal tissue and that the color produced will not be masked or quenched by other plant compounds.

EXAMPLE 14

Expression of colored proteins in Arabidopsis

Transformation of Arabidopsis

Construction of pCGP960 (35S:gus:ocs binary)

The binary vector pCGP960 was prepared to use as a control in plant transformation experiments. A CaMV35S:GUS:ocs3' expression cassette was isolated from pKIWI101 (Klee *et al., Bio/Technology 3:* 637-642, 1985) and inserted into the pWTT2132 (DNAP) binary vector backbone which contains a CaMV 35S:*SuRB* selectable marker gene.

The binary vectors pCGP2772 (Figure 24), pCGP2765 (Figure 21), pCGP3259 (Figure 36), pCGP2785 (Figure 33), pCGP3258 (Figure 39), pCGP2926 (Figure 44), pCGP3263 (Figure 38), pCGP2787 (Figure 34), pCGP2782 (Figure 27), pCGP960 (see above), pCGP3261 (Figure 45), pCGP3260 (Figure 46), pBINmGFP4ER (Haseloff *et al.*, 1997, *supra*) were introduced into *Agrobacterium tumefaciens* strain AGL0 as described in Example 1.

Arabidopsis thaliana ecotype WS-2 was transformed with the above constructs using the floral dip method as mentioned in Example 1. Seeds from dipped plants were plated on selection and transgenic plants were allowed to grow until flowering. Plants can be allowed to self-fertilize to produce seed. The T2 seed can then be germinated on selection (e.g. 100 µg/mL chlorsulfuron selection for those transformed with a CaMV 35S: *SuRB* selectable marker gene) and allowed to grow to flowering. A number of the T2 generation would be expected to be homozygous for the introduced transgenes with the expectation that these plants would have increased coloured protein gene expression and protein production than the heterozygous parental lines.

Northern analysis

Leaves from a random selection of 2 events per construct (pCGP2772, pCGP2765, pCGP3259, pCGP2785, pCGP3258, pCGP3261, pCGP960, pBIN35Smgfp4ER, pCGP3260) were analysed for the presence of transcripts of the introduced T1 or A8 colored protein genes. Total RNA was isolated from these events using a Plant RNAeasy kit (QIAGEN) following procedures recommended by the manufacturer.

RNA samples (5 µg) were electrophoresed through 2.2 M formaldehyde/1.2% w/v agarose gels using running buffer containing 40 mM morpholinopropanesulphonic acid (pH 7.0), 5 mM sodium acetate, 0.1 mM EDTA (pH 8.0). The RNA was transferred to Hybond-N filters (Amersham) as described by the manufacturer.

The RNA blot was initially probed with ^{32}P-labelled fragments of a *Bam*HI/*Hin*dIII fragment isolated from pCGP2921 (T1) (Figure 10) (10^8 cpm/µg, 2 x 10^6 cpm/mL). Prehybridization (1 hour at 42°C) and hybridization (16 hours at 42°C) of the membrane were carried out in 50% v/v formamide, 1 M NaCl, 1% w/v SDS, 10% w/v dextran sulphate. The filter was washed in 2 x SSC, 1% w/v SDS at 65°C for between 1 to 2 hours and then 0.2 x SSC, 1% w/v SDS at 65°C for between 0.5 to 1 hour. The filter was exposed to Kodak XAR film with an intensifying screen at -70°C for 22 hours.

The T1 probe hybridized with transcripts of expected sizes (see Table 20) in RNA of transgenic plants that had been transformed with constructs carrying the T1 or A8 clones (lanes 1, 2, 5, 6, 7, 8, 13, 16 and 17) (eg. pCGP2772, pCGP2765, pCGP3259, pCGP2785, pCGP3258, pCGP3261) (Figure 41A) (Table 20). Under the conditions used, no hybridizing transcript was detected by Northern analysis of total RNA isolated from non transgenic control plants (lanes 9 and 10) or transgenic plants transformed with non-T1 carrying constructs (lanes 3, 4, 11, 12, 14 and 15) (e.g. pCGP960 (GUS), pBIN35Smgfp4, pCGP3260 (ER:mGFP4).

The ^{32}P-labelled T1 DNA probe was then stripped from the RNA blot by soaking the membrane in 0.1% SDS at 100°C and incubating it in a 65°C oven for 30 minutes with a final incubation step at room temperature for around 30 minutes.

The RNA blot was then probed with ^{32}P-labelled fragments of a ~0.8 kb *Hin*dIII fragment from pCGP1651 (*SuRB*) (10^8 cpm/µg, 2 x 10^6 cpm/mL). Prehybridization and hybridization were carried out as described above. The plasmid pCGP1651 contains a 0.8 kb *Hin*dIII fragment from the *SuRB* coding region contained in the binary plasmid vector pWTT2132 (DNAP).

The *SuRB* probe hybridized with a 2.2 kb transcript in transgenic plants that had been transformed with the constructs carrying the CaMV 35S: *SuRB* transgene (Figure 41 B) (lanes 1 to 8, 13 to 17) (eg. pCGP2772, pCGP2765, pCGP3259, pCGP2785, pCGP3258, pCGP3261) (Table 20). Under the conditions used, no hybridizing transcript was detected by Northern analysis of total RNA isolated from non transgenic control plants (lanes 9 and 10) or transgenic plants transformed with non-*SuRB* constructs (lanes 11 and 12) (e.g. pBIN35Smgfp4ER).

Detection of colored proteins in transgenic Arabidopsis

Polyclonal rabbit antibodies to T1 protein

T1 protein was extracted from cultures of *E. coli* harbouring pCGP2921 (Figure 10) as described previously in Example 6.

Polyclonal rabbit antibodies against the T1 protein were produced by Institute of Medical and Veterinary Sciences, Veterinary Services Division, 101 Blacks Rd, Gilles Plains, South Australia 5086, Australia. An amount of 300 µg of T1 protein (with Freunds complete adjuvent) was initially administered. Serial doses of 300 µg T1 protein (with Freunds incomplete adjuvent) were subsequently administered 22 days and 36 days after the initial dose. Antibodies collected in the first bleed (which was taken at 45 days after the initial dose) were used to probe Western blots in the first instance.

Protein extraction from plants

Leaf material (20 -120 mg) was collected from *Arabidopsis* plants, snap frozen in liquid nitrogen and then ground to a fine powder using a mortar and pestle. An equal volume (w/v) of extraction buffer (100 mM Na_2PO_4 pH 6.8, 150 mM NaCl, 10 mM EDTA, 10 mM DTT, 0.3 % Tween 20, 0.05 % Triton X) was then added to the fine powder and the mixture was further ground using the mortar and pestle. The resultant slurry was centrifuged at 10 000 rpm for 10 min and the supernatant was collected.

Western blot analysis of proteins extracted from transgenic Arabidopsis

Aliquots (8 µL) of the protein extracts were mixed with 2 µL of 5 x SDS loading buffer 10% v/v glycerol, 3% w/v SDS, 3% β-mercaptoethanol, 0.025% w/v bromophenol blue) electrophoresed through precast SDS PAGE gels (12% w/v resolving, 4% w/v stacking gel) (Ready Gels, Biorad) at 100 V for 1h 15 min in a Min-Protean System (Bio-Rad) using conditions as described previously in Example 6. The proteins were then transferred

to Immun-Blot PVDF membrane (Bio-Rad) using a Mini Trans-Blot Electrophoretic Transfer Cell (Bio-Rad) in Towbin buffer (25 mM Tris, 20 % methanol, 192 mM glycine) at 100 V for 1 h. PVDF membranes were incubated in blocking buffer (5 % non-fat dry milk, 0.2 % Tween-20, 75 mM NaPi pH 7.4, 68 mM NaCl) at room temperature for 1 h. Membranes were then further incubated with Rabbit anti-T1 antibody (diluted 1/200 in blocking buffer) for 2 h at room temperature then washed twice for 5 min in wash buffer (0.2 % Tween, NaPi pH 7.4, 68 mM NaCl). The membranes were finally incubated with goat anti-rabbit-IgG-alkaline phosphatase congugate (Bio-Rad) (diluted 1/300 in blocking buffer) for 1 h at room temperature followed by 4 washes for 10 min each in wash buffer. Colorimetric detection was carried out with Western Blue Stabilized Substrate for Alkaline Phosphatase (Promega).

The polyclonal T1 antibody detected a protein band running at the same position as T1 protein extracted from *E.coli* cultures harbouring pCGP2921 in extracts from *Arabidopsis*/2772 event 1.2, *Arabidopsis*/3259 event 1.5. The same T1 protein band was not detected in extracts from the non-transgenic controls.

The protein content in a 2 µL sample of the protein extracts was estimated using a Bio-Rad Protein Assay as per the manufacturers instructions (Microassay Procedure). The absorbance of each extract at 595 nm was compared with BSA standard curves (0 - 10 µg/mL) to estimate protein concentrations.

Samples of protein extract and a dilution series of known amounts of purified His-tagged colored protein (T1) were electrophoresed through SDS PAGE gels as described previously. The proteins were transferred to PVDF membranes (as described above) and probed with rabbit anti-T1 antibodies. The amounts of T1 colored protein in the protein extracts was estimated by comparison with the purified His-tagged colored protein dilution series. This allowed an estimation of expression of colored protein in *Arabidopsis* leaf as a percentage of total soluble protein (Table 21).

EXAMPLE 15

Expression of colored proteins in Petunia

Transformation of petunia

Petunia hybrida cultivar Mitchell produces white flowers. Mitchell was transformed with the binary constructs pCGP2772 (Figure 24), pCGP2765 (Figure 21), pCGP3259 (Figure 36) pCGP2785 (Figure 33) and pCGP2926 (Figure 44) *via Agrobacterium*-mediated transformation as described in Example 1.

Northern analysis

Flowers from a random selection of events transformed with the T-DNAs of pCGP2772 and pCGP2765 were analysed for the presence of transcripts of the introduced T1 or A8 colored protein. Total RNA was isolated using a Plant RNAeasy kit (Qiagen) following procedures recommended by the manufacturer. Northern analysis was performed as described above for analysis of the *Arabidopsis* transgenic plants.

The T1 probe hybridized with transcripts of around 0.9 kb in petal RNA of transgenic Mitchell plants that had been transformed with constructs carrying the T1 or A8 clones (Figure 40A) (pCGP2772 (lanes 7 to 12) and pCGP2765 (lanes 1 to 6), respectively). Under the conditions used no hybridising transcript was detected in RNA isolated from petals of a non transgenic control (data not shown).

The *SuRB* probe hybridized with a 2.2 kb transcript in transgenic plants that had been transformed with the constructs carrying the CaMV 35S: *SuRB* transgene (Figure 40B).

Under the conditions used no hybridizing transcript was detected in RNA isolated from petals of a non transgenic control (data not shown).

Detection of colored proteins in transgenic P. hybrida

Western blot analysis of proteins extracted from transgenic Petunia

Proteins were extracted from leaf and flower material (petal tube, petal limb, anthers, pistil, stigma and style) (100 - 300 mg) of transgenic and non-transgenic *P. hybrida* cv, Mitchell plants as described for *Arabidopsis*.

Western blot analysis of these protein extracts was performed as described for *Arabidopsis*.

The polyclonal T1 antibody detected a protein band running at the same position as T1 protein extracted from *E.coli* cultures harbouring pCGP2921 in extracts from *Petunia* accession 24534 (pCGP2765) and *Petunia* accession 24444 (pCGP2772). The same T1 protein band was not detected in the non-transgenic controls.

An estimation of expression of colored protein in *Petunia* leaf and petal as a percentage of total soluble protein was made as described above for *Arabidopsis* extracts (Table 22).

The T1 protein was produced in *Arabidopsis* leaf (Example 14) and *Petunia* leaf and flower tissue (Example 15). It is expected that an increase in protein accumulation will produce stronger colours in flower and leaf tissue. The first generation of transformed plants are selfed to give homozygous second generation transformants with higher T1 protein or other CFM accumulation and stronger colour.

Alternatively, different transgenic events are crossed to produce second generation transformants with higher T1 protein or other CFM accumulation and stronger colour. Methods envisaged to increase total T1 protein or other CFM accumulating in transformed plants include targeting T1 or other CFM to the chloroplast using a chloroplast transit peptide such as that from the small subunit of ribulose-bisphosphate from tobacco (see Example 11 or Table 17). These chloroplast transit peptides will facilitate the movement and accumulation of CFMs into chloroplasts which are abundant in leaves and chromoplasts which are abundant in flowers petals. Another method envisaged to produce

higher levels of CFMs in plant tissues is the use of chloroplast/plastid transformation techniques which have been used in the past to generate plants expressing recombinant proteins at levels of up to 46 % of total soluble protein (De Cosa *et al.*, *Nat. Biotechnol. 19*, 71-74, 2001; Daniell *et al.*, *Trends in Plant Sci. 7:* 84-91, 2002, see Example 11, Table 18). It is also envisaged that the co-expression of a suitable chaperonin in conjunction with one or more CFMs allows the efficient folding and packaging of CFMs into stable structures which are accumulated in higher amounts than would normally be expected. It is also envisaged that producing a fusion of CFM with ubiquitin in plants will increase levels of accumulated CFMs in transgenic plants as has been demonstrated in yeast (Baker, *Curr. Opinions in Biotech, 7:* 541-546, 1996 and references within). It is also envisaged that targeting T1 or other CFM to the endoplasmic reticulum (see Example 11) will increase the levels of accumulated recombinant protein in plant tissues (Haseloff *et al.*, 1997, *supra*).

Detection of correctly folded CFMs in plant extracts.

CFMs that are folded correctly in heterologous systems (such as when expressed in flowers or other plant tissues) are expected to retain characteristic absorbance and corresponding colour (see Example 13). The level of CFM production or accumulation may initially be too low for significant color change in plant tissue. A method for detecting low levels of correctly folded CFMs in plant extracts is described for leaf material from *Petunia* transformed with pCGP2772 and pCGP2765, however, this method can be used with other plant tissues such as but not limited to *Petunia* or rose or gerbera.

Total soluble proteins were extracted from transgenic leaves of Mitchell/pCGP2772 and Mitchell/pCGP2765) (see Example 15). These samples were frozen in liquid nitrogen and ground using a mortar and pestle. An equal volume (w/v) of extraction buffer (100 mM NaPO4 pH 6.8, 150 mM NaCl, 10 mM EDTA, 10 mM DTT, 0.3 % Tween 20, 0.05 % Triton X) was added to the sample and further ground. The resultant slurry was centrifuged at 10 000 rpm for 10 min and the supernatant collected.

The extracts were used undiluted or diluted 1:2 in water and their absorbance characteristics determined between 400 nm and 700 nm using a Varian Cary 50 Bio UV-Visible Spectrophotometer. The absorbance spectra were compared to those of extracts of non-transgenic control tissue and non-transgenic control tissue spiked with either T1 or T3 His-tagged purified protein (see Example 8). Detectable color was observed through the detection of peaks at approximately 580-590 nm in the extracts from transgenic plant tissue that were not evident in non-transgenic control tissue.

Methods envisaged to increase protein levels are as described above or by Bailey-Serres and Gallie (*American Society of Plant Physiologists,* Look beyond transcription, UCLA, USA, 1998) or by modification of mRNA sequence to optimize 5' and 3' untranslated sequences thereby improving message stability and/or translation efficiency, optimisation of codon usage in the introduced gene to more closely match that found in highly expressed genes (that is genes which give rise to high levels or encoded protein synthesis) in particular those of target crops, augmentation of protein stability via the attachment for example of stabilising sequences such as ubiquitin, changes to specific N-terminal amino acid residues to promote altered aggregation of monomeric forms of the protein, more effective targeting of the synthesized polypeptide to intracellular organelles or compartments, duplication and there for amplification of introduced genes leading to increased levels of protein biosynthesis for example using 'Gene Amplification Technology' (Borisjuk *et al., Nature Biotechnology 18*: 1303-1306, 2000).

EXAMPLE 16

Expression of colored proteins in other plants

The horticultural industry relies on the production of novel traits such as new colors, fragrances, productivity and disease resistance. Introduction of colored protein sequences (*via* genetic engineering) into commercially important plant lines such as, for example, but not limited to roses, carnations and gerberas provides a means to produce novel colors in flowers or plants that lack such colors.

Introduction of colored protein genes into roses is achieved using methods such as those described, for example, in International Patent Application Number PCT/US91/04412, or by Robinson and Firoozabady (*Scientia Horticulturae, 55*: 83-99, 1993), Rout *et al.* (*Scientia Horticulturae, 81*: 201-238, 1999) or Marchant *et al.* (*Molecular Breeding 4*: 187-194, 1998) or by any other method well known in the art.

Introduction of colored protein genes into carnations is achieved using methods such as those described, for example, in International Patent Application Number PCT/US92/02612 or by Lu *et al.* (*Bio/Technology 9*: 864-868, 1991), Robinson and Firoozabady (1993, *supra*) or by any other method known in the art.

Introduction of colored protein genes into carnations is achieved using methods such as those described, for example, by Robinson and Firoozabady (1993, *supra*).

The cotton industry relies on the production of dyed cotton, using dyes that can have concomitant detrimental effects on the environment. Introduction of colored protein sequences (*via* genetic engineering) into commercially important cotton lines, or other plant lines that allow for production of fabrics (such as, but not limited to, hemp), and also relies on use of colored dyes to dye said fabrics, is achieved using methods such as those described, for example, in an International Patent Application having Publication Number WO 00/77230.

EXAMPLE 17

Generation of transformed animals

The use of the CFMs of the present invention are employed to produce transgenic animals which exhibit novel color, for example, sheep with blue or red colored fleece, cows with red colored hide *inter alia*. The transgenic animals of the present invention can be produced by any number of method know in the art. Such as, but not limited to transgenic animals are produced by any number of methods, for example, microinjection of constructs

comprising a CFM nucleotide sequence into the pronucleus of a fertilized ovum, or injection of embryonic stem (ES) cells into embryos.

Microinjection

Following fertilization a single celled embryo is removed from the animal (e.g. sheep, cow, pig, goat). Micromanipulators on a specially equipped microscope are used to grasp each embryo. A glass pipette drawn to a fine point immobilizes the embryo on one side. On the opposite side, a construct containing a CFM nucleotide sequence is injected into the embryo's pronucleus with a second finely drawn injection needle. Following the injection, the embryos are transferred back into the hormonally prepared or pseudopregnant recipient females or foster mothers. The recipients follow normal pregnancy and deliver full-term young.

Injection of embryonic stem cells

ES cells are isolated from the inner cell mass of blastocyst-stage embryos (about 7 days postfertilization), ES cells are grown in the lab for many generations to produce an unlimited number of identical cells capable of developing into fully formed adults. These ES cells are altered genetically by injection of a construct containing a CFM nucleotide sequence.

Transgenic individuals are produced by microinjection of embryonic stem (ES) cells containing the CFM construct into embryos to produce "hybrid" embryos of two or more distinct cell types. Following the injection, the embryos are transferred back into the hormonally prepared or pseudopregnant recipient females or foster mothers. The recipients follow normal pregnancy and deliver full-term young.

EXAMPLE 18

Generation of a far red fluorescent monomeric protein

Cloning and expression

cDNA encoding the colored protein Rtms-5 (SEQ ID NO:166) was isolated from *Montipora efflorescens* (Scleractina Acropodiae). Under daylight illumination, *Montipora efflorescens* was a purply-red colour, but fluoresced yellow under blue illumination and red under green illumination.

To further characterise the protein, the cDNA was tagged with hexahistidine at its C-terminus and expressed at high levels in *Escherichia coli*. For expression in bacteria, the nucleotide sequence encoding Rtms-5.pep (SEQ ID NO:166) was retrieved from pGEM-T cloning vector (Promega) using forward oligonucleotide primers consisting of the Not*I* restriction binding site, a ribosomal binding site, a spacer and 15 bases encoding the N-terminus of the protein (MSV-RBS, SEQ ID NO:213; SVIAK-RBS, SEQ ID NO:214) and a reverse oligonucleotide primer encoding H6-tag (POC220-H6, SEQ ID NO:215).

SEQ ID NO:213 MSV-RBS

GGC TCT AGA AAG GAG ATA TAC AAG TGT GAT CGC TAC ACA AAT GA

SEQ ID NO:214 SVIAK-RBS

GGC TCT AGA AAG GAG ATA TAC AAT GTC CGT TAT CGC TAA ACA GAT

SEQ ID NO:215 POC220-H6

GGC AAG CTT TCA GTG GTG GTG GTG GTG GTG GGC GAC CAC AGG TTT GCG TG

PCR product was gel purified and diluted (x10) prior to cloning into pCRII-TOPO (Invitrogen) and transforming into Top 10 cells (Invitogen). Cells were induced with 0.5mM IPTG, and protein was purified on Ni-columns (Pro-Bond, Invitrogen) eluting with 50mM, 200 mM, 350 mM and 500 mM Imidazole in PBS pH 6.0, prior to overnight dialysis against 50 mM Potassium Phosphate pH 6.65.

Fluorescence charcteristics of Rtms-5

E. coli colonies were blue in colour in daylight, and weakly red fluorescent when excited with light of wavelength 595 nm.

An alignment of the amino acid sequence of Rtms-5 (SEQ ID NO:166) with other fluorescent proteins was constructed (Table 19). Rtms-5 (SEQ ID NO:166) contains the key amino acids (Tyr-66 and Gly-67) that correspond to those that form the fluorophore in other well-characterised proteins, dsRed583 (also known herein as drFP583, SEQ ID NO:221) and GFP (SEQ ID NO:222). Overall, 67% and 20% of the Rtms-5 (SEQ ID NO:166) sequence is identical to dsRed583 (SEQ ID NO:221) and GFP (SEQ ID NO:222), respectively. The protein shares a high degree of identity with a number of chromoproteins recently isolated from the *Anthozoa* species (Gurskaya *et al., FEBS Lett. 507:* 16-20, 2001).

The absorption and excitation emission spectra were measured for the purified "wild-type" Rtms-5 (SEQ ID NO:166). The protein displays a major absorption peak at 592 nm, with an extinction that is highly variable (ε_{592} = 53,000 M^{-1} cm^{-1}–111,000 M^{-1} cm^{-1}) and a shoulder peak at 454 nm (Figure 42. The variability in the extinction coefficient is similar to that observed for drFP583 (SEQ ID NO:221) and, similarly, it is dependant on the state of maturity, as well as the conditions under which the protein is expressed (Baird *et al.,* 2000, *supra*).

Site directed mutagenesis

Rtms-5 (SEQ ID NO:166) was only weakly fluorescent. To enhance this, site-directed mutagenesis was carried out. The alignment of the Rtms-5 sequence (SEQ ID NO:166) with other sequences (Table 19) indicated that position 142 was occupied by the residue histine. A variant Rtms-5-H142S, containing the substitution H142S, was engineered by mutagenesis of pCRII-TOPO::RTms5 to produce pCRII-TOPO::RTms5-H142S. This

single substitution increased the quantum yield of far-red fluorescence by 170-fold to a quantum yield of less than 0.02. Minor effects on the excitation and emission spectra and the absorption spectra were observed (4 nm shift towards the blue end of the spectrum, refer to Figure 42A,B,C).

Analysis of oligomeric structure

dsRed583 (SEQ ID NO:221) is known to be an obligate tetramer. The formation of oligomers by fluorescent proteins can present a serious problem when expressed fused to other proteins of interest. Consequently, it was important to establish the degree of oligomerisation of Rtms-5 (SEQ ID NO:166). The protein has a predicted size of 25,820 Da (with H6). When subjected to SDS-PAGE under reducing conditions, purified Rtms-5 (SEQ ID NO:166) migrated with an M_r of 26,900. However, under non-reducing conditions the majority of the protein migrated with an M_r of 114,000. These results indicated that native Rtms-5 (SEQ ID NO:166) was predominantly a tetramer.

Further site directed mutagenesis and analysis of structure

A second round of site-directed mutagenesis was carried out, to mutagenise CRII-TOPO::RTms5-H142S to produce the variant pCRII-TOP-RTms5-H142S-F158H (pCRII::Rtms-5v). This colored peptide contained the additional substitutions F158H and R145H, and is designated Rtms-5v (SEQ ID NO:216).

Rtms-5v (SEQ ID NO:216) was expressed in *E. coli* and the purified six His-tagged protein was subjected to analytical ultracentrifugation. The results indicated that the mutagenised variant sedimented predominantly as a monomer (82%, 30,700 Da) with the remaining proportion sedimenting as a dimer (18%, 50,800 Da). This colored protein fluoresced in the far-red range (see Figure 42C), and can be used effectively in yeast cells and mammalian cells.

Effect of site directed mutagenesis of other colored proteins

Site directed mutagenesis of residue H or N 142 to S, in other colored protein sequences, also leads to the generation of far-red fluorescence. Examples of the excitation and emission spectra for two other colored proteins, Aams-4 (SEQ ID NO:90)-H142S, and Rtms-1 (SEQ ID NO:162)-N142S are shown in Figure 43.

EXAMPLE 19

Expression in yeast, mammals and as a fusion protein

The subject inventors sought to demonstrate that the instant CFMs can be expressed in yeast and mammalian cells and can be used as fusion proteins for genetic marking of cells.

(a) *Expression in yeast*

For expression in yeast cells a *Bam*HI/*Not*1 DNA cassette encoding dsRed or YGFP3 (an enhanced variant for expression in yeast) or a *Bgl*II/*Not*1 cassette encoding the novel fluorescent protein, Rtms-5v (SEQ ID NO:216), were retrieved using the pair of oligonucleotide primers RFPUP1 (SEQ ID NO:234), /RFPDO1 (SEQ ID NO:235), YGFP3UP (SEQ ID NO:232), /YGFP3DO (SEQ ID NO:233), or MSVIATUP (SEQ ID NO:236)/COFPDO (SEQ ID NO:237), respectively, using as templates the vectors pYGFP3 (Cormack *et al*., *Microbiology 143:* 303-11, 1977), pDsRed-1 [Clontech Industries] or cDNA for pCRII-TOPO::RTms-5v. In the case of YGFP3UP, the *Not*1 site was retrieved after digesting the PCR product from pGEM-T (Promega). The PCR product was cloned into the *Bam*HI/*Not*I site of the multi-copy yeast expression vector pAS1NB to produce pAS1NB::dsRedL, pAS1NB::YEGFP3L or pAS1NB::Rtms-5v from which the DNA cassette encoding wild-type GFP had been removed but retaining the multiple cloning sites of that vector and linker sequence of that vector [Prescott *et al*., *FEBS Letts. 411:* 97-101, 1997]. pASN1B is a derivative of pAS1N (Prescott *et al*., 1997, *supra*) in which a *Bam*H1 restriction site has been removed from the PGK promoter region. This

series of vectors allows the expression of fluorescent proteins not fused to a partner protein and provides.

SEQ ID NO:232 YGFP3UP

5'- GGATCCATCGCCACCATGTCTAAAGGTGAAGAATTATTCACTGG

SEQ ID NO:233 YGFP3DO

5'- CAGCTGTTATTTGTACAATTCATCCATACCATGG

SEQ ID NO:234 RFPUP1

5'- CGGGATCCATCGCCACCATGAGGTCTTCCAAGAATGTTATC

SEQ ID NO:235 RFPDO1

5'- GAGGATCCGCGGCCGCTAAAGGAACAGATGG

SEQ ID NO:236 MSVIATUP

5'- GAAGATCTAAAACAATGAGTGTGATCGCTACACAAATG

SEQ ID NO:237 COFPDO

5'- TATCAAATCGCCGGCGTCAGGCGACCACAGGTTTG

(b) Expression as a fusion protein

Two DNA cassettes encompassing segments of the yeast genes ATP4 and ATP7 for subunit b and d of ATP synthase, respectively, were recovered by PCR from YRD15

genomic DNA using the oligonucleotide primer pairs ATP4PROMUP2 (SEQ ID NO:238)/ATP4DO2 (SEQ ID NO:239), or ATP7TUP (SEQ ID NO:240)/ATP3TDO (SEQ ID NO:241), respectively. The first, ATP4PO, encompasses the open reading frame for ATP4 and 500 bp of sequence upstream of the initiation codon flanked by *Bgl*II and *Bam*HI restriction sites at the 5' and 3', respectively. The *Bam*H1 restriction site allows for an in frame-fusion between the C-terminus of subunit b and each of the three fluorescent protein cassettes. The second, ATP7T, encompasses the transcription terminator cassette representing the terminator region of the ATP7 gene flanked at the 5' and 3' ends by restriction sites for *Not*I and *Sac*II, respectively. These restriction sites were obtained on cloning the PCR product into GEM-T. The ATP4PO & ATP7T DNA cassettes were cloned sequentially into the *Bam*HI and *NotI/Sac*II sites, respectively of the yeast expression vector pRS413 to produce the expression vector construction denoted pRS413::ATP4PO:ATP7T. A *Bgl*IIHI/*Not*I DNA fragment encoding YGFP3L was excised from pAS1NB::YEGFP3L and then cloned into the *Bgl*II/*Not*I site of pRS413::ATP4PO:ATP7T to produce a vector (pRS306::ATP4PO:YEGFP3L:ATP7T) encoding subunit b fused to YEGFP3 with a polypeptide linker of 25 amino acids. A vector (pRS413::ATP4PO:RTms-5:ATP7T or pRS413::ATP4PO:dsRed:ATP7T) encoding subunit b fused to RTms-5B or dsRed with a polypeptide linker of 27 amino acids was derived from pRS306::ATP4PO:YGFP3L:ATP7T by replacing the *Bam*HI/*Not*I fragment encoding YEGFP3 with an equivalent fragment encoding Rtms-5v or dsRed.

SEQ ID NO:238 ATP4PROMUP2

5'- <u>AGATCT</u>GTGTTGTGACGCAACTGCAACTCC

SEQ ID NO:239 ATP4DO2

5'- GTGATCAGC<u>GGATCC</u>CTTCAATTTAGAAAGCAATTGTTC

SEQ ID NO:240 ATP7TUP

5'- CCTCTATATATTACGCACCATATTC

SEQ ID NO:241 ATP7TDO

5'- ATACGTGACGACATTGGTAGTC

(c) Results were visualised using Clear Native Gels.

These were run essentially as described hereinafter. Briefly, 200 μg of mitochondrial protein was pelleted for 5 min at 100,000 g. Yeast mitochondria were isolated from spheropblasts (Law *et al.*, *Methods in Enzymol. 260:* 122-163, 1995). The pellet was solubilized in buffer (40 μl) containing in dodceyl β-maltoside to isolate the monomer form or digitonin (20 g/g protein) to isolate the dimer form and incubated on ice for 20 min and centrifuged 100,000 g for 30 min. Supernatants (30 μl) were loaded into wells of 4-16% gradient gels (13 cm x 10 cm x 0.075 cm). After running and while still between the glass plates, gels were imaged for fluorescence using a Perkin-Elmer multi-wavelength imager in 'edge-illumination mode' using appropriate filters for excitation (GFP, 480±20 nm; dsRed and Rtms-5v, 540±25 nm) and emission (GFP, 535±20 nm; dsRed, 590±35 nm; Rtms-5v, 620±30 nm).

DNA cassettes encoding subunit b fused to the N-terminus of each of the three fluorescent proteins were expressed in a yeast strain lacking expression of endogenous subunit b. The ATP synthase in each of these strains was established to be assembled and functional as cells of each strain were able to grow using the non-fermentable substrate ethanol as carbon source. Yeast cells lacking endogenous subunit b do not assemble functional mtATPase and cannot grow using ethanol as the sole carbon source. Yeast cells of each strain expressing the individual fusion proteins were visualized using fluorescence microscopy. For cells of each strain the distribution of fluorescence in the cell was similar and consistent with localisation to the mitochondrion.

Mitochondria were isolated from cells of each of the strains and, after extraction, ATP synthase complexes were subjected to analysis by clear native gel electrophoresis (CNGE). ATP synthase isolated from yeast is a large membrane bound complex (~800 kDa for the monomeric form) made up of 20 different types of subunits some of which are present in the complex as more than one copy. The complex can be isolated as a monomer or a dimer depending on the detergent, dodceyl β-maltoside or digitonin, respectively, used to extract the complex from mitochondrial membranes. Subunit b is present in a single copy in the monomer. ATP synthase in this experiment was extracted from each preparation of mitochondria under conditions that favour the isolation of the monomer. Subunit b is present in a single copy in the monomer. Samples were subjected to analysis by CNGE and the gel imaged for fluorescence using conditions of illumination and light detection specific for each fluorescent protein (Figure 47). A single fluorescent band corresponding to the position of assembled monomeric ATP synthase was observed for complexes containing the b-GFP fusion protein (Figure 47, lane 1). The position of GFP not fused to another protein is shown (Figure 47, lane 4). A single fluorescent band was seen for complexes containing the fusion protein b-Rtms-5v (Figure 47, lane 2). However, multiple bands were observed for samples containing b-dsRed Figure 47, lane 3). It is possible that, in order of decreasing mobility, each fluorescent band corresponds to a monomer, dimer, trimer and tetramer.

(d) *For expression in mammals*

For expression in mammalian cells, a *SmaI/Not*I fragment encoding Rtms-5v (SEQ ID NO:216) was excised from pAS1NB::RTms-5v and cloned into the expression site of the mammalian expression vector pCI-Neo (Promega Corporation, Madison USA). This vector allows the expression of Rtms-5v not fused to a partner protein.

A major benefit of fluorescent protein technology is the ability to simultaneously monitor using spectrally distinct variants more than one event in the living cell. The spectral properties of Rtms-5v suggest that should be feasible to image both dsRed and Rtms-5v

expressed in the same cell. This would allow Rtms-5 to be used in combination with dsRed rather than substitute for dsRed. The emission maxima for dsRed and Rtms-5v are separated by 50 nm. We tested the possibility of imaging dsRed, RTms-5v and EGFP expressed in the same cell. Three individual DNA cassettes were constructed encoding dsRed fused at its N-terminus to the 16 amino acid mitochondrial targeting sequence of human 3-oxoacyl-CoA thiolase, EGFP fused to the C-terminus of Rab6 and Rtms-5v not fused to any other protein. Cells were imaged using a Zeiss 510 Meta confocal laser scanning microscopy (Zeiss). The distribution of fluorescence arising from each of the Rtms-5v, dsRed and EGFP fusions was consistent with the locations expected (cytosol/nucleus, mitochondrion and golgi, respectively). These results show that Rtms-5v is able to fluorescently label other compartments of the cell such as the mitochondrion in addition to the cytoplasm. The position of a non-transfected and, therefore, non-fluorescent cell is shown in the transmitted light image by the white arrow Rtms-5v showed no evidence of aggregation. Similar results were observed for the expression of Rtms-5v not targeted in yeast cells. Multiple fluorescent proteins are commonly (eg. GFP, dsRed, CFP) imaged in the same cell.

EXAMPLE 20

Additional color proteins from coral

The inventors sought additional color proteins from two corals, *Montipora efforescens* and *Pavona decussaca.*

(a) *Montipora efforescens*

Standard purification techniques (Dove *et al.*, 2001, *supra*) were adopted for the purification of a red fluorescent protein from phosphate buffer extract of *M. efforescens*. A protein was purified using gel filtration and subject to N-terminal amino acid sequencing. A polymorphism was identified, comprising F and R residues. The N-terminal amino acid sequences are represented as follows:

SPPDY TLE**F**P KKXVA	SEQ ID NO:242
SPPDY TLE**R**P KKGVA	SEQ ID NO:243

The polymorphism is indicated in bold larger type.

(b) *Pavona decussaca*

Similar techniques as those described in (a), above, were used to identify and purify a green fluorescent protein from *P. decussaca.* Gel electrophoresis showed that the proteins ran as two bands and N-terminal amino acid sequencing identified polymorphic variants, shown in bold larger type, below:

Top band:

(D)SS(P)E SYL**K**N GIAEE MKTDV MEGI	**SEQ ID NO:244**

Lower band:

S**YLP**N GIAEE MKTDL MEGIV NG	**SEQ ID NO:245**
S**LYQ**N GIAEE MKTDL MEGIV NG	**SEQ ID NO:246**

The protein fraction was generating these N-terminal sequences had absorbed maximally at 440 nm with maximal excitation at 440 nm and emission at 488 nm.

Oligonucleotide probes were designed in both forward and reverse directions for PCR amplification from a ZAP express cDNA library of *Acropora millepora* (Scleractinian coral). The oligonucleotide primers used were as follows:

Forward

MEGIVNG-A	ATG GAA GGG ATA GTC GAT GG	**SEQ ID NO:247**
MEGIVNG-T	ATG GAA GGG ATT GTC GAT GG	**SEQ ID NO:248**

MEGIVNG-C	ATG GAA GGG ATC GTC GAT GG	**SEQ ID NO:249**

Reverse

REV-MEG-T	CCT CGA CAA TCC CTT CCA T	**SEQ ID NO:250**
REV-MEG-C	CCT CGA CGA TCC CTT CCA T	**SEQ ID NO:251**

DNA was amplified and separated using gel electrophoresis. Bands were purified and cloned into pCRII-TOPO and transfected into TOP 10 cells (Invitrogen). Plasmids were then purified and subjected to nucleotide sequencing. The complete sequence is shown in Table 23.

In this experiment, therefore, a protein identified from *P. decussaca* was used to identify a clone from *Acropora millepora.*

Those skilled in the art will appreciate that the invention described herein is susceptible to variations and modifications other than those specifically described. It is to be understood that the invention includes all such variations and modifications. The invention also includes all of the steps, features, compositions and compounds referred to or indicated in this specification, individually or collectively, and any and all combinations of any two or more of said steps or features.

TABLE 2

Class	SubClass	Order	GFP	Initial studies	Sequence information	%identity$^{(length)}$ *
Hydrozoa		Hydroida	yes	Shimomura *et al., J. Cell. Comp. Physiol. 59:* 223-239, 1962; Morise *et al., Biochemistry 13:*2656-2662, 1974; Morin & Hastings , *J. Cell Physiol. 77:* 313-318, 1971	Prasher et al. (1992) Gene 111:229-33; Chalfie et al. (1994) Science 263:802-5; Inouye & Tsuji (1994) FEBS Lett. 341:277-80.	$23^{(238)}$
		Milliporina	yes		Invention	$95.0^{(220)}$ - $97.3^{(221)}$
		Stylasterine				
		Trachylina				
		Siphonophora				
		Chondrophora				
		Actinulida				
Anthozoa	Octocorallia (=Alcyonaria)	Gorgonacea				
		Telestacea				
		Pennatulacea (see pens & sea pansies)	yes	Morin & Hastings, *J. Cell Physiol. 77:* 313-318, 1977	WO 99/49019	$43.5^{(225)}$ & $43.5^{(225)}$
		Alcyonacea				
		Helioporacea				
		Stolonifera	yes		Matz *et al., Nature Biotechnology 17:* 969-973, 1999	$52.7^{(226)}$
	Hexacorallia (=Zoantharia)	Actiniaria (sea anemones)	yes		Matz *et al., Nature Biotechnology 17:* 969-973; 1999; Lukyanov *et al., JBC 275:* 25879-25882, 2000	$46.2^{(227)}$ & $47.2^{(223)}$
		Scleractinia (true or stony corals)	yes	Kawaguti, *Paloa Trop. Boil. Stn. Stud. 2:* 617-673, 1994; Dove *et al. Biol. Bull. 189:* 288-297, 1995	WO 00/46233; Dove *et al., Coral Reefs 19:*197-204, 2001; Invention.	$93.2^{(220)}$ - $100^{(255)}$
		Zoanthidea	yes		Matz *et al., Nature Biotechnology 17:* 969-973, 1999	$44.1^{(231)}$ & $45.5^{(236)}$
		Corallimorpharia (coral-like anemones)	yes		Matz *et al., Nature Biotechnology 17:* 969-973, 1999	$57.8^{(225)}$ & $62.5^{(224)}$
	Ceriantipatharia	Antipatharia				

Class	SubClass	Order	GFP	Initial studies	Sequence information	%identity$^{(length)}$ *
		Ceriantharia				
Cubozoa						
Scyphozoa (jellyfish)		Stauromedusae	no			
		Coronatae				
		Semaeostomae				
		Rhizostaomae				

* Best fit in relation to Aams2-pep (SEQ ID NO:88) over 220-238 amino acids as indicated in length

TABLE 3 Fluorescent properties

Excitation region	Exciter filter	Dichroic mirror	Additional barrier filter
Ultra-violet	UG-1	DM400 + L420	L435
Violet	BP 405	DM455 +Y455	Y475
Blue	BP 490	DM500 + O515	O515
Green	BP 545	DM580 + O590	R610

TABLE 4 Class: Anthozoa; Order: Scleractinia

Family	Genus, Species	Color morph	Fluorescent properties
Pocilloporidae	*Pocillopora damicormis*	Pink	Faintgreen fluorescence under blue light
	Pocillopora damicormis	Green	Fluoresce blue-green, green, green and red under UV, violet, blue and green light, respectively
Acroporidae	*Acropora aspera*	Blue tipped	Tentacles and calices fluoresce violet, blue, green, and faint red under UV, violet, blue and green light, respectively
	Acropora aspera	Blue light fluorescent	Fluoresces green under UV and violet light
	Acropora nobilis	Green	Calices and tentacles fluorescent violet, blue, green and red under UV, violet, blue and green light, respectively
	Montipora sp. *(plating)*	Red/red fluorescent	Yellow fluorescence under blue light, red fluorescence under green light
Poritidae	*Porites murrayensis*	Purple	Calices fluoresce faint green under violet and blue light
Agariciidae	*Pavona decussaca*	Green	Blue under UV light; green under violet light; and blue and moderate red under green light
Mussidae	*Acanthasthastrea*	Green	Calices and polyps fluorescent violet, blue, green and faint under UV, violet, blue and green light, respectively
Faviidae	*Platygyra* sp.	Green	Blue under UV and violet light; green under blue light
	Caulastrea sp.	Green	Blue under UV light; green under violet and blue light

TABLE 5 Class: Hydrozoa; Order: Milleporina

Genus	Color	Fluorescent properties
Millepora	Green	Blue under UV and violet light; green under blue light

TABLE 6

N-terminus	Genus species	Name	Type	Amino acids within 5 Å of fluorophore
sgiat	*Acropora aspera*	Aams-5.pep	1	QVLSPQCQYGSIFWRNSYEHENMERLQCE
sviat	*Acropora aspera*	Aams-2.pep	1	QVLSPQCQYGSIFWRNSYEHENMERLQCE
sviat	*Acropora aspera*	Aams-4.pep	1	QVLSPQCQYGSIFWRNSYEHENMERLQCE
sviat	*Acropora aspera*	Aams-6.pep	1	QVLSPQCQYGSIFWRNSYEHENMERLQCE
sviat	*Acanthastrea sp.*	Acams-2.pep	6*	QVLSPQYQYGSIYWRNSYENENMERLQCE
sviat	*Acanthastrea sp.*	Acams-3.pep	6	QVLSPQYQYGSIYWRNSYENENMERLQCE
sviat	*Acanthastrea sp.*	Acams-4.pep	3	QVLSPQYQYGSIYWRNSHENENMERLQCE
sviat	*Acanthastrea sp.*	Acams-5.pep	*	
sviat	*Caulastrea sp.*	Cems-F.pep	5	QVLSPQCQYGNIFWRNSYEHENMGRLQCE
sviat	*Caulastrea sp.*	Cems-G.pep	5	QVLSPQCQYGNIFWRNSYEHENMGRLQCE
sviat	*Caulastrea sp.*	Cems-H.pep	5	QVLSPQCQYGNIFWRNSYEHENMGRLQCE
sviat	*Caulastrea sp.*	Cems-I.pep	16*	QVLSPQCQYGNIFWRNSYEHENMERLQCE
sviat	*Acropora nobilis*	LGAms-5.pep	6	QVLSPQYQYGSIYWRNSYENENMERLQCE
sviat	*Acropora nobilis*	LGAms-6.pep	18*	QVLSPQYQYGSIFWRNSYENENMERLQCE
sviat	*Millepora sp.*	Mi68Dms.pep	1	QVLSPQCQYGSIFWRNSYEHENMERLQCE
sviat	*Millepora sp.*	Mims-A.pep	1	QVLSPQCQYGSIFWRNSYEHENMERLQCE
sviat	*Millepora sp.*	Mims-B.pep	1	QVLSPQCQYGSIFWRNSYEHENMERLQCE
sviat	*Millepora sp.*	Mims-C.pep	1	QVLSPQCQYGSIFWRNSYEHENMERLQCE
sviat	*Pavona decussata*	Pav5ms.pep	6	QVLSPQYQYGSIYWRNSYENENMERLQCE
sviat	*Pavona decussata*	Pavms-2.pep	6*	QVLSPQYQYGSIYWRNSYENENMERLQCE
sviat	*Pavona decussata*	Pavms-3.pep	6	QVLSPQYQYGSIYWRNSYENENMERLQCE
sviat	*Pavona decussata*	Pavms-4.pep	11	QVLSPQYQYGSIYWGNSYENENMERLQCE
sviat	*Porites murrayensis*	PMms-A.pep	2	QVLSPQSQYGSIYWRNSYENENMERLQCE
sviat	*Porites murrayensis*	PMms-B.pep	2	QVLSPQSQYGSIYWRNSYENENMERLQCE
sviat	*Porites murrayensis*	PMms-C.pep	9	QVLSPQTQYGSIYWRNSYENGNMERLQCE
sviat	*Porites murrayensis*	PMms-D.pep	2	QVLSPQSQYGSIYWRNSYENENMERLQCE
sviat	*Porites murrayensis*	PMms-E.pep	2	QVLSPQSQYGSIYWRNSYENENMERLQCE
sviat	*Pink Pocillopora*	PPd57-1ms.pep	12	QVLSPQTQYGSIYWRNSYENENMERLQCE

N-terminus	Genus species	Name	Type	Amino acids within 5 Å of fluorophore
sviat	*Pink Pocillopora*	PPd57-2ms.pep	1	QVLSPQCQYGSIFWRNSYEHENMERLQCE
sviat	*Pink Pocillopora*	PPd57-3.pep	1	QVLSPQCQYGSIFWRNSYEHENMERLQCE
sviat	*Pink Pocillopora*	PPd57-4ms.pep	2	QVLSPQSQYGSIYWRNSYENENMERLQCE
sviat	*Platygyra sp.*	PPms-1.pep	8	RVLSPQCQYGNIFWRNSYEHENMGRLQCE
sviat	*Platygyra sp.*	PPms-2.pep	19*	QVLSPQYQYGSIFWRNSYENENMERLRCE
sviat	*Platygyra sp.*	PPms-E.pep	5	QVLSPQCQYGNIFWRNSYEHENMGRLQCE
sviat	*Platygyra sp.*	PPms-G.pep	13	QVLSPQCQYGNIFWGNSYEHENMGRLQCE
sviat	*Montipora sp.*	RTms-1.pep	6	QVLSPQYQYGSIYWRNSYENENMERLQCE
sviat	*Montipora sp.*	RTms-5.pep	1	QVLSPQCQYGSIFWRNSYEHENMERLQCE
svivt	*Montipora sp.*	RTms-6.pep	6	QVLSPQYQYGSIYWRNSYENENMERLQCE
svsat	*Montipora sp.*	RTms-2.pep	6	QVLSPQYQYGSIYWRNSYENENMERLQCE

TABLE 7

N-terminus	Species	Name	Type	Amino acids within 5 Å of fluorophore
sviak	*Acropora aspera*	Aasv-1.pep	15	QVLSPQSQYGSIYWRNSYENGNMERLQCE
sviak	*Acropora aspera*	Aasv-3.pep	14	QVLSPQSQYGSIYWRNSYENENMERLQRE
sviak	*Acropora aspera*	Aasv-P.pep	2	QVLSPQSQYGSIYWRNSYENENMERLQCE
sviak	*Acanthastria sp.*	Acasv-A.pep	4	QVLSPRCQYGNIFWRNSYEHENMGRLQCE
sviak	*Acanthastria sp.*	Acasv-C.pep	14	QVLSPQSQYGSIYWRNSYENENMERLQRE
sviak	*Acanthastria sp.*	Acasv-D.pep	1	QVLSPQCQYGSIFWRNSYEHENMERLQCE
sviak	*Caulastrea ap.*	Ce61-3sv.pep	14	QVLSPQSQYGSIYWRNSYENENMERLQRE
sviak	*Caulastrea ap.*	Ce61-4sv.pep	20	QVXSPQSQYGSXYWRNSYEHENMERLQCE
sviak	*Caulastrea ap.*	Ce61-5sv-rep.pep	18	QVLSPQCQYGSIFWRNSYEHENMESIQCE
sviak	*Caulastrea ap.*	Ce61-7sv-rep.pep	1	QVLSPQCQYGSIFWRNSYEHENMERLQCE
sviak	*Green Pocillopora*	GPd58-2sv.pep	2	QVLSPQSQYGSIYWRNSYENENMERLQCE
sviak	*Acropora nobilis*	LGAsv-A.pep	2	QVLSPQSQYGSIYWRNSYENENMERLQCE
sviak	*Acropora nobilis*	LGAsv-C.pep	1	QVLSPQCQYGSIFWRNSYEHENMERLQCE
sviak	*Acropora nobilis*	LGAsv-D.pep	2	QVLSPQSQYGSIYWRNSYENENMERLQCE
sviak	*Acropora nobilis*	LGAsv-E.pep	2	QVLSPQSQYGSIYWRNSYENENMERLQCE
sviak	*Millepora sp. (Hydrozoan)*	Misv-A.pep	14	QVLSPQSQYGSIYWRNSYENENMERLQRE
sviak	*Millepora sp. (Hydrozoan)*	Misv-B.pep	14	QVLSPQSQYGSIYWRNSYENENMERLQRE
sviak	*Millepora sp. (Hydrozoan)*	Misv-F.pep	14	QVLSPQSQYGSIYWRNSYENENMERLQRE
sviak	*Pavona decussaca*	Pavsv-A.pep	7	QVLSPQSQYGSVYWRNSYVNENMERLQCE
sviak	*Pavona decussaca*	Pavsv-B.pep	1	QVLSPQCQYGSIFWRNSYEHENMERLQCE
sviak	*Pavona decussaca*	Pavsv-C.pep	17	QVLSPQSQYGSVYWRNSYENENMERLQRE
sviak	*Porites Murrayensis*	PM1Asv-rep.pep	15	QVLSPQSQYGSIYWRNSYENGNMERLQCE
sviak	*Porites Murrayensis*	PM1Csv-rep.pep	2	QVLSPQSQYGSIYWRNSYENENMERLQCE
sviak	*Porites Murrayensis*	PMsv-4.pep	2*	QVLSPQSQYGSIYWRNSYENENM*
sviak	*Porites Murrayensis*	PMsv-5.pep	2	QVLSPQSQYGSIYWRNSYENENMERLQCE
sviak	*Platygyra sp.*	PPsv-1.pep	5	QVLSPQCQYGNIFWRNSYEHENMGRLQCE
sviak	*Platygyra sp.*	PPsv-2.pep	5	QVLSPQCQYGNIFWRNSYEHENMGRLQCE
sviak	*Platygyra sp.*	PPsv-3.pep	5	QVLSPQCQYGNIFWRNSYEHENMGRLQCE

N-terminus	Species	Name	Type	Amino acids within 5 Å of fluorophore
sviak	*Platygyra sp.*	PPsv-4.pep	4	QVLSPRCQYGNIFWRNSYEHENMGRLQCE
sviak	*Platygyra sp.*	PPsv-5.pep	2	QVLSPQSQYGSIYWRNSYENENMERLQCE
sviak	*Platygyra sp.*	PPsv-6.pep	10	QVLSPQSQYGSIYWRNSYENENMERLQCG
sviak	*Montipora sp.*	RTsv-1.pep	2	QVLSPQSQYGSIYWRNSYENENMERLQCE
sviak	*Montipora sp.*	RTsv-2.pep	2	QVLSPQSQYGSIYWRNSYENENMERLQCE
sviak	*Montipora sp.*	RTsv-3.pep	2	QVLSPQSQYGSIYWRNSYENENMERLQCE

TABLE 8 Percentage DNA sequence similarities generated using LALIGN

	A8	D1	D10	S1	S3	T1	T3
A8		97.3	98.7	97.7	99.6	97.5	99.9
D1			97.5	98.1	96.9	99.6	97.2
D10				98.2	98.2	97.6	98.5
S1					97.9	98.2	97.5
S3						97.0	99.4
T1							97.3
T3							

TABLE 9 Percentage amino acid sequence similarities generated using LALIGN

	A8	D1	D10	S1	S3	T1	T3
A8		95.5	98.2	97.3	99.1	96.0	100.0
D1			94.6	96.4	94.6	98.7	95.5
D10				96.4	97.3	95.1	98.2
S1					97.3	96.9	97.3
S3						95.1	99.1
T1							96.0
T3							

TABLE 10

Blue: λ_{max} = 589 - 593 nm
Type 1: QVLSPQCQYGSIFWRNSYEHENMERLQCE

Acasv-D = PavsvB
PPd57-2ms=PPd57-3

Mims-A =Mims-B
Aams-2 =Aams4

			λ_{max} =	
eq ID No: 166	RTms5.pep	BLUE	592	M S V I A T Q M T Y K V Y M S G T V N G H Y F E V E G D G K G K P Y E G E Q T V K L T V T K G G P L P F A W D I
eq ID No: 30	Acasv-D.pep	CLEAR		M S V I A K Q M T Y K V Y M S G T V N G H Y F E V E G D G K G K P Y E G E Q T V K L T V T K G G P L P F A W D I
eq ID No: 30	Acasv-D P161L.pep	BLUE		M S V I A K Q M T Y K V Y M S G T V N G H Y F E V E G D G K G K P Y E G E Q T V K L T V T K G G P L P F A W D I
eq ID No: 44	LGAsv-C.pep	BLUE	591	M S V I A K Q M T Y K V Y M S G T V N G H Y F E V E G D G K G K P Y E G E Q T V K L T V T K G G P L P F A W D I
eq ID No: 38	Ce61-7sv.pep	BLUE	591.5	M S V I A K Q M T Y X X Y X S G T V X G H Y F E V E G D G K G K P Y E G E Q T V K L T V T K G G P L P F A W D I
eq ID No: 122	Mims-A.pep	BLUE	589	M S V I A T Q M T Y K V Y M S G T V D G H Y F E V E G D G K G K P Y E G E Q T V K L T V T K G G P L P F A W D I
eq ID No: 124	Mims-B.pep	CLEAR		M S V I A T Q M T Y K V Y M S G T V D G H Y F E V E G D G K G K P Y E G E Q T V K L T V T K G G P L P F A W D I
eq ID No: 140	PPd57-2ms.pep	BLUE	593	M S V I A T Q M T Y K V Y M S G T V N G H Y F E V E G D G K G K P Y E G E Q T V R L T A T K G G P L P F A W D I
eq ID No: 88	Aams-2.pep	BLUE	592.5	M S V I A T Q M T Y K V Y M S G T V N G H Y F E V E G D G K G K P Y E G E Q T V R L T A T K G G P L P F A W D I

RTms5.pep	BLUE	592	L S P Q C Q Y G S I P F T K Y P E D I - - P D Y V K Q S F P E G F T W E R I M N F E D G A V C T V S N D S S I Q G N C F
Acasv-D.pep	CLEAR		L S P Q C Q Y G S I P F T K Y P E D I - - P D Y V K Q S F P E G F T W E R I M N F E D G A V C T V S N D S S I Q G N C F
Acasv-D P161L.pep	BLUE		L S P Q C Q Y G S I P F T K Y P E D I - - P D Y V K Q S F P E G F T W E R I M N F E D G A V C T V S N D S S I Q G N C F
LGAsv-C.pep	BLUE	591	L S P Q C Q Y G S I P F T K Y P E D I - - P D Y V K Q S F P E G F T W E R I M N F E D G A V C T V S N D S S I Q G N C F
Ce61-7sv.pep	BLUE	591.5	L S P Q C Q Y G S I P F T K Y P E D I - - P D Y V K Q S F P E G F T W E R I M N F E D G A V C T V S N D S S I Q G N C F
Mims-A.pep	BLUE	589	L S P Q C Q Y G S I P F T K Y P E D I - - P D Y V K Q S F P E G F T W E R I M N F E D G A V C T V S N D S S I Q G N C F
Mims-B.pep	CLEAR		L S P Q C Q Y G S I P F T K Y P E D I - - P D Y V K Q S F P E G F T W E R I M N F E D G A V C T V S N D S S I Q G N C F
PPd57-2ms.pep	BLUE	593	L S P Q C Q Y G S I P F T K Y P E D I - - P D Y V K Q S F P E G F T W E R I M N F E D G A V C T V S N G S S I Q G N C F
Aams-2.pep	BLUE	592.5	L S P Q C Q Y G S I P F T K Y P E D I - - P D Y V K Q S F P E G F T W E R I M N F E D G A V C T V S N D S S I Q G N C F

RTms5.pep	BLUE	592	T Y H V K F S G L N F P P N G P V M - Q K K T Q G W E P H S E R L F A - - R G G M L I G N N F M A L K L E G G G H Y L
Acasv-D.pep	CLEAR		T Y H V K F S G L N F P P N G P V M - Q K K T Q G W E P H S E R L F A - - R G G M L I G N N F M A R K L E G G G H Y L
Acasv-D P161L.pep	BLUE		T Y H V K F S G L N F P P N G P V M - Q K K T Q G W E P H S E R L F A - - R G G M L I G N N F M A L K L E G G G H Y L
LGAsv-C.pep	BLUE	591	T Y H V K F S G L D F P P D G P V M - Q K K T Q G W E P H S E R L F A - - R G G M L I G N N F M A L K L E G G G H Y L
Ce61-7sv.pep	BLUE	591.5	T Y H V K F S G L N F P P N G P V M - Q K K T Q G W E P H S E R L F A - - R G G M L I G N N F M A L K L E G G G H Y L
Mims-A.pep	BLUE	589	T Y H V K F S G L N F P P N G P V M - Q K K T Q G W E P H S E R L F A - - R G G M L I G N N F M A L K L E G G G H Y L
Mims-B.pep	CLEAR		T Y H V K F S G L N F P P N G P V M - Q K K T Q G W E P H S E R L F A - - R G G M L I G N N F M A L K L G G G G H Y L
PPd57-2ms.pep	BLUE	593	[illegible] Y H V K F S G L N F P P N G P V M - Q K K T Q G W E P H S E R L F A - - R D G M L I G N N F M A L K L E G G G H Y L
Aams-2.pep	BLUE	592.5	[illegible] Y H V K F S G L N F P P N G P V M - Q K K T Q G W E P H S E R L F A - - R D G M L I G N N F M A L K L E G G G H Y L

RTms5.pep	BLUE	592	C E F K T T Y K A K K - P V K M P G Y H Y V D R K L D V T N H N K D Y T S - V E Q C E I S I A R K P V V A
Acasv-D.pep	CLEAR		C E F K T T Y K A K K - P V K M P G Y H Y V D R K L D V T N H N K D Y T S - V E Q C E I S I A R K P V V A
Acasv-D P161L.pep	BLUE		C E F K T T Y K A K K - P V K M P G Y H Y V D R K L D V T N H N K D Y T S - V E Q C E I S I A R K P V V A
LGAsv-C.pep	BLUE	591	C E F K T T Y K A K K - P V K M P G Y H Y V D R K L D V T N H N K D Y T S - V E Q C E I S I A R K P V V A
Ce61-7sv.pep	BLUE	591.5	C E F K T T Y K A K K - P V K M P G Y H Y V D R K L D V T N H N K D Y T S - V E Q C E I S I A R K P V V A
Mims-A.pep	BLUE	589	C E F K T T Y K A K K - P V K M P G Y H Y V D R K L D V T N H N K D Y T S - V E Q C E I S I A R K P V V A
Mims-B.pep	CLEAR		C E F K T T Y R A K K - P V K M P G Y H Y V D R K L D V T N H N K D Y T S - V E Q C E I S I A R K P V V A
PPd57-2ms.pep	BLUE	593	C E F K T T Y K A K K - P V K M P G Y H Y V D R K L D V T N H N K D Y T S - V E Q C E I S I A R K P V V A
Aams-2.pep	BLUE	592.5	C E F K T T Y K A K K - P V K M P G Y H Y V D R K L D V T N H N K D Y T S - V E Q C E I S I [illegible] R K P V V A

TABLE 11

Type 2: QVLSPQSQYGSIYWRNSYENENVERLQCE

PMms-B = PMms-E = PPd57-4ms
LGAsv-A = LGAsv-D = GPd58-2sv = PPsv5

RTsv-2 = Rtsv-3
gtCP* from Gurskaya *et al.* 2001 *FEBS Letters* 507

			λ_{max} =		
Seq ID No:82	RTsv-1.pep	purple		1	MSVIAKQMTYKVYMSGTVNGHYFEAEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDI
Seq ID No:48	LGAsv-E.pep	purple		1	MSVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDI
Seq ID No:46	LGAsv-D.pep	purple	579	1	MSVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDI
Seq ID No:84	RTsv-2.pep	purple	579.5	1	MSVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTEGGPLPFAWDI
Seq ID No:58	PM1Csv.pep	purple		1	MSVIAKQMTYKVYMSGTVNGHYFEVEGDGKGRPYEGEQTVKLTVTKGGPLPFAWDI
Seq ID No:62	PMsv-5.pep	purple	579	1	MSVIAKQMTYKVYMSGTVNGHYFEVQGDGKGKPYEGEQTVKLTVTKGGPLPFAWDI
Seq ID No:128	PMms-A.pep	clear		1	MSVIATQMTYKVYMRGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDI
Seq ID No:130	PMms-B.pep	purple	579.5	1	MSVIATQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDI
Seq ID No: 217	gtCP*	purple	580	1	MSVIAKQMTYKVYMSGTVNGHYFEVQGDGKGKPYEEEQTVKLTVTKGGPLPFAWDI

RTsv-1.pep	purple		57	LSPCSQYGSIPFTKYPEDI--PDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCF
LGAsv-E.pep	purple		57	LSPCSQYGSIPFTKYPEDI--PDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCF
LGAsv-D.pep	purple	579	57	LSPCSQYGSIPFTKYPEDI--PDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCF
RTsv-2.pep	purple	579.5	57	LSPCSQYGSIPFTKYPEDI--PDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCF
PM1Csv.pep	purple		57	LSPCSQYGSIPFTKYPEDI--PDYVKQSFPEGYTWERIMKFEDGAVCTVSNDSSMQGNCF
PMsv-5.pep	purple	579	57	LSPCSQYGSIPFTKYPEDI--PDYVKQSFPEGYTWERIMNFKDGAVCTVSNDSSIQGNCF
PMms-A.pep	clear		57	LSPCSQYGSIPFTKYPEDI--PDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCF
PMms-B.pep	purple	579.5	57	LSPCSQYGSIPFTKYPEDI--PDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCF
gtCP*	purple	580	57	LSPCSQYGSIPFTKYPEDI--PDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCF

RTsv-1.pep	purple		115	IYHVKFSGLNFPPNGPVM-QKKTQGWEPNTERLFA--RDGMLIGNNFMALKLEGGG HYL
LGAsv-E.pep	purple		115	IYHVKFSGLNFPPNGPVM-QKKTQGWEPNTERLFA--RDGMLIGNNFMALKLEGGG HYL
LGAsv-D.pep	purple	579	116	IYHVKFSGLNFPPNGPVM-QKKTQGWEPNTERLFA--RDGMLIGNNFMALKLEGGG HYL
RTsv-2.pep	purple	579.5	116	IYHVKFSGLNFPPCGPVM-QKKTQGWEPNTERLFA--RDGMLIGNNFMALKLEGGG HYL
PM1Csv.pep	purple		115	IYHVKFSGLNFPPNGPVM-QKKTQGWEPNTERLYA--RDGMLIGNNFMALKLEG[illegible]G HY[illegible]
PMsv-5.pep	purple	579	115	IYHVKFSGLNFPPNGPVM-QKKTQGWEPNTERLFA--RDGMLIGNNFMALKLEGGG HYL
PMms-A.pep	clear		115	IYHVKFSGLNFPPNGPVM-QKKTQGWEPNTERLYA--RDGMLIGNNFMALKLEGGG HYL
PMms-B.pep	purple	579.5	115	IYHVKFSGLNFPPNGPVM-QKKTQGWEPNTERLFA--RDGMLIGNNFMALKLEGGG HYL
gtCP*	purple	580	115	IYNVKFSGLNFPPNGPVM-QKKTQGWEPNTERLFA--RDGMLIGNNFMALKLEGGG HYL

RTsv-1.pep	purple		171	CEFKSTYKAKK-PVKMPGYHYVDRKLDVTNHNKDYTS-VEQCEISIARKPVVA
LGAsv-E.pep	purple		171	CEFKSTYKAKK-PVKMPGYHYVDRKLDVTNHNKDYTS-VEQCEISIARKPVVA
LGAsv-D.pep	purple	579	170	CEFKSTYKAKK-PVKMPGYHYVDRKLDVTNHNKDYTS-VEQCEISIARKPVVA
RTsv-2.pep	purple	579.5	171	CEFKSTYKAKK-PVKMPGYHYVDRKLDVTNHNKDYTS-VEQCEISIARKPVVA
PM1Csv.pep	purple		171	CEFKSTYKAKK-PVKMPGYHYVDRKLDVTNHNKDYTS-VEQCEISIARKPVVA
PMsv-5.pep	purple	579	171	CEFKSTYKAKK-PVKMPGYHYVDRKLDVTNHNKDYTS-VEQCEISIARKPVVA
PMms-A.pep	clear		171	CEFKSTYKAKK-PVKMPGYHYVDRKLDVTNHNKDYTS-VEQCEISIARKPVVA
PMms-B.pep	purple	579.5	171	CEFKSTYKAKK-PVKMPGYHYVDRKLDVTNHNKDYTS-VEQCEISIARKPVVA
gtCP*	purple	580	170	CEFKSTYKAKK-PVKMPGYHYVDRKLDVTNHN[illegible]DYTS-VEQCEISIARKPVVA

TABLE 12

Typo14: QVLSPQSQYGSIYWRNSYENENMERLQRE

Misv-B=Misv-F

			λ_{max} =		
Seq ID No:22	Aasv-3.pep	purple		1	MSVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLTVTKGGPLPFAWDI
Seq ID No:28	Acasv-C.pep	purple	579.5	1	MSVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLTVTKGGPLPFAWDI
Seq ID No:32	Ce61-3sv.pep	pink		1	MSVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLTVTKGGPLPFAWDI
Seq ID No:60	Misv-A.pep	purple		1	MSVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDI
Seq ID No:52	Misv-B.pep	purple	579	1	MSVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLTVTKGGPLPFAWDI
	Aasv-3.pep	purple		57	LSPQSQYGSIPFTKYPEDI--PDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCF
	Acasv-C.pep	purple	579.5	57	LSPQSQYGSIPFTKYPEDI--PDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCF
	Ce61-3sv.pep	pink		57	LSPQSQYGSIPFTKYPEDI--PDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCF
	Misv-A.pep	purple		57	LSPQSQYGSIPFTKYPEDI--PDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCF
	Misv-B.pep	purple	579	57	LSPQSQYGSIPFTKYPEDI--PDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCF
	Aasv-3.pep	purple		115	IYHVKFSGLNFPPNGPVM-QKKTQGWEPNTERLLA--RDGMLIGNNFMALKLEGGG-HYL
	Acasv-C.pep	purple	579.5	115	IYHVKFSGLNFPPNGPVM-QKKTQGWEPNTERLSA--RDGMLIGNNFMALKLEGGG-HYL
	Ce61-3sv.pep	pink		116	IYHVKFSGLNFPPNGPVM-QKKTQGWEPNTERLSA--RDGMLIGNNFMALKLEGGG-HYL
	Misv-A.pep	purple		115	IYHVKFSGLNFPPNGPVM-QKKTQGWEPNTERLFA--RDGMLIGNNFMALKLEGGG-HYL
	Misv-B.pep	purple	579	115	IYHVKFSGLNFPPNGPVM-QKKTQGWEPNTERLFA--RDGMLIGNNFMALKLEGGG-HYL
	Aasv-3.pep	purple		171	CEFKSTYKARK-PVKMPGYHYVDRKLDVTNHNKDYTS-VEQREISIARKPVVA
	Acasv-C.pep	purple	579.5	170	CEFKSTYKARK-PVKMPGYHCVDRKLDVTNHNKDYTS-VEQREISIARKPVVA
	Ce61-3sv.pep	pink		171	CEFKSTYKARK-PVKMPGYHYVDRKLDVTNHNKDYTS-VEQREISIARKPVVA
	Misv-A.pep	purple		171	CEFKSTYKARK-PVKMPGYHYVDRKLDVTNHNKDYTS-VEQREISIARKPVVA
	Misv-B.pep	purple	579	171	CEFKSTYKARK-PVKMPGYHYVDRKLDVTNHNKDYTS-VEQREISIARKPVVA

TABLE 13

Type 6: QVLSPQYQYGSIYWRNSYENENMERLQCE

			λ_{max} =		
Seq ID No:116	LGAms-5.pep	purple	583.5	1	MSVIATQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLTVTKGGPLPFAWDI
Seq ID No:162	RTms-1.pep	purple	584	1	MSVIATQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDI
Seq ID No:158	Pavms-3.pep	clear		1	MSVIATQVTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDI
Seq ID No:168	RTms-6.pep	purple	585.5	1	MSVIATQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDI
Seq ID No:164	RTms-2.pep	clear		1	MSVIATQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDI
	LGAms-5.pep	purple	583.5	57	LSPQYQYGSIPFTKYPEDI--PDYVKQFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCF
	RTms-1.pep	purple	584	57	LSPQYQYGSIPFTKYPEDI--PDYVKQFPEGYTWERIMNFEDGAVCAVSNDSSIQGNCF
	Pavms-3.pep	clear		57	LSPQYQYGSIPFTKYPEDI--PDYVKQFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCF
	RTms-6.pep	purple	585.5	57	LSPQYQYGSIPFTKYPEDI--PDYVKQFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCF
	RTms-2.pep	clear		57	LSPQYQYGSIPFTKYPEDI--PDYVKQFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCF
	LGAms-5.pep	purple	583.5	115	IYHVKFSGLNFPPNGPVM-QKKTQGWEPNTERLSA--RDGMLIGNNFMALKLEGGGHYL
	RTms-1.pep	purple	584	115	IYHVKFSGLNFPPNGPVM-QKKTQGWEPNTERLFA--RDGMLIGNNFMALKLEGGGHYL
	Pavms-3.pep	clear		116	IYHVKFSGLNFPPNGPVM-QKKTQGWEPNTERLFA--RDGMLIGNNFMALKLEGGGHYL
	RTms-6.pep	purple	585.5	115	IYHVKFSGLNFPPNGPVM-QKKTQGWEPNTERLFA--RDGMLIGNNFMALKLEGGGHYL
	RTms-2.pep	clear		115	IYHVKFSGLNFPPNGPVM-QKKTQGWEPNTERLFA--RDGMLIGNNFMALKLEGGGHYL
	LGAms-5.pep	purple	583.5	171	CEFKSTYKAKK-PVKMPGYHYVDRKLDVTNHNKDYTS-VEQCEISIARKPVVA

TABLE 14

Sequence types with no 520-600 nm absorbance producing non-coloured bacteria (clear)

Amino acids within 5 nm of chromophore with M of MSVIA = 1:

	name	Type	38	40	57	58	59	60	61	62	63	64	65	66	87	89	91	105	107	116	140	142	144	157	159	172	193	195	209	210	##	predominant coral pigment
Srq ID No:64	PPsv-1.pep	5	Q	V	L	S	P	Q	C	Q	Y	G	N	I	F	W	R	N	S	Y	E	H	E	N	M	G	R	L	Q	C	E	green fluorescent
Seq ID No:66	PPsv-2.pep	5	Q	V	L	S	P	Q	C	Q	Y	G	N	I	F	W	R	N	S	Y	E	H	E	N	M	G	R	L	Q	C	E	green fluorescent
Seq ID No:68	PPsv-3.pep	5	Q	V	L	S	P	Q	C	Q	Y	G	N	I	F	W	R	N	S	Y	E	H	E	N	M	G	R	L	Q	C	E	green fluorescent
Seq ID No:110	Cems-G.pep	5	Q	V	L	S	P	Q	C	Q	Y	G	N	I	F	W	R	N	S	Y	E	H	E	N	M	G	R	L	Q	C	E	green fluorescent
Seq ID No:112	Cems-H.pep	5	Q	V	L	S	P	Q	C	Q	Y	G	N	I	F	W	R	N	S	Y	E	H	E	N	M	G	R	L	Q	C	E	green fluorescent
Seq ID No:150	PPms-E.pep	5	Q	V	L	S	P	Q	C	Q	Y	G	N	I	F	W	R	N	S	Y	E	H	E	N	M	G	R	L	Q	C	E	green fluorescent
Seq ID No:108	Cems-F.pep	5	Q	V	L	S	P	Q	C	Q	Y	G	N	I	F	W	R	N	S	Y	E	H	E	N	M	G	R	L	Q	C	E	green fluorescent
Seq ID NO:152	PPms-G.pep	13	Q	V	L	S	P	Q	C	Q	Y	G	N	I	F	W	G	N	S	Y	E	H	E	N	M	G	R	L	Q	C	E	green fluorescent
Seq ID No:146	PPms-1.pep	8	R	V	L	S	P	Q	C	Q	Y	G	N	I	F	W	R	N	S	Y	E	H	E	N	M	G	R	L	Q	C	E	green fluorescent
Seq ID No:26	Acasv-A.pep	4	Q	V	L	S	P	R	C	Q	Y	G	N	I	F	W	R	N	S	Y	E	H	E	N	M	G	R	L	Q	C	E	green fluorescent
Seq ID No:70	PPsv-4.pep	4	Q	V	L	S	P	R	C	Q	Y	G	N	I	F	W	R	N	S	Y	E	H	E	N	M	G	R	L	Q	C	E	green fluorescent
Seq ID No:20	Aasv-1.pep	15	Q	V	L	S	P	Q	S	Q	Y	G	S	I	Y	W	R	N	S	Y	E	N	G	N	M	E	R	L	Q	C	E	green fluorescent
Seq ID No:56	PMlAsv.pep	15	Q	V	L	S	P	Q	S	Q	Y	G	S	I	Y	W	R	N	S	Y	E	N	G	N	M	E	R	L	Q	C	E	green fluorescent
Seq ID No:80	Pavsv-C.pep	17	Q	V	L	S	P	Q	S	Q	Y	G	S	V	Y	W	R	N	S	Y	E	N	E	N	M	E	R	L	Q	R	E	purple
Seq ID No:76	Pavsv-A.pep	7	Q	V	L	S	P	Q	S	Q	Y	G	S	V	Y	W	R	N	S	Y	V	N	E	N	M	E	R	L	Q	C	E	green fluorescent

Sequence types with some 520-600 nm absorbance producing pinky-purple bacteria

Amino acids within 5 nm of chromophore with M of MSVIA = 1:

name	Type	38	40	57	58	59	60	61	62	63	64	65	66	87	89	91	105	107	116	140	142	144	157	159	172	193	195	209	210	##	predominant coral pigment
Ce61-4sv	20	Q	V	X	S	P	Q	S	Q	Y	G	S	X	Y	W	R	N	S	Y	E	H	E	N	M	E	R	L	Q	C	E	green fluorescent
PPd57-1ms	12	Q	V	L	S	P	Q	[illegible]	Q	Y	G	S	I	Y	W	R	N	S	Y	E	N	E	N	M	E	R	L	Q	C	E	pink

TABLE 15 Conserved amino acid differences between blue and purple colored proteins

Position	Amino acid in blue proteins (n = 2)	Amino acid in purple proteins (n = 4)	Amino acid in blue-purple protein (n = 1)
41	Arg (charged, polar)	Lys (charged, polar)*	Arg
43	Ala (nonpolar)	Thr (uncharged, polar)	Ala
61	Cys (uncharged, polar)	Ser (uncharged, polar)	Cys
87	Phe (nonpolar)	Tyr (uncharged, polar)	Phe
142	His (charged, polar)	Asn (uncharged, polar)	Asn
143	Ser (uncharged, polar)	Thr (uncharged, polar)	Thr
175	Thr (uncharged, polar)	Ser (uncharged, polar)	Ser
198	Ile (nonpolar)	Thr (uncharged, polar)	Thr

* Amino acid position 41 of the purple protein encoded by D10 (SEQ ID NO:192) is Arg.

TABLE 16: Amount of colored protein (expressed as a percentage of total soluble protein) produced in cultures of *E. coli* and *S. cerevisiae*.

Species	Plasmid	CP clone	Colour	RHSCC	%CP
E.coli	pCGP2921	T1	blue	102A	50%
S. cerevisiae	pCGP3269	A8	purple	82B	8%
S. cerevisiae	pCGP3270	T1	blue	101C	6%

RHSCC = Royal Horticultural Society Colour Chart (Kew, UK)

TABLE 17 Summary of recombinant protein accumulation levels in plants after nuclear DNA transformation.

Protein	Plant	Targeting	Accumulation	Reference
Endoglucanase	Tobacco	Chloroplast (Tomato-Rubisco small subunit protein)	Up to 1.35 % TSP in leaves.	*Transgenic Res 9:* 43-54, 2000
PEPC	Rice	cytosol	Up to 12 % TSP in leaves.	*Nat Biotechnol. 17:* 22-23, 1999
Cystatin	Rice	cytosol	Up to 2 % TSP.	*Plant Mol Biol 30:* 149-157, 1996
Antibody	Arabid.	ER-retained (DIKDEL), ER-secreted	Up to 6 % TSP	*Eur J Biochem*
Spider Silk	Tobacco Potato	ER-retained	2 % + TSP in leaves and potato tubers	*Nat Biotechnol 19:* 573-577. 2000
Cry9Aa	Tobacco Potato Cauliflower Turnip	cytosol	0.3 % TSP in Tobacco leaves. Expression in other plants 0.1-0.03 %.	*Plant Sci 160:* 341-353, 2001
Xylanase GFP Alkaline phosphatase	Tobacco	ER-excreted in guttation fluid	3 % TSP (alk. phos.)	*Plant Physiol 124:* 927-934, 2000
GUS-Peptide vaccine	?	cytosol	Up to 3 %TSP	*FEBS Lett 488:* 13-17, 2001
Bt, NPTII	Tobacco	cytosol	Bt: 0.02% TSP NPTII: 0-07-0.27 % TSP	*Nature 328:* 33-37, 1987
AlMV-CP	Tobacco Tomato	cytosol	0.1 - 0.4 % TSP Tobacco 0.1 - 0.8 % TSP Tomato	*EMBO 6:* 1181 -1 1188, 1987
sGFP	Rice	Chloroplast (rbsS-Tp)	10 % of TSP. Much higher than cytoplasmic control (0.5 % TSP)	Plant & Animal Genome VII Conference 1999 abstract

TSP = total soluble protein

TABLE 18 Summary of recombinant protein accumulation levels in plants after Plastid DNA transformation.

Protein	Plant	Targeting	Accumulation	Reference
GFP	tobacco	Chloroplast expression	5 % TSP in leaves	*Plant Journal 27:* 257 - 265
Bt (cry2Aa2)	tobacco	Chloroplast expression	2-3 % TSPin leaves	*Proc Natl Acad Sci* 1840-1845, 1999
Bt (cry2Aa2)	?	Chloroplast expression	45.3 % TSP	*Nat Biotechnol 19:* 71-74, 2001
Somatotropin	Tobacco	Chloroplast expression	7 % + "more than 300-fold higher than a similar gene expressed using a nuclear transgenic approach"	*Nat Biotechnol 18:* 333-338, 2000
Bt (cry1Ac)	Tobacco	Chloroplast expression	3-5 % TSP in leaves	*Biotechnology 13:* 362-365, 1995
EPSPS	Tobacco	Chloroplast expression	10 % + TSP in leaves	*Plant J 25:* 261-270, 2001

TSP = total soluble protein

TABLE 19

```
Seq ID No:216  RTms5-v    1        MSVIATCMTYKVYMSGTVNGHYFEVEGDGKGKPYEGECTVKLTVTKGGPLPFAWDI
Seq ID No:166  RTms5      1        MSVIATCMTYKVYMSGTVNGHYFEVEGDGKGKPYEGECTVKITVTKGGPLPFAWDI
Seq ID No:217  gtCP       1        MSVIAKCMTYKVYMSGTVNGHYFEVQGDGKSKPYEGECTVKLTVTKGGPLPFAWDI
Seq ID No:218  poc4       1         SVTAKCMTYKVYMSGTVNGHYFEVEGDGKGKPYEGECTVRLTVTKGGPLPFAWDI
Seq ID No:219  baspoc3    1         SVIAKCMTYKVYMSGTVNGHYFEVEGDGKGKPYEGECTVRLAVTKGGPLPFAWDI
Seq ID No:220  dsFP593    1    MSCSKNVIKEFMRFKVRMEGTVNGHEFEIKGEGEGRPYEGHCSVKLMVTKGGPLPFAFDI
Seq ID No:221  drFP583    1    MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI
Seq ID No:222  gfp        1    MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTT-GKLPVPWPT

               RTms5-v   57    LSPCFCYGSIPFTKYPEDI--PDYVKCSFPEGFTWERIMNFEDGAVCTVSNDSSICGNCF
               RTms5     57    LSPCFCYGSIPFTKYPEDI--PDYVKCSFPEGFTWERIMNFEDGAVCTVSNDSSICGNCF
               gtCP      57    LSPCSCYGSIPFTKYPEDI--PDYVKCSFPEGYTWERIMNFEDGAVCTVSNDSSICGNCF
               poc4      56    LSPCSCYGSIPFTKYPEDI--PDYVKCSFPEGYTWERIMNFEDGAVCTVSNDSSICGNGF
               baspoc3   56    LSPCFCYGSIPFTKYPEDI--PDYVKCSFPGRYTWERIMNFEDGAVCTVSNDSSICGNGF
               dsFP593   61    LSPCFCYGSKVYVKHPADI--PDYKKLSFPEGFKWERVMNFEDGGVVTVSCDSSLKDGCF
               drFP583   61    LSPCFCYGNKVYVKHPADI--PDYKKLSFPEGFKWERVMNFEDGGVVTVTCDSSLGDGCF
               gfp       60    LVTTFSYGVCCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL

               RTms5-v  115    TYHVKFSGLNFPPNGPVM-GKKTCGWEPSSEHLFA--RGGMLIGNNHMALKLEGGG-HYL
               RTms5    115    TYHVKFSGLNFPPNGPVM-GKKTCGWEPHSERLFA--RGGMLIGNNFMALKLEGGG-HYL
               gtCP     115    IYNVKFSGLNFPPNGPVM-GKKTCGWEPNTERLFA--RDGMLLGNNFMALKLEGGG-HYL
               poc4     114    IYHVKFSGLNFPPNGPVM-GKKTCGWEPNTERLFA--RDGMLLGNNFMALKLEGGG-HYL
               baspoc3  114    IYHVKFSGLNFPPNGPVM-GKKTCGWEPNTERLFA--RDGMLLGNNFMALKLEGGG-HYL
               dsFP593  119    IYEVKFIGVNFPSDGPVM-CRRTRGWEASSERLYP--RDGVLKGDIHMALRLEGGG-HYL
               drFP583  119    IYKVKFIGVNFPSDGPVM-GKKTMGWEASTKRLYP--RDGVLKGEIHKALKLKDGG-HYL
               gfp      120    VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKCKNGIKVNFKIRHNIEDGSVQLA

               RTms5-v  171    CEFKTTYKAKK-PVKMPGYHYVDRKLDVTNHNKDYTS-VECCEISIARKPVVA
               RTms5    171    CEFKTTYKAKK-PVKMPGYHYVDRKLDVTNHNKDYTS-VECCEISIARKPVVA
               gtCP     171    CEFKSTYKAKK-PVKMPGYHYVDRKLDVTNHNIDYTS-VECCEISIARKPVVA
               poc4     170    CEFKSTYKAKK-PVRMPGYHYVDRKLDVTNHNKDYTS-VECCEISIARKPVVAWCFFRV>
               baspoc3  170    CEFKSTYKARK-PVKMPGYHYVDRKLDVTNHNKDYTS-VEGREISIARKPLVA
               dsFP593  175    VEFKSIYMVKKPSVCLPGYYYVDSKLDMTSHNEDYTIV-VEGYEKTCGRHHPFIKPLC
               drFP583  175    VEFKSIYMAKK-PVCLPGYYYVDSKLDITSHNEDYTI-VEGYERTEGRHHLFL
               gfp      180    DHYCCNTPIGDGPVLLPDNHYLSTCSALSKDPNEKRDHMVLLEFVTAAGIT
```

TABLE 20 Summary of Northern analysis of *Arabidopsis* transgenic plants

Construct number	**CP Cassette**	**Selectable marker**	**T1**	**SuRB**
pCGP2772	35S: T1: 35S	35S: SuRB	~0.9 kb	~2.2 kb
pCGP2765	35S: A8: 35S	35S: SuRB	~0.9 kb	~2.2 kb
pCGP3259	35S: ER:T1: 35S	35S: SuRB	~1.0 kb	~2.2 kb
pCGP2785	35S: SSU:T1: 35S	35S: SuRB	~1.1 kb	~2.2 kb
pCGP3258	35S: T1:GFP: 35S	35S: SuRB	~1.6 kb	~2.2 kb
pCGP3261	35S: ER:T1:GFP: 35S	35S: SuRB	~1.7 kb	~2.2 kb
pCGP960	35S: GUS	35S: SuRB	none	~2.2 kb
pBINmgfp4	35S: mGFP4: nos	35S : *npt*II	none	none
non transgenic	NA	NA	none	none

CP cassette = Colored protein cassette contained in construct;

SM cassette = the selectable marker gene contained in construct;

NA = not applicable;

none = no transcripts detected

TABLE 21 Estimations of T1 protein in leaf samples from 2 transgenic *Arabidopsis* events (expressed as a percentage of total protein)

Construct	Cassette	Acc #	Sample	%T1
pCGP3259	35S:ERT:T1:35S	1.5	leaf	0.005%
pCGP2772	35S:T1:35S	1.2b	leaf	0.005%

Construct = Binary vector used in transformation;

Cassette refers to the chimaeric T1 transgene contained in the T-DNA;

Acc# refers to the accession number of the transgenic plant.

TABLE 22: Estimations of T1 protein in petal and/or leaf samples from 2 transgenic *P. hybrida* events (expressed as a percentage of total protein)

Construct	Cassette	Acc #	Sample	%T1
pCGP3259	35S:ERT:T1:35S	24444	leaf	0.009%
pCGP2765	35S:A8:35S	24534	petal	0.02%
pCGP2765	35S:A8:35S	24534	leaf	0.006%

TABLE 23 Complete amino acid sequence of PdGFP-T3.pep

S Y L P N G I A E E M K T D L
Given N-terminal polymorphy ,

Continuing…

PdGFP-T3.pep

```
      1  MEGIVDGHKF VITGHGNGNP FEGKQTMNLC VVEGGPLPFS EDILSAAFDY

     51  GNRVFTEYPQ GMVDFFKNSC PAGYTWHRSL LFEDGAVCTT SADITVSVEE

    101  NCFYHNSKFH GVNFPADGPV MKKMTTNWEP SCEKIIPVPR QGILKGDIAM

    151  YLLLKDGGRY RCQFDTIYKA KSDPKEMPEW HFIQHKLTRE DRSDAKNQKW

    201  QLVEHAVASR SALPG*
```

```
  1  ATGGAAGGGA TTGTCGATGG GCATAAATTT GTGATCACGG GCCACGGCAA
 51  TGGAAATCCT TTCGAAGGGA AACAGACTAT GAATCTGTGT GTGGTTGAAG
101  GGGGACCCCT GCCATTCTCC GAAGACATTT TGTCTGCTGC GTTTGACTAC
151  GGAAACAGGG TCTTCACTGA ATATCCTCAA GGCATGGTTG ACTTTTTCAA
201  GAATTCATGT CCAGCTGGAT ACACATGGCA CAGGTCTTTA CTCTTTGAAG
251  ATGGAGCAGT TTGCACAACT AGTGCAGATA TAACAGTGAG TGTTGAGGAG
301  AACTGCTTTT ATCACAATTC CAAGTTTCAT GGAGTGAACT TTCCTGCTGA
351  TGGACCTGTG ATGAAAAAGA TGACAACTAA TTGGGAGCCA TCCTGCGAGA
401  AAATCATACC AGTACCTAGA CAGGGGATAT TGAAAGGGGA TATTGCCATG
451  TACCTTCTTC TGAAGGATGG TGGGCGTTAT CGGTGCCAGT TCGACACAAT
501  TTACAAAGCA AAGTCTGACC CGAAAGAGAT GCCGGAGTGG CACTTCATCC
551  AACATAAGCT CACCCGGGAA GACCGCAGCG ATGCTAAGAA CCAGAAATGG
601  CAACTGGTAG AACATGCTGT TGCTTCCCGA TCCGCATTGC CCGGATAAGA
651  ACATGATATA GTTCAAACAT GTTGTTACAT GCGCATGCTT ATTACTNTGA
701  TGACAATGTA GTTCGAGCCA GGCCAGTAGC AATAAAGCAC ATTTCAANCA
751  AAAAAAAAAA AAAAAAA
```

CLAIMS

1. An isolated nucleic acid molecule comprising a nucleotide sequence encoding a color-facilitating molecule (CFM) which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to said cell when visualized by a human eye in the absence of excitation by extraneous non-white light or particle emission.

2. The isolated nucleic acid molecule of Claim 1 wherein the CFM is derived from *Anemonia majano, Anemonia sulcata, Clavularia* sp, *Zoanthus* sp, *Discosoma* sp (e.g. *Discosoma striata*), *Aequorea* sp (e.g. *Aequorea victoria*), *Anthozoa* sp, *Cassiopea* sp, (e.g. *Cassiopea xamachana*), *Millepora* sp, *Acropora* sp (e.g. *Acropora aspera* and *Acropora nobilis*), *Montipora* sp, *Porites murrayensis*, *Pocillopora damicornis*, *Pavona descussaca*, *Acanthastrea* sp, *Platygyra* sp or *Caulastrea* sp.

3. The isolated nucleic acid molecule of Claim 1 or Claim 2 wherein the CFM comprises an amino acid sequence in its N-terminal end selected from SVIAK (SEQ ID NO:5), (M)SVIAT (SEQ ID NO:6), SGIAT (SEQ ID NO:7), SVIVT (SEQ ID NO:8) or SVSAT (SEQ ID NO:9).

4. The isolated nucleic acid molecule of Claim 3 wherein the CFM comprises an amino acid sequence selected from the list comprising SVIAT QMTY KVYM SGT (SEQ ID NO:10), SVIAT QMTY KVYM PGT (SEQ ID NO:11), SVIAT QVTY KVYM SGT (SEQ ID NO:12), SGIAT QMTY KVYM SGT (SEQ ID NO:13), SVIVT QMTY KVYM SGT (SEQ ID NO:14), SVSAT QMTY KVYM SGT (SEQ ID NO:15), SVIAK QMTY KVNM SGT (SEQ ID NO:16), SVIAK QMTY KVYM SDT (SEQ ID NO:17) and SVIAK QMTY $X_1X_2YX_3$ SGT (SEQ ID NO:18) wherein X_1, X_2 and X_3 may be any amino acid provided that X_1 is not K; X_2 is not V; X_3 is not M.

5. The isolated nucleic acid molecule of Claim 3 or Claim 4 wherein the CFM comprises an amino acid sequence selected from the list comprising SEQ ID NOs:20, 22,

24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 190, 192, 194, 196, 198, 200 and 202 provided that, where the said amino acid sequence comprises the sequence SVIAK QMTY $X_1X_2YX_3$ SGT, X_1 is not lysine, X_2 is not valine, and X_3 is not methionine or an amino acid sequence having at least 60% similarity to any one or more of the above referenced sequences.

6. The isolated nucleic acid molecule of Claim 5 comprising a nucleotide sequence encoding a color-facilitating molecule (CFM), wherein the nucleotide sequence is selected from the list comprising SEQ ID NOs:19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 189, 191, 193, 195, 197, 199 and 201 or a nucleotide sequence having at least 60% similarity to one or more of the above referenced sequences or a nucleotide sequence capable of hybridizing to one of the above referenced sequences or a complementary form thereof under low stringency conditions.

7. The isolated nucleic acid molecule of any one of Claims 1 to 6 wherein the cell is a prokaryotic cell.

8. The isolated nucleic acid molecule of any one of Claims 1 to 6 wherein the cell is a eukaryotic cell.

9. The isolated nucleic acid molecule of Claim 8 wherein the eukaryotic cell is a mammalian animal cell.

10. The isolated nucleic acid molecule of Claim 8 wherein the eukaryotic cell is a non-mammalian animal cell.

11. The isolated nucleic acid molecule of Claim 10 wherein the eukaryotic cell is a plant cell.

12. The isolated nucleic acid molecule of Claim 11 wherein the plant cell is part of a plant callus or a whole plant.

13. The isolated nucleic acid molecule of Claim 12 wherein the whole plant is an ornamental or flowering plant or a part thereof.

14. The isolated nucleic acid molecule of Claim 13 wherein the plant part is a flower, root, leaf, stem, seed, fruit or fiber.

15. The isolated nucleic acid molecule of Claim 13 wherein the plant is selected from a rose, carnation, lisianthus, petunia, lily, tulip, pansy, gerbera or chrysanthemum.

16. The isolated nucleic acid molecule of of any one of Claims 1 to 15 wherein the CFM is a GFP or derivative or homolog thereof.

17. The isolated nucleic acid molecule of Claim 16 wherein the homolog of GFP is a non-fluorescent GFP.

18. An isolated color-facilitating molecule (CFM) comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to said cell when visualized by a human eye in the absence of excitation by extraneous non-white light or particle emission.

19. The isolated CFM of Claim 18 wherein the CFM is derived from *Anemonia majano, Anemonia sulcata, Clavularia* sp, *Zoanthus* sp, *Discosoma* sp (e.g. *Discosoma striata*), *Aequorea* sp (e.g. *Aequorea victoria*), *Anthozoa* sp, *Cassiopea* sp, (e.g. *Cassiopea xamachana*), *Millepora* sp, *Acropora* sp (e.g. *Acropora aspera* and *Acropora nobilis)*,

Montipora sp, *Porites murrayensis*, *Pocillopora damicormis*, *Pavona descussaca*, *Acanthastrea* sp, *Platygyra* sp or *Caulastrea* sp.

20. The isolated CFM of Claim 19 wherein the CFM comprises an amino acid sequence in its N-terminal end selected from SVIAK (SEQ ID NO:5), (M)SVIAT (SEQ ID NO:6), SGIAT (SEQ ID NO:7), SVIVT (SEQ ID NO:8) or SVSAT (SEQ ID NO:9).

21. The isolated CFM of Claim 20 wherein the CFM comprises an amino acid sequence selected from the list comprising SVIAT QMTY KVYM SGT (SEQ ID NO:10), SVIAT QMTY KVYM PGT (SEQ ID NO:11), SVIAT QVTY KVYM SGT (SEQ ID NO:12), SGIAT QMTY KVYM SGT (SEQ ID NO:13), SVIVT QMTY KVYM SGT (SEQ ID NO:14), SVSAT QMTY KVYM SGT (SEQ ID NO:15), SVIAK QMTY KVNM SGT (SEQ ID NO:16), SVIAK QMTY KVYM SDT (SEQ ID NO:17) and SVIAK QMTY $X_1X_2YX_3$ SGT (SEQ ID NO:18) wherein X_1, X_2 and X_3 may be any amino acid provided that X_1 is not K; X_2 is not V; X_3 is not M.

22. The isolated CFM of Claim 21 wherein the CFM comprises a polypeptide having an amino acid sequence selected from the list comprising SEQ ID NOs:20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 190, 192, 194, 196, 198, 200 and 202 provided that, where the said amino acid sequence comprises the sequence SVIAK QMTY $X_1X_2YX_3$ SGT, X_1 is not lysine, X_2 is not valine, and X_3 is not methionine or an amino acid sequence having at least 60% similarity to any one or more of the above referenced sequences.

23. The isolated CFM of Claim 18 wherein the cell is a prokaryotic cell.

24. The isolated CFM of Claim 18 wherein the cell is a eukaryotic cell.

25. The isolated CFM of Claim 24 wherein the eukaryotic cell is a mammalian animal cell.

26. The isolated CFM of Claim 24 wherein the eukaryotic cell is a non-mammalian animal cell.

27. The isolated CFM of Claim 26 wherein the non-mammalian animal cell is a plant cell.

28. The isolated CFM of Claim 27 wherein the plant cell is part of a plant callus or a whole plant.

29. The isolated CFM of Claim 28 wherein the whole plant is an ornamental or flowering plant or a part thereof.

30. The isolated CFM of Claim 29 wherein the plant part is a flower, root, leaf, stem, seed, fruit or fiber.

31. The isolated CFM of Claim 29 wherein the plant is selected from a rose, carnation, lisianthus, petunia, lily, tulip, pansy, gerbera or chrysanthemum.

32. The isolated CFM of any one of Claims 18 to 31 wherein the CFM is a GFP or derivative or homolog thereof.

33. The isolated CFM of Claim 32 wherein the homolog of GFP is a non-fluorescent GFP.

34. An isolated cell wherein said cell or a parent cell is genetically modified to enable the production of a color-facilitating molecule (CFM) which alone or together with one or more other molecules imparts an altered visual characteristic to said cell when visualized by a human eye in the absence of excitation by extraneous non-white light or

particle emission.

35. The isolated cell of Claim 34 wherein the CFM is derived from *Anemonia majano, Anemonia sulcata, Clavularia* sp, *Zoanthus* sp, *Discosoma* sp (e.g. *Discosoma striata*), *Aequorea* sp (e.g. *Aequorea victoria*), *Anthozoa* sp, *Cassiopea* sp, (e.g. *Cassiopea xamachana*), *Millepora* sp, *Acropora* sp (e.g. *Acropora aspera* and *Acropora nobilis)*, *Montipora* sp, *Porites murrayensis*, *Pocillopora damicormis*, *Pavona descussaca*, *Acanthastrea* sp, *Platygyra* sp or *Caulastrea* sp.

36. The isolated cell of Claim 35 wherein the CFM comprises an amino acid sequence in its N-terminal end selected from SVIAK (SEQ ID NO:5), (M)SVIAT (SEQ ID NO:6), SGIAT (SEQ ID NO:7), SVIVT (SEQ ID NO:8) or SVSAT (SEQ ID NO:9).

37. The isolated cell of Claim 36 wherein the CFM comprises a polypeptide having an amino acid sequence selected from the list comprising SVIAT QMTY KVYM SGT (SEQ ID NO:10), SVIAT QMTY KVYM PGT (SEQ ID NO:11), SVIAT QVTY KVYM SGT (SEQ ID NO:12), SGIAT QMTY KVYM SGT (SEQ ID NO:13), SVIVT QMTY KVYM SGT (SEQ ID NO:14), SVSAT QMTY KVYM SGT (SEQ ID NO:15), SVIAK QMTY KVNM SGT (SEQ ID NO:16), SVIAK QMTY KVYM SDT (SEQ ID NO:17) and SVIAK QMTY $X_1X_2YX_3$ SGT (SEQ ID NO:18) wherein X_1, X_2 and X_3 may be any amino acid provided that X_1 is not K; X_2 is not V; X_3 is not M.

38. The isolated cell of Claim 36 or 37 wherein the CFM comprises a polypeptide having an amino acid sequence selected from the list comprising SEQ ID NOs:20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 190, 192, 194, 196, 198, 200 and 202 provided that, where the said amino acid sequence comprises the sequence SVIAK QMTY $X_1X_2YX_3$ SGT, X_1 is not lysine, X_2 is not valine, and X_3 is not methionine or an amino acid sequence having at least 60% similarity to any

one or more of the above referenced sequences.

39. The isolated cell of Claim 34 wherein the cell is a prokaryotic cell.

40. The isolated cell of Claim 34 wherein the cell is a eukaryotic cell.

41. The isolated cell of Claim 40 wherein the eukaryotic cell is a mammalian cell such as from a livestock animal (e.g. sheep, pig, horse, goat, llama, cow) or part thereof (e.g. wool, leather).

42. The isolated cell of Claim 40 wherein the eukaryotic cell is a non-mammalian animal cell (e.g. avian species such as ostrichs, emus, ducks, chickens, turkeys).

43. The isolated cell of Claim 40 wherein the eukaryotic cell is a plant cell.

44. The isolated plant cell of Claim 43 wherein the cell is part of a plant callus or a whole plant.

45. The isolated plant cell of Claim 44 wherein the whole plant is an ornamental or flowering plant or a part thereof.

46. The isolated plant cell of Claim 45 wherein the plant part is a flower, root, leaf, stem, seed, fruit or fiber.

47. The isolated plant cell of Claim 45 wherein the plant is selected from a rose, carnation, lisianthus, petunia, lily, tulip, pansy, gerbera or chrysanthemum.

48. The isolated cell of Claim 34 wherein the CFM is a GFP or derivative or homolog thereof.

49. The isolated cell of Claim 48 wherein the homolog of GFP is a non-fluorescent GFP homolog thereof.

50. A plant or part of a plant wherein said plant or plant part comprises cells genetically modified to enable production of a CFM which alone or in combination with one or other molecules imparts an altered visual characteristic to said cells when visualized by a human eye in the absence of excitation by extraneous non-white light or particle emission.

51. The plant or part of a plant of Claim 50 wherein the CFM is derived from *Anemonia majano, Anemonia sulcata, Clavularia* sp, *Zoanthus* sp, *Discosoma* sp (e.g. *Discosoma striata*), *Aequorea* sp (e.g. *Aequorea victoria*), *Anthozoa* sp, *Cassiopea* sp, (e.g. *Cassiopea xamachana*), *Millepora* sp, *Acropora* sp (e.g. *Acropora aspera* and *Acropora nobilis)*, *Montipora* sp, *Porites murrayensis*, *Pocillopora damicormis*, *Pavona descussaca*, *Acanthastrea* sp, *Platygyra* sp or *Caulastrea* sp.

52. The plant or part of a plant of Claim 51 wherein the CFM comprises an amino acid sequence in its N-terminal end selected from SVIAK (SEQ ID NO:5), (M)SVIAT (SEQ ID NO:6), SGIAT (SEQ ID NO:7), SVIVT (SEQ ID NO:8) or SVSAT (SEQ ID NO:9).

53. The plant or part of a plant of Claim 51 wherein the CFM comprises a polypeptide having an amino acid sequence selected from the list comprising SVIAT QMTY KVYM SGT (SEQ ID NO:10), SVIAT QMTY KVYM PGT (SEQ ID NO:11), SVIAT QVTY KVYM SGT (SEQ ID NO:12), SGIAT QMTY KVYM SGT (SEQ ID NO:13), SVIVT QMTY KVYM SGT (SEQ ID NO:14), SVSAT QMTY KVYM SGT (SEQ ID NO:15), SVIAK QMTY KVNM SGT (SEQ ID NO:16), SVIAK QMTY KVYM SDT (SEQ ID NO:17) and SVIAK QMTY $X_1X_2YX_3$ SGT (SEQ ID NO:18) wherein X_1, X_2 and X_3 may be any amino acid provided that X_1 is not K; X_2 is not V; X_3 is not M.

54. The plant or part of a plant of Claim 53 wherein the CFM comprises a

polypeptide having an amino acid sequence selected from the list comprising SEQ ID NOs:20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 190, 192, 194, 196, 198, 200 and 202 provided that, where the said amino acid sequence comprises the sequence SVIAK QMTY $X_1X_2YX_3$ SGT, X_1 is not lysine, X_2 is not valine, and X_3 is not methionine or an amino acid sequence having at least 60% similarity to any one or more of the above referenced sequences.

55. The plant or part of a plant of Claim 50 wherein the whole plant is an ornamental or flowering plant or a part thereof.

56. The plant or part of a plant of Claim 55 wherein the plant part is a flower, root, leaf, stem, seed, fruit or fiber.

57. The plant or part of a plant of Claim 55 wherein the plant is selected from a rose, carnation, lisianthus, petunia, lily, tulip, pansy, gerbera or chrysanthemum.

58. The plant or part of a plant of Claim 50 wherein the CFM is a GFP or derivative or homolog thereof.

59. The plant or part of a plant of Claim 58 wherein the homolog of GFP is a non-fluorescent GFP.

60. A cut flower from a plant of any one of Claims 50 to 59.

61. An extract from a plant or part of a plant of any one of Claims 50 to 59.

62. The extract of Claim 61 wherein the extract is a flavoring or food additive, beverage or juice, or coloring agent.

63. Isolated hemp material from a plant of any one of Claims 50 to 54, 58 or 59.

64. Cotton from a plant of any one of Claims 50 to 54, 58 or 59.

65. A composition comprising a CFM of any one of Claims 18 to 33.

66. A method for generating a transgenic plant or part of a plant, wherein said plant or plant part comprises cells genetically modified to enable production of a CFM which alone or in combination with one or other molecules imparts an altered visual characteristic to said cells when visualized by a human eye in the absence of excitation by extraneous non-white light or particle emission, said method comprising introducing into said cells an isolated nucleic acid molecule comprising a nucleotide sequence selected from the list comprising SEQ ID NOs:19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 189, 191, 193, 195, 197, 199 and 201 or a nucleotide sequence having at least 60% similarity to one or more of the above referenced sequences or a nucleotide sequence capable of hybridizing to one of the above referenced sequences or a complementary form thereof under low stringency conditions and regenerating a transgenic plant therefrom.

67. The method of Claim 66 wherein said CFM is derived from *Anemonia majano, Anemonia sulcata, Clavularia* sp, *Zoanthus* sp, *Discosoma* sp (e.g. *Discosoma striata*), *Aequorea* sp (e.g. *Aequorea victoria*), *Anthozoa* sp, *Cassiopea* sp, (e.g. *Cassiopea xamachana*), *Millepora* sp, *Acropora* sp (e.g. *Acropora aspera* and *Acropora nobilis*), *Montipora* sp, *Porites murrayensis*, *Pocillopora damicornis*, *Pavona descussaca*, *Acanthastrea* sp, *Platygyra* sp or *Caulastrea* sp.

68. The method of Claim 67 wherein the CFM comprises an amino acid

sequence in its N-terminal end selected from SVIAK (SEQ ID NO:5), (M)SVIAT (SEQ ID NO:6), SGIAT (SEQ ID NO:7), SVIVT (SEQ ID NO:8) or SVSAT (SEQ ID NO:9).

69. The method of Claim 67 wherein the CFM comprises a polypeptide having an amino acid sequence selected from the list comprising SVIAT QMTY KVYM SGT (SEQ ID NO:10), SVIAT QMTY KVYM PGT (SEQ ID NO:11), SVIAT QVTY KVYM SGT (SEQ ID NO:12), SGIAT QMTY KVYM SGT (SEQ ID NO:13), SVIVT QMTY KVYM SGT (SEQ ID NO:14), SVSAT QMTY KVYM SGT (SEQ ID NO:15), SVIAK QMTY KVNM SGT (SEQ ID NO:16), SVIAK QMTY KVYM SDT (SEQ ID NO:17) and SVIAK QMTY $X_1X_2YX_3$ SGT (SEQ ID NO:18) wherein X_1, X_2 and X_3 may be any amino acid provided that X_1 is not K; X_2 is not V; X_3 is not M.

70. The method of Claim 69 wherein the CFM comprises a polypeptide having an amino acid sequence selected from the list comprising SEQ ID NOs:20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 190, 192, 194, 196, 198, 200 and 202 provided that, where the said amino acid sequence comprises the sequence SVIAK QMTY $X_1X_2YX_3$ SGT, X_1 is not lysine, X_2 is not valine, and X_3 is not methionine or an amino acid sequence having at least 60% similarity to any one or more of the above referenced sequences.

71. The method of Claim 66 wherein the plant part is plant callus.

72. The method of Claim 66 wherein the plant part is a flower, root, leaf, stem, seed, fruit or fiber.

73. The method of Claim 66 wherein the plant is an ornamental or flowering plant or a part thereof.

74. The method of Claim 73 wherein the plant is selected from a rose, carnation, lisianthus, petunia, lily, tulip, pansy, gerbera or chrysanthemum.

75. The method of Claim 66 wherein the CFM is a GFP or derivative or homolog thereof.

76. The method of Claim 75 wherein the homolog of GFP is a non-fluorescent GFP homolog thereof.

77. An isolated antibody specific for a CFM, said CFM comprising an amino acid sequence in its N-terminal end selected from SVIAK (SEQ ID NO:5), (M)SVIAT (SEQ ID NO:6), SGIAT (SEQ ID NO:7), SVIVT (SEQ ID NO:8) or SVSAT (SEQ ID NO:9).

78. The isolated antibody of Claim 77 wherein the CFM comprises a polypeptide having an amino acid sequence selected from the list comprising SVIAT QMTY KVYM SGT (SEQ ID NO:10), SVIAT QMTY KVYM PGT (SEQ ID NO:11), SVIAT QVTY KVYM SGT (SEQ ID NO:12), SGIAT QMTY KVYM SGT (SEQ ID NO:13), SVIVT QMTY KVYM SGT (SEQ ID NO:14), SVSAT QMTY KVYM SGT (SEQ ID NO:15), SVIAK QMTY KVNM SGT (SEQ ID NO:16), SVIAK QMTY KVYM SDT (SEQ ID NO:17) and/or SVIAK QMTY $X_1X_2YX_3$ SGT (SEQ ID NO:18) wherein X_1, X_2 and X_3 may be any amino acid provided that X_1 is not K; X_2 is not V; X_3 is not M.

79. The isolated antibody of Claim 77 or 78, wherein the CFM comprises a polypeptide having an amino acid sequence selected from the list comprising SEQ ID NOs:20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 190, 192, 194, 196, 198, 200 and/or 202 or an amino acid sequence having at least 60% similarity to any one or more of the above referenced sequences.

80. A biomatrix comprising a CFM, said CFM comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to said cell when visualized by a human eye in the absence of excitation by extraneous non-white light or particle emission.

81. The biomatrix of Claim 80 wherein the CFM is derived from *Anemonia majano, Anemonia sulcata, Clavularia* sp, *Zoanthus* sp, *Discosoma* sp (e.g. *Discosoma striata*), *Aequorea* sp (e.g. *Aequorea victoria*), *Anthozoa* sp, *Cassiopea* sp, (e.g. *Cassiopea xamachana*), *Millepora* sp, *Acropora* sp (e.g. *Acropora aspera* and *Acropora nobilis)*, *Montipora* sp, *Porites murrayensis, Pocillopora damicormis, Pavona descussaca, Acanthastrea* sp, *Platygyra* sp or *Caulastrea* sp.

82. The biomatrix of Claim 81 wherein the CFM comprises an amino acid sequence in its N-terminal end selected from SVIAK (SEQ ID NO:5), (M)SVIAT (SEQ ID NO:6), SGIAT (SEQ ID NO:7), SVIVT (SEQ ID NO:8) or SVSAT (SEQ ID NO:9).

83. The biomatrix of Claim 82 wherein the CFM comprises a polypeptide having an amino acid sequence selected from the list comprising SVIAT QMTY KVYM SGT (SEQ ID NO:10), SVIAT QMTY KVYM PGT (SEQ ID NO:11), SVIAT QVTY KVYM SGT (SEQ ID NO:12), SGIAT QMTY KVYM SGT (SEQ ID NO:13), SVIVT QMTY KVYM SGT (SEQ ID NO:14), SVSAT QMTY KVYM SGT (SEQ ID NO:15), SVIAK QMTY KVNM SGT (SEQ ID NO:16), SVIAK QMTY KVYM SDT (SEQ ID NO:17) and SVIAK QMTY $X_1X_2YX_3$ SGT (SEQ ID NO:18) wherein X_1, X_2 and X_3 may be any amino acid provided that X_1 is not K; X_2 is not V; X_3 is not M.

84. The biomatrix of Claim 83 wherein the CFM comprises a polypeptide having an amino acid sequence selected from the list comprising SEQ ID NOs:20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150,

152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 190, 192, 194, 196, 198, 200 and 202 provided that, where the said amino acid sequence comprises the sequence SVIAK QMTY $X_1X_2YX_3$ SGT, X_1 is not lysine, X_2 is not valine, and X_3 is not methionine or an amino acid sequence having at least 60% similarity to any one or more of the above referenced sequences.

85. The biomatrix of Claim 80 wherein the cell is a prokaryotic cell.

86. The biomatrix of Claim 80 wherein the cell is a eukaryotic cell.

87. The biomatrix of Claim 86 wherein the eukaryotic cell is a mammalian animal cell.

88. The biomatrix of Claim 86 wherein the eukaryotic cell is a non-mammalian animal cell.

89. The biomatrix of Claim 88 wherein the non-mammalian animal cell is a plant cell.

90. The biomatrix of Claim 89 wherein the plant cell is part of a plant callus or a whole plant.

91. The biomatrix of Claim 90 wherein the whole plant is an ornamental or flowering plant or a part thereof.

92. The biomatrix of Claim 91 wherein the plant part is a flower, root, leaf, stem, seed, fruit or fiber.

93. The biomatrix of Claim 91 wherein the plant is selected from a rose, carnation, lisianthus, petunia, lily, tulip, pansy, gerbera or chrysanthemum.

94. The biomatrix of any one of Claims 80 to 93, wherein the CFM is a GFP or derivative or homolog thereof.

95. The biomatrix of Claim 94 wherein the homolog of GFP is a non-fluorescent GFP.

96. The biomatrix of any one of Claims 80 to 95 wherein the said biomatrix is a sunscreen.

97. The biomatrix of any one of Claims 80 to 95 wherein the said biomatrix is a cosmetic,

98. The biomatrix of any one of Claims 80 to 95 wherein the said biomatrix is a light-filtering composition.

99. The biomatrix of any one of Claims 80 to 95 wherein the said biomatrix is a photon trap.

100. The biomatrix of any one of Claims 80 to 95 wherein the said biomatrix is a reporter molecule.

101. A diagnostic assay comprising screening for the presence of a CFM wherein the nucleic acid molecule encoding said CFM is expressed in a cell.

102. The diagnostic assay of Claim 101 wherein said nucleic acid molecule comprises a nucleotide sequence encoding a CFM comprising a polypeptide having an amino acid sequence in its N-terminal end selected from SVIAK (SEQ ID NO:5), (M)SVIAT (SEQ ID NO:6), SGIAT (SEQ ID NO:7), SVIVT (SEQ ID NO:8) or SVSAT (SEQ ID NO:9).

103. The diagnostic assay of Claim 102 wherein said nucleic acid molecule

comprises a nucleotide sequence encoding a CFM comprising a polypeptide having an amino acid sequence selected from the list comprising SVIAT QMTY KVYM SGT (SEQ ID NO:10), SVIAT QMTY KVYM PGT (SEQ ID NO:11), SVIAT QVTY KVYM SGT (SEQ ID NO:12), SGIAT QMTY KVYM SGT (SEQ ID NO:13), SVIVT QMTY KVYM SGT (SEQ ID NO:14), SVSAT QMTY KVYM SGT (SEQ ID NO:15), SVIAK QMTY KVNM SGT (SEQ ID NO:16), SVIAK QMTY KVYM SDT (SEQ ID NO:17) and SVIAK QMTY $X_1X_2YX_3$ SGT (SEQ ID NO:18) wherein X_1, X_2 and X_3 may be any amino acid provided that X_1 is not K; X_2 is not V; X_3 is not M.

104. The diagnostic assay of Claim 103 wherein said nucleic acid molecule comprises a nucleotide sequence encoding a CFM comprising the CFM comprises a polypeptide having an amino acid sequence selected from the list comprising SEQ ID NOs:20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 190, 192, 194, 196, 198, 200 and 202 provided that, where the said amino acid sequence comprises the sequence SVIAK QMTY $X_1X_2YX_3$ SGT, X_1 is not lysine, X_2 is not valine, and X_3 is not methionine or an amino acid sequence having at least 60% similarity to any one or more of the above referenced sequences.

105. The diagnostic assay of any one of Claims 101 to 104 wherein said nucleic acid molecule comprises a nucleotide sequence selected from the list comprising SEQ ID NOs:19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 189, 191, 193, 195, 197, 199 and 201 or a nucleotide sequence having at least 60% similarity to one or more of the above referenced sequences or a nucleotide sequence capable of hybridizing to one of the above referenced sequences or a complementary form thereof under low stringency conditions.

106. The diagnostic assay of Claim 101 wherein the CFM comprises an amino acid sequence in its N-terminal end selected from SVIAK (SEQ ID NO:5), (M)SVIAT (SEQ ID NO:6), SGIAT (SEQ ID NO:7), SVIVT (SEQ ID NO:8) or SVSAT (SEQ ID NO:9).

107. The diagnostic assay of Claim 101 wherein the CFM comprises a polypeptide having an amino acid sequence selected from the list comprising SVIAT QMTY KVYM SGT (SEQ ID NO:10), SVIAT QMTY KVYM PGT (SEQ ID NO:11), SVIAT QVTY KVYM SGT (SEQ ID NO:12), SGIAT QMTY KVYM SGT (SEQ ID NO:13), SVIVT QMTY KVYM SGT (SEQ ID NO:14), SVSAT QMTY KVYM SGT (SEQ ID NO:15), SVIAK QMTY KVNM SGT (SEQ ID NO:16), SVIAK QMTY KVYM SDT (SEQ ID NO:17) and SVIAK QMTY $X_1X_2YX_3$ SGT (SEQ ID NO:18) wherein X_1, X_2 and X_3 may be any amino acid provided that X_1 is not K; X_2 is not V; X_3 is not M.

108. The diagnostic assay of Claim 107 wherein the CFM comprises a polypeptide having an amino acid sequence selected from the list comprising SEQ ID NOs:20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 190, 192, 194, 196, 198, 200 and 202 provided that, where the said amino acid sequence comprises the sequence SVIAK QMTY $X_1X_2YX_3$ SGT, X_1 is not lysine, X_2 is not valine, and X_3 is not methionine or an amino acid sequence having at least 60% similarity to any one or more of the above referenced sequences.

109. Use of a nucleic acid molecule encoding a CFM, said CFM, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to said cell when visualized by a human eye in the absence of excitation by extraneous non-white light or particle emission, in the manufacture of a cell which produces said CFM.

110. Use of the CFM of Claim 109 wherein the cell is a prokaryotic cell.

111. Use of the CFM of Claim 109 wherein the cell is a eukaryotic cell.

112. Use of the CFM according to Claim 111 wherein the eukaryotic cell is a mammalian animal cell.

113. Use of the CFM according to Claim 111 wherein the eukaryotic cell is a non-mammalian cell.

114. Use of the CFM according to Claim 113, wherein the non-mammalian cell is a plant cell.

```
[SEQ ID NO:20]   Aasv-1.pep         SVIAKQMTYKVYMSDTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQS
[SEQ ID NO:22]   Aasv-3.pep         SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLTVTKGGPLPFAWDILSPQS
[SEQ ID NO:24]   Aasv-P.pep         SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQS
[SEQ ID NO:26]   Acasv-A.pep        SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPRC
[SEQ ID NO:28]   Acasv-C.pep        SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLTVTKGGPLPFAWDILSPQS
[SEQ ID NO:30]   Acasv-D.pep        SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQC
[SEQ ID NO:32]   Ce61-3sv.pep       SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLTVTKGGPLPFAWDILSPQS
[SEQ ID NO:34]   Ce61-4sv.pep       SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTXGGPLPFAWDIXSPQS
[SEQ ID NO:36]   Ce61-5sv.pep       SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQC
[SEQ ID NO:38]   Ce61-7sv.pep       SVIAKQMTY  Y SGTVXGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQC
[SEQ ID NO:40]   GPd58-2sv.pep      SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQS
[SEQ ID NO:42]   LGAsv-A.pep        SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQS
[SEQ ID NO:44]   LGAsv-C.pep        SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQC
[SEQ ID NO:46]   LGAsv-D.pep        SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQS
[SEQ ID NO:48]   LGAsv-E.pep        SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTEGGPLPFAWDILSPQS
[SEQ ID NO:50]   Misv-A.pep         SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQS
[SEQ ID NO:52]   Misv-B.pep         SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLTVTKGGPLPFAWDILSPQS
[SEQ ID NO:54]   Misv-F.pep         SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLTVTKGGPLPFAWDILSPQS
[SEQ ID NO:56]   PM1Asv-rep.pep     SVIAKQMTYKVYMSDTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQS
[SEQ ID NO:58]   PM1Csv-rep.pep     SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGRPYEGEQTVKLTVTKGGPLPFAWDILSPQS
[SEQ ID NO:60]   PMsv-4.pep         SVIAKQMTYKVYMSGTVNGHYFXVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQS
[SEQ ID NO:62]   PMsv-5.pep         SVIAKQMTYKVYMSGTVNGHYFEVQGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQS
[SEQ ID NO:64]   PPsv-1.pep         SVIAKQMTYKVYMSGTVNGHYFEVEGDRKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQC
[SEQ ID NO:66]   PPsv-2.pep         SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQC
[SEQ ID NO:68]   PPsv-3.pep         SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQC
[SEQ ID NO:70]   PPsv-4.pep         SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPRC
[SEQ ID NO:72]   PPsv-5.pep         SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQS
[SEQ ID NO:74]   PPsv-6.pep         SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQS
[SEQ ID NO:76]   Pavsv-A.pep        SVIAKQMTYKVNMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTEGGPLPFAWDILSPQS
[SEQ ID NO:78]   Pavsv-B.pep        SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQC
[SEQ ID NO:80]   Pavsv-C.pep        SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTEGGPLPFAWDILSPQS
[SEQ ID NO:82]   RTsv-1.pep         SVIAKQMTYKVYMSGTVNGHYFEAEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQS
[SEQ ID NO:84]   RTsv-2.pep         SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQS
[SEQ ID NO:86]   RTsv-3.pep         SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQS
                                    *********    * ******** .** **.********.**** *************..
```

Figure 1

```
[SEQ ID NO:20]   Aasv-1.pep         QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYNVKFS
[SEQ ID NO:22]   Aasv-3.pep         QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS
[SEQ ID NO:24]   Aasv-P.pep         QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIVNFEDGAVCTVSNDSSIQGNCFIYNVKFS
[SEQ ID NO:26]   Acasv-A.pep        QYGNIPFTKYPEDVPDYVKQSFPEGFTWERIMNFEDGAVCTVSNDSSIQGNCFTYHVKFS
[SEQ ID NO:28]   Acasv-C.pep        QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS
[SEQ ID NO:30]   Acasv-D.pep        QYGSIPFTKYPEDIPDYVKQSFPEGFTWERIMNFEDGAVCTVSNDSSIQGNCFTYHVKFS
[SEQ ID NO:32]   Ce61-3sv.pep       QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS
[SEQ ID NO:34]   Ce61-4sv.pep       QYGSXPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS
[SEQ ID NO:36]   Ce61-5sv.pep       QYGSIPFTKYPEDIPDYVKQSFPEGFTWERIMNFEDGAVCTVSNDSSIQGNCFTYHVKFS
[SEQ ID NO:38]   Ce61-7sv.pep       QYGSIPFTKYPEDIPDYVKQSFPEGFTWERIMNFEDGAVCTVSNDSSIQGNCFTYHVKFS
[SEQ ID NO:40]   GPd58-2sv.pep      QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYNVKFS
[SEQ ID NO:42]   LGAsv-A.pep        QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYNVKFS
[SEQ ID NO:44]   LGAsv-C.pep        QYGSIPFTKYPEDIPDYVKQSFPEGFTWERIMNFEDGAVCTVSNDSSIQGNCFTYHVKFS
[SEQ ID NO:46]   LGAsv-D.pep        QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYNVKFS
[SEQ ID NO:48]   LGAsv-E.pep        QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYNVKFS
[SEQ ID NO:50]   Misv-A.pep         QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS
[SEQ ID NO:52]   Misv-B.pep         QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS
[SEQ ID NO:54]   Misv-F.pep         QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS
[SEQ ID NO:56]   PM1Asv-rep.pep     QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYNVKFS
[SEQ ID NO:58]   PM1Csv-rep.pep     QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMKFEDGAVCTVSNDSSMQGNCFIYNVKFS
[SEQ ID NO:60]   PMsv-4.pep         QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIVNFEDGAVCTVSNDSSIQGNCFIYNVKFS
[SEQ ID NO:62]   PMsv-5.pep         QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFKDGAVCTVSNDSSIQGNCFIYNVKFS
[SEQ ID NO:64]   PPsv-1.pep         QYGNIPFTKYPEDVPDYVKQSFPEGFTWERIMNFEDGAVCTVSNDSSIQGNCFTYHVKFS
[SEQ ID NO:66]   PPsv-2.pep         QYGNIPFTKYPEDVPDYVKQSFPEGFTWERIMNFEDGAVCTVSNDSSIQGNCFTYHVKFS
[SEQ ID NO:68]   PPsv-3.pep         QYGNIPFTKYPEDVPDYVKQSFPEGFTWERIMNFEDGAVCTVSNDSSIQGNCFTYHVKFS
[SEQ ID NO:70]   PPsv-4.pep         QYGNIPFTKYPEDVPDYVKQSFPEGFTWERIMNFEDGAVCTVSNDSSIQGNCFTYHVKFS
[SEQ ID NO:72]   PPsv-5.pep         QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYNVKFS
[SEQ ID NO:74]   PPsv-6.pep         QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGSCFIYNVKFS
[SEQ ID NO:76]   Pavsv-A.pep        QYGSVPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYNVKFS
[SEQ ID NO:78]   Pavsv-B.pep        QYGSIPFTKYPEDIPDYVKQSFPEGFTWERIMNFEDGAVCTVSNDSSIQGNCFTYHVKFS
[SEQ ID NO:80]   Pavsv-C.pep        QYGSVPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS
[SEQ ID NO:82]   RTsv-1.pep         QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYNVKFS
[SEQ ID NO:84]   RTsv-2.pep         QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYNVKFS
[SEQ ID NO:86]   RTsv-3.pep         QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYNVKFS
                                    ***  ********.***********.*****. * ************.** ** *.****
```

Figure 1 continued

```
[SEQ ID NO:20]  Aasv-1.pep         GLNFPPNGPVMQKKTQGWEPNTGRLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKK
[SEQ ID NO:22]  Aasv-3.pep         GLNFPPNGPVMQKKTQGWEPNTERLLARDGMLIGNNFMALKLEGGGHYLCEFKSTYKARK
[SEQ ID NO:24]  Aasv-P.pep         GLNFPPNGPVMQKKTQGWEPNTERLYARDGMLIGNNFMALKLEGGQRSL*----------
[SEQ ID NO:26]  Acasv-A.pep        GLNFPPNGPVMQKKTRGWEPHSERLFARGGMLIGNNFMALKLEGGGHYLCGFKTTYKAKK
[SEQ ID NO:28]  Acasv-C.pep        GLNFPPNGPVMQKKTQGWEPNTERLSARDGMLIGNNFMALKLEGGGHYLCEFKSTYKARK
[SEQ ID NO:30]  Acasv-D.pep        GLNFPPNGPVMQKKTQGWEPHSERLFARGGMLIGNNFMAPKLEGGGHYLCEFKTTYKAKK
[SEQ ID NO:32]  Ce61-3sv.pep       GLNFPPNGPVMQKKTQGWEPNTERLSARDGMLIGNNFMALKLEGGGHYLCEFKSTYKARK
[SEQ ID NO:34]  Ce61-4sv.pep       GLNFPPNGPVMQKKTQGWEPHSERLFARDGMLIGNNFMALKXEGGGXYLCEFKSTYKAKK
[SEQ ID NO:36]  Ce61-5sv.pep       GLNFPPNGPVMQKKTQGWEPHSERLFARGGMLIGNNFMALKLEGGGHYLCEFKTTYKAKK
[SEQ ID NO:38]  Ce61-7sv.pep       GLNFPPNGPVMQKKTQGWEPHSERLFARGGMLIGNNFMALKLEGGGHYLCEFKTTYKAKK
[SEQ ID NO:40]  GPd58-2sv.pep      GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKK
[SEQ ID NO:42]  LGAsv-A.pep        GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKK
[SEQ ID NO:44]  LGAsv-C.pep        GLDFPPNGPVMQKKTQGWEPHSERLFARGGMLIGNNFMALKLEGGGHYLCEFKTTYKAKK
[SEQ ID NO:46]  LGAsv-D.pep        GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKK
[SEQ ID NO:48]  LGAsv-E.pep        GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKK
[SEQ ID NO:50]  Misv-A.pep         GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKARK
[SEQ ID NO:52]  Misv-B.pep         GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKARK
[SEQ ID NO:54]  Misv-F.pep         GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKARK
[SEQ ID NO:56]  PM1Asv-rep.pep     GLNFPPNGPVMQKKTQGWEPNTGRLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKK
[SEQ ID NO:58]  PM1Csv-rep.pep     GLNFPPNGPVMQKKTQGWEPNTERLYARDGMLIGNNFMALKLEGSGHYTCEFKSTYKAKK
[SEQ ID NO:60]  PMsv-4.pep         GLNFPPNGPVMQKKTQGWEPNTERLYARDGMLIGNNFMALKLEGGQRSL*----------
[SEQ ID NO:62]  PMsv-5.pep         GLNFPPNGPVMQKKTQGWEPNTERLFARDGVLIGNNFMALKLEGGGHYLCEFKSTYKAKK
[SEQ ID NO:64]  PPsv-1.pep         GLNFPPNGPVMQKKTQGWEPHSERLFARGGMLIGNNFMALKLEGGGHYLCGFKTTYKAKK
[SEQ ID NO:66]  PPsv-2.pep         GLNFPPNGPVMQKKTQGWEPHSERLFARGGMLIGNNFMALKLEGGGHYLCGFKTTYKAKK
[SEQ ID NO:68]  PPsv-3.pep         GLNFPPNGPVMQKKTQGWEPHSERLFARGGMLIGNNFMALKLEGGGHYLCGFKTTYKAKK
[SEQ ID NO:70]  PPsv-4.pep         GLNFPPNGPVMQKKTRGWEPHSERLFARGGMLIGNNFMALKLEGGGHYLCGFKTTYKAKK
[SEQ ID NO:72]  PPsv-5.pep         GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKK
[SEQ ID NO:74]  PPsv-6.pep         GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKK
[SEQ ID NO:76]  Pavsv-A.pep        GLNFPPNGPVMQKKTQGWVPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKK
[SEQ ID NO:78]  Pavsv-B.pep        GLNFPPNGPVMQKKTQGWEPHSERLFARGGMLIGNNFMAPKLEGGGHYLCEFKTTYKAKK
[SEQ ID NO:80]  Pavsv-C.pep        GLNFPPNGPVMQKKTQGWEPNTERLSARDGMLIGNNFMALKLEGGGHYLCEFKSTYKARK
[SEQ ID NO:82]  RTsv-1.pep         GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKK
[SEQ ID NO:84]  RTsv-2.pep         GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKK
[SEQ ID NO:86]  RTsv-3.pep         GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKK
                                   ** ************.** *.. ** ** *.******** ****       ** **** *
```

Figure 1 continued

```
[SEQ ID NO:20]  Aasv-1.pep        PVMMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA----------
[SEQ ID NO:22]  Aasv-3.pep        PVKMPGYHYVDRKLDVTNHNKDYTSVEQREISIARKPVVA----------
[SEQ ID NO:24]  Aasv-P.pep        --------------------------------------------------
[SEQ ID NO:26]  Acasv-A.pep       PVKMPGYHYVDRKLDVTNHNKDYISVEQCEISIARKPVVA----------
[SEQ ID NO:28]  Acasv-C.pep       PVKMPGYHCVDRKLDVTNHNKDYTSVEQREISIARKPVVA----------
[SEQ ID NO:30]  Acasv-D.pep       PVKMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA----------
[SEQ ID NO:32]  Ce61-3sv.pep      PVKMPGYHYVDRKLDVTNHNKDYTSVEQREISIARKPVVA----------
[SEQ ID NO:34]  Ce61-4sv.pep      PVMMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA----------
[SEQ ID NO:36]  Ce61-5sv.pep      PVKMPGYHYVYSTIHVTNHNKDYTSVEQCEISXXRKPVVA----------
[SEQ ID NO:38]  Ce61-7sv.pep      PVKMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA----------
[SEQ ID NO:40]  GPd58-2sv.pep     PVMMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA----------
[SEQ ID NO:42]  LGAsv-A.pep       PVMMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA----------
[SEQ ID NO:44]  LGAsv-C.pep       PVKMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA----------
[SEQ ID NO:46]  LGAsv-D.pep       PVMMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA----------
[SEQ ID NO:48]  LGAsv-E.pep       PVMMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA----------
[SEQ ID NO:50]  Misv-A.pep        PVKMPGYHYVDRKLDVTNHNKDYTSVEQREISIARKPVVA----------
[SEQ ID NO:52]  Misv-B.pep        PVKMPGYHYVDRKLDVTNHNKDYTSVEQREISIARKPVVA----------
[SEQ ID NO:54]  Misv-F.pep        PVKMPGYHYVDRKLDVTNHNKDYTSVEQREISIARKPVVA----------
[SEQ ID NO:56]  PM1Asv-rep.pep    PVMMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA----------
[SEQ ID NO:58]  PM1Csv-rep.pep    PVMMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA----------
[SEQ ID NO:60]  PMsv-4.pep        --------------------------------------------------
[SEQ ID NO:62]  PMsv-5.pep        PVMMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA*RFFRVKSRHK
[SEQ ID NO:64]  PPsv-1.pep        PVKMPGYHYVDRKLDVTNHNKDYISVEQCEISIARKPVVA----------
[SEQ ID NO:66]  PPsv-2.pep        PVKMPGYHYVDRKLDVTNHNKDYISVEQCEISIARKPVVA----------
[SEQ ID NO:68]  PPsv-3.pep        PVKMPGYHYVDRKLDVTNHNKDYISVEQCETSIARKPVVA----------
[SEQ ID NO:70]  PPsv-4.pep        PVKMPGYHYVDRKLDVTNHNKDYISVEQCEISIARKPVVA----------
[SEQ ID NO:72]  PPsv-5.pep        PVMMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA----------
[SEQ ID NO:74]  PPsv-6.pep        PVMMPGYHYVDRKLDVTNHNKDYTSVEQCGISIARKPVVA----------
[SEQ ID NO:76]  Pavsv-A.pep       PVMMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA----------
[SEQ ID NO:78]  Pavsv-B.pep       PVKMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA----------
[SEQ ID NO:80]  Pavsv-C.pep       PVKMPGYHYVDRKLDVTNHNKDYTSVEQREISIARKPVVA----------
[SEQ ID NO:82]  RTsv-1.pep        PVMMPGYHYVDRKLDVTNHNKDYTSVEQCEIPIARKPVVA----------
[SEQ ID NO:84]  RTsv-2.pep        PVMMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA----------
[SEQ ID NO:86]  RTsv-3.pep        PVMMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA----------
```

Figure 1 continued

```
[SEQ ID NO:19]  Aasv-1         TCCGTTATCGCTAAACAGATGACCTACAAGGTTTATATGTCAGACACGGTCAATGGACAC
[SEQ ID NO:21]  Aasv-3         TCCGTTATCGCTAAACAGATGACCTACAAAGTTTATATGTCAGGCACGGTCAATGGACAC
[SEQ ID NO:23]  Aasv-P         TCCGTTATCGCTAAACAGATGACCTACAAAGTTTATATGTCAGGCACGGTCAATGGACAC
[SEQ ID NO:25]  Acasv-A        TCCGTTATCGCTAAACAGATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACAC
[SEQ ID NO:27]  Acasv-C        TCCGTTATCGCTAAACAGATGACCTACAAAGTTTATATGTCAGGCACGGTCAATGGACAC
[SEQ ID NO:29]  Acasv-D        TCCGTTATCGCTAAACAGATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACAC
[SEQ ID NO:31]  Ce61-3sv       TCCGTTATCGCTAAACAGATGACCTACAAAGTTTATATGTCAGGCACGGTCAATGGACAC
[SEQ ID NO:33]  Ce61-4sv       TCCGTTATCGCTAAACAGATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACAC
[SEQ ID NO:35]  Ce61-5sv-rep   TCCGTTATCGCTAAACAGATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACAC
[SEQ ID NO:37]  Ce61-7sv-rep   TCCGTTATCGCTAAACAGATGACCTACATNGNTTATNTGTCAGGCACNGTCNATGGACAC
[SEQ ID NO:39]  GPd58-2sv      TCCGTTATCGCTAAACAGATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACAC
[SEQ ID NO:41]  LGAsv-A        TCCGTTATCGCTAAACAGATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACAC
[SEQ ID NO:43]  LGAsv-C        TCCGTTATCGCTAAACAGATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACAC
[SEQ ID NO:45]  LGAsv-D        TCCGTTATCGCTAAACAGATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACAC
[SEQ ID NO:47]  LGAsv-E        TCCGTTATCGCTAAACAGATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACAC
[SEQ ID NO:49]  Misv-A         TCCGTTATCGCTAAACAGATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACAC
[SEQ ID NO:51]  Misv-B         TCCGTTATCGCTAAACAGATGACCTACAAAGTTTATATGTCAGGCACGGTCAATGGACAC
[SEQ ID NO:53]  Misv-F         TCCGTTATCGCTAAACAGATGACCTACAAAGTTTATATGTCAGGCACGGTCAATGGACAC
[SEQ ID NO:55]  PM1Asv-rep     TCCGTTATCGCTAAACAGATGACCTACAAGGTTTATATGTCAGACACGGTCAATGGACAC
[SEQ ID NO:57]  PM1Csv-rep     TCCGTTATCGCTAAACAGATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACAC
[SEQ ID NO:59]  PMsv-4         TCCGTTATCGCTAAACAGATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACAC
[SEQ ID NO:61]  PMsv-5         TCCGTTATCGCTAAACAGATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACAC
[SEQ ID NO:63]  PPsv-1         TCCGTTATCGCTAAACAGATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACAC
[SEQ ID NO:65]  PPsv-2         TCCGTTATCGCTAAACAGATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACAC
[SEQ ID NO:67]  PPsv-3         TCCGTTATCGCTAAACAGATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACAC
[SEQ ID NO:69]  PPsv-4         TCCGTTATCGCTAAACAGATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACAC
[SEQ ID NO:71]  PPsv-5         TCCGTTATCGCTAAACAGATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACAC
[SEQ ID NO:73]  PPsv-6         TCCGTTATCGCTAAACAGATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACAC
[SEQ ID NO:75]  Pavsv-A        TCCGTTATCGCTAAACAGATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACAC
[SEQ ID NO:77]  Pavsv-B        TCCGTTATCGCTAAACAGATGACCTACAAGGTTAATATGTCAGGCACGGTCAATGGACAC
[SEQ ID NO:79]  Pavsv-C        TCCGTTATCGCTAAACAGATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACAC
[SEQ ID NO:81]  RTsv-1         TCCGTTATCGCTAAACAGATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACAC
[SEQ ID NO:83]  RTsv-2         TCCGTTATCGCTAAACAGATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACAC
[SEQ ID NO:85]  RTsv-3         TCCGTTATCGCTAAACAGATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACAC
                               ****************************  * * ** ****** *** *** ********
```

Figure 2

```
[SEQ ID NO:19]   Aasv-1          TACTTTGAGGTTGAAGGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAAG
[SEQ ID NO:21]   Aasv-3          TACTTTGAGGTCGAAGGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAGG
[SEQ ID NO:23]   Aasv-P          TACTTTGAGGTCGAAGGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAGG
[SEQ ID NO:25]   Acasv-A         TACTTTGAGGTCGAAGGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAAG
[SEQ ID NO:27]   Acasv-C         TACTTTGAGGTCGAAGGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAGG
[SEQ ID NO:29]   Acasv-D         TACTTTGAGGTCGAAGGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAAG
[SEQ ID NO:31]   Ce61-3sv        TACTTTGAGGTCGAAGGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAGG
[SEQ ID NO:33]   Ce61-4sv        TACTTTGAGGTNGAAGGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAAG
[SEQ ID NO:35]   Ce61-5sv-rep    TACTTTGAGGTCGAAGGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAAG
[SEQ ID NO:37]   Ce61-7sv-rep    TACTTTGAGGTCGAAGGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAAG
[SEQ ID NO:39]   GPd58-2sv       TACTTTGAGGTTGAAGGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAAG
[SEQ ID NO:41]   LGAsv-A         TACTTTGAGGTTGAAGGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAAG
[SEQ ID NO:43]   LGAsv-C         TACTTTGAGGTCGAAGGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAAG
[SEQ ID NO:45]   LGAsv-D         TACTTTGAGGTTGAAGGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAAG
[SEQ ID NO:47]   LGAsv-E         TACTTTGAGGTTGAAGGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAAG
[SEQ ID NO:49]   Misv-A          TACTTTGAGGTTGAAGGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAAG
[SEQ ID NO:51]   Misv-B          TACTTTGAGGTCGAAGGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAGG
[SEQ ID NO:53]   Misv-F          TACTTTGAGGTCGAAGGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAGG
[SEQ ID NO:55]   PM1Asv-rep      TACTTTGAGGTTGAAGGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAAG
[SEQ ID NO:57]   PM1Csv-rep      TACTTTGAGGTTGAAGGCGATGGAAAAGGAAGGCCTTACGAGGGGGAGCAGACGGTAAAG
[SEQ ID NO:59]   PMsv-4          TACTTTGAGGTTGAAGGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAAG
[SEQ ID NO:61]   PMsv-5          TACTTTGAGGTCCAAGGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAAG
[SEQ ID NO:63]   PPsv-1          TACTTTGAGGTCGAAGGCGATAGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAAG
[SEQ ID NO:65]   PPsv-2          TACTTTGAGGTCGAAGGCGATGGGAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAAG
[SEQ ID NO:67]   PPsv-3          TACTTTGAGGTCGAAGGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAAG
[SEQ ID NO:69]   PPsv-4          TACTTTGAGGTCGAAGGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAAG
[SEQ ID NO:71]   PPsv-5          TACTTTGAGGTTGAAGGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAAG
[SEQ ID NO:73]   PPsv-6          TACTTTGAGGTTGAAGGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAAG
[SEQ ID NO:75]   Pavsv-A         TACTTTGAGGTTGAAGGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAAG
[SEQ ID NO:77]   Pavsv-B         TACTTTGAGGTCGAAGGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAAG
[SEQ ID NO:79]   Pavsv-C         TACTTTGAGGTTGAAGGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAAG
[SEQ ID NO:81]   RTsv-1          TACTTTGAGGCTGAAGGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAAG
[SEQ ID NO:83]   RTsv-2          TACTTTGAGGTTGAAGGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAAG
[SEQ ID NO:85]   RTsv-3          TACTTTGAGGTTGAAGGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAAG
                                 **********   ******** * ******* ************************** *
```

Figure 2 continued

```
[SEQ ID NO:19]  Aasv-1          CTCACTGTCACCAAGGGCGGACCTCTGCCATTTGCTTGGGATATTCTATCACCACAGAGT
[SEQ ID NO:21]  Aasv-3          CTGACTGTCACCAAGGGCGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACAGTCA
[SEQ ID NO:23]  Aasv-P          CTGACTGTCACCAAGGGCGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACAGTCA
[SEQ ID NO:25]  Acasv-A         CTCACTGTCACCAAGGGCGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACGGTGT
[SEQ ID NO:27]  Acasv-C         CTGACTGTCACCAAGGGCGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACAGTCA
[SEQ ID NO:29]  Acasv-D         CTCACTGTCACCAAGGGCGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACAGTGT
[SEQ ID NO:31]  Ce61-3sv        CTGACTGTCACCAAGGGCGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACAGTCA
[SEQ ID NO:33]  Ce61-4sv        CTCACTGTCACCNAGGGCGGACCTCTGCCATTTGCTTGGGATATTNTATCACCACAGAGT
[SEQ ID NO:35]  Ce61-5sv-rep    CTCACTGTCACCAAGGGCGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACAGTGT
[SEQ ID NO:37]  Ce61-7sv-rep    CTCACTGTCACCAAGGGCGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACAGTGT
[SEQ ID NO:39]  GPd58-2sv       CTCACTGTCACCAAGGGCGGACCTCTGCCATTTGCTTGGGATATTCTATCACCACAGAGT
[SEQ ID NO:41]  LGAsv-A         CTCACTGTCACCAAGGGCGGACCTCTGCCATTTGCTTGGGATATTCTATCACCACAGAGT
[SEQ ID NO:43]  LGAsv-C         CTCACTGTCACCAAGGGCGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACAGTGT
[SEQ ID NO:45]  LGAsv-D         CTCACTGTCACCAAGGGCGGACCTCTGCCATTTGCTTGGGATATTCTATCACCACAGAGT
[SEQ ID NO:47]  LGAsv-E         CTCACTGTCACCGAGGGCGGACCTCTGCCATTTGCTTGGGATATTCTATCACCACAGAGT
[SEQ ID NO:49   Misv-A          CTCACTGTCACCAAGGGCGGACCTCTGCCATTTGCTTGGGATATTCTATCACCACAGAGT
[SEQ ID NO:51]  Misv-B          CTGACTGTCACCAAGGGCGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACAGTCA
[SEQ ID NO:53]  Misv-F          CTGACTGTCACCAAGGGCGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACAGTCA
[SEQ ID NO:55]  PM1Asv-rep      CTCACTGTCACCAAGGGCGGACCTCTGCCATTTGCTTGGGATATTCTATCACCACAGAGT
[SEQ ID NO:57]  PM1Csv-rep      CTCACTGTCACCAAGGGCGGACCTCTGCCATTTGCTTGGGATATTCTATCACCACAGAGT
[SEQ ID NO:59]  PMsv-4          CTCACTGTCACCAAGGGCGGACCTCTGCCATTTGCTTGGGATATTCTATCACCACAGAGT
[SEQ ID NO:61]  PMsv-5          CTCACTGTCACCAAGGGCGGACCTCTGCCATTTGCTTGGGATATTCTATCACCACAGAGT
[SEQ ID NO:63]  PPsv-1          CTCACTGTCACCAAGGGCGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACAGTGT
[SEQ ID NO:65]  PPsv-2          CTCACTGTCACCAAGGGCGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACAGTGT
[SEQ ID NO:67]  PPsv-3          CTCACTGTCACCAAGGGCGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACAGTGT
[SEQ ID NO:69]  PPsv-4          CTCACTGTCACCAAGGGCGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACGGTGT
[SEQ ID NO:71]  PPsv-5          CTCACTGTCACCAAGGGCGGACCTCTGCCATTTGCTTGGGATATTCTATCACCACAGAGT
[SEQ ID NO:73]  PPsv-6          CTCACTGTCACCAAGGGCGGACCTCTGCCATTTGCTTGGGATATTCTATCACCACAGAGT
[SEQ ID NO:75]  Pavsv-A         CTCACTGTCACCGAGGGCGGACCTCTGCCATTTGCTTGGGATATTCTATCACCACAGAGT
[SEQ ID NO:77]  Pavsv-B         CTCACTGTCACCAAGGGCGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACAGTGT
[SEQ ID NO:79]  Pavsv-C         CTCACTGTCACCGAGGGCGGACCTCTGCCATTTGCTTGGGATATTCTATCACCACAGAGT
[SEQ ID NO:81]  RTsv-1          CTCACTGTCACCAAGGGCGGACCTCTGCCATTTGCTTGGGATATTCTATCACCACAGAGT
[SEQ ID NO:83]  RTsv-2          CTCACTGTCACCAAGGGCGGACCTCTGCCATTTGCTTGGGATATTCTATCACCACAGAGT
[SEQ ID NO:85]  RTsv-3          CTCACTGTCACCAAGGGCGGACCTCTGCCATTTGCTTGGGATATTCTATCACCACAGAGT
                                ** ********* ********************************* ********* *
```

Figure 2 continued

```
[SEQ ID NO:19] Aasv-1         CAGTACGGAAGCATACCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAG
[SEQ ID NO:21] Aasv-3         CAGTACGGAAGCATACCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAG
[SEQ ID NO:23] Aasv-P         CAGTACGGAAGCATACCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAG
[SEQ ID NO:25] Acasv-A        CAGTACGGAAACATACCATTCACCAAGTACCCTGAAGACGTCCCTGACTATGTAAAGCAG
[SEQ ID NO:27] Acasv-C        CAGTACGGAAGCATACCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAG
[SEQ ID NO:29] Acasv-D        CAGTACGGAAGCATACCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAG
[SEQ ID NO:31] Ce61-3sv       CAGTACGGAAGCATACCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAG
[SEQ ID NO:33] Ce61-4sv       CAGTACGGAAGCNTACCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAG
[SEQ ID NO:35] Ce61-5sv-rep   CAGTACGGAAGCATACCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAG
[SEQ ID NO:37] Ce61-7sv-rep   CAGTACGGAAGCATACCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAG
[SEQ ID NO:39] GPd58-2sv      CAGTACGGAAGCATACCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAG
[SEQ ID NO:41] LGAsv-A        CAGTACGGAAGCATACCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAG
[SEQ ID NO:43] LGAsv-C        CAGTACGGAAGCATACCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAG
[SEQ ID NO:45] LGAsv-D        CAGTACGGAAGCATACCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAG
[SEQ ID NO:47] LGAsv-E        CAGTACGGAAGCATACCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAG
[SEQ ID NO:49] Misv-A         CAGTACGGAAGCATACCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAG
[SEQ ID NO:51] Misv-B         CAGTACGGAAGCATACCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAG
[SEQ ID NO:53] Misv-F         CAGTACGGAAGCATACCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAG
[SEQ ID NO:55] PM1Asv-rep     CAGTACGGAAGCATACCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAG
[SEQ ID NO:57] PM1Csv-rep     CAGTACGGAAGCATACCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAG
[SEQ ID NO:59] PMsv-4         CAGTACGGAAGCATACCATTCACCAAGTACCCTGAGGACATCCCTGACTATGTAAAGCAG
[SEQ ID NO:61] PMsv-5         CAGTACGGAAGCATACCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAG
[SEQ ID NO:63] PPsv-1         CAGTACGGAAACATACCATTCACCAAGTACCCTGAAGACGTCCCTGACTATGTAAAGCAG
[SEQ ID NO:65] PPsv-2         CAGTACGGAAACATACCATTCACCAAGTACCCTGAAGACGTCCCTGACTATGTAAAGCAG
[SEQ ID NO:67] PPsv-3         CAGTACGGAAACATACCATTCACCAAGTACCCTGAAGACGTCCCTGACTATGTAAAGCAG
[SEQ ID NO:69  PPsv-4         CAGTACGGAAACATACCATTCACCAAGTACCCTGAAGACGTCCCTGACTATGTAAAGCAG
[SEQ ID NO:71] PPsv-5         CAGTACGGAAGCATACCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAG
[SEQ ID NO:73] PPsv-6         CAGTACGGAAGCATACCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAG
[SEQ ID NO:75] Pavsv-A        CAGTACGGAAGCGTACCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAG
[SEQ ID NO:77] Pavsv-B        CAGTACGGAAGCATACCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAG
[SEQ ID NO:79] Pavsv-C        CAGTACGGAAGCGTACCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAG
[SEQ ID NO:81] RTsv-1         CAGTACGGAAGCATACCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAG
[SEQ ID NO:83] RTsv-2         CAGTACGGAAGCATACCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAG
[SEQ ID NO:85] RTsv-3         CAGTACGGAAGCATACCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAG
                              ********** * ********************** *** ********************
```

Figure 2 continued

```
[SEQ ID NO:19] Aasv-1          TCATTCCCTGAGGGATATACATGGGAGAGGATCATGAACTTCGAAGATGGTGCAGTGTGT
[SEQ ID NO:21] Aasv-3          TCATTCCCGGAGGGATATACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGT
[SEQ ID NO:23] Aasv-P          TCATTCCCGGAGGGATATACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGT
[SEQ ID NO:25] Acasv-A         TCATTCCCGGAGGGATTTACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGT
[SEQ ID NO:27] Acasv-C         TCATTCCCGGAGGGATATACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGT
[SEQ ID NO:29] Acasv-D         TCATTCCCGGAGGGATTTACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGT
[SEQ ID NO:31] Ce61-3sv        TCATTCCCGGAGGGATATACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGT
[SEQ ID NO:33] Ce61-4sv        TCATTCCCTGAGGGATATACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGT
[SEQ ID NO:35] Ce61-5sv-rep    TCATTCCCGGAGGGATTTACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGT
[SEQ ID NO:37] Ce61-7sv-rep    TCATTCCCGGAGGGATTTACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGT
[SEQ ID NO:39] GPd58-2sv       TCATTCCCTGAGGGATATACATGGGAGAGGATCATGAACTTCGAAGATGGTGCAGTGTGT
[SEQ ID NO:41] LGAsv-A         TCATTCCCTGAGGGATATACATGGGAGAGGATCATGAACTTCGAAGATGGTGCAGTGTGT
[SEQ ID NO:43] LGAsv-C         TCATTCCCGGAGGGATTTACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGT
[SEQ ID NO:45] LGAsv-D         TCATTCCCTGAGGGATATACATGGGAGAGGATCATGAACTTCGAAGATGGTGCAGTGTGT
[SEQ ID NO:47] LGAsv-E         TCATTCCCTGAGGGATATACATGGGAGAGGATCATGAACTTCGAAGATGGTGCAGTGTGT
[SEQ ID NO:49] Misv-A          TCATTCCCTGAGGGATATACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGT
[SEQ ID NO:51] Misv-B          TCATTCCCGGAGGGATATACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGT
[SEQ ID NO:53] Misv-F          TCATTCCCGGAGGGATATACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGT
[SEQ ID NO:55] PM1Asv-rep      TCATTCCCTGAGGGATATACATGGGAGAGGATCATGAACTTCGAAGATGGTGCAGTGTGT
[SEQ ID NO:57] PM1Csv-rep      TCATTCCCTGAGGGATATACATGGGAGAGGATCATGAAGTTTGAAGATGGTGCAGTATGT
[SEQ ID NO:59] PMsv-4          TCATTCCCTGAGGGATATACATGGGAGAGGATCGTGAACTTCGAAGATGGTGCAGTGTGT
[SEQ ID NO:61] PMsv-5          TCATTCCCTGAGGGATATACATGGGAGAGGATCATGAACTTCAAAGATGGTGCAGTGTGT
[SEQ ID NO:63] PPsv-1          TCATTCCCGGAGGGATTTACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGT
[SEQ ID NO:65] PPsv-2          TCATTCCCGGAGGGATTTACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGT
[SEQ ID NO:67] PPsv-3          TCATTCCCGGAGGGATTTACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGT
[SEQ ID NO:69] PPsv-4          TCATTCCCGGAGGGATTTACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGT
[SEQ ID NO:71] PPsv-5          TCATTCCCTGAGGGATATACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGT
[SEQ ID NO:73] PPsv-6          TCATTCCCTGAGGGATATACATGGGAGAGGATCATGAACTTCGAAGATGGTGCAGTGTGT
[SEQ ID NO:75] Pavsv-A         TCATTCCCTGAGGGATATACATGGGAGAGGATCATGAACTTCGAAGATGGTGCAGTGTGT
[SEQ ID NO:77] Pavsv-B         TCATTCCCGGAGGGATTTACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGT
[SEQ ID NO:79] Pavsv-C         TCATTCCCGGAGGGATATACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGT
[SEQ ID NO:81] RTsv-1          TCATTCCCTGAGGGATATACATGGGAGAGGATCATGAACTTCGAAGATGGTGCAGTGTGT
[SEQ ID NO:83] RTsv-2          TCATTCCCTGAGGGATATACATGGGAGAGGATCATGAACTTCGAAGATGGTGCAGTGTGT
[SEQ ID NO:85] RTsv-3          TCATTCCCTGAGGGATATACATGGGAGAGGATCATGAACTTCGAAGATGGTGCAGTGTGT
               ******** ******* **************** **** **   ************* ***
```

Figure 2 continued

```
[SEQ ID NO:19] Aasv-1          ACTGTCAGCAATGATTCCAGCATCCAAGGTAACTGTTTCATCTACAATGTCAAGTTCTCT
[SEQ ID NO:21] Aasv-3          ACTGTCAGCAATGATTCCAGCATCCAAGGCAACTGTTTCATCTACCATGTCAAGTTCTCT
[SEQ ID NO:23] Aasv-P          ACTGTCAGCAATGATTCCAGCATCCAAGGCAACTGTTTCATCTACCATGTCAAGTTCTCT
[SEQ ID NO:25] Acasv-A         ACTGTCAGCAATGATTCCAGCATCCAAGGCAACTGTTTCACCTACCATGTCAAGTTCTCT
[SEQ ID NO:27] Acasv-C         ACTGTCAGCAATGATTCCAGCATCCAAGGCAACTGTTTCATCTACCATGTCAAGTTCTCT
[SEQ ID NO:29] Acasv-D         ACTGTCAGCAATGACTCCAGCATCCAAGGCAACTGTTTCACCTACCATGTCAAGTTCTCT
[SEQ ID NO:31] Ce61-3sv        ACTGTCAGCAATGATTCCAGCATCCAAGGCAACTGTTTCATCTACCATGTCAAGTTCTCT
[SEQ ID NO:33] Ce61-4sv        ACTGTCAGCAATGATTCCAGCATCCAAGGTAACTGTTTCATCTACCATGTCAAGTTCTCT
[SEQ ID NO:35] Ce61-5sv-rep    ACTGTCAGCAATGATTCCAGCATCCAAGGCAACTGTTTCACCTACCATGTCAAGTTCTCT
[SEQ ID NO:37] Ce61-7sv-rep    ACTGTCAGCAATGATTCCAGCATCCAAGGCAACTGTTTCACCTACCATGTCAAGTTCTCT
[SEQ ID NO:39] GPd58-2sv       ACTGTCAGCAATGATTCCAGCATCCAAGGTAACTGTTTCATCTACAATGTCAAGTTCTCT
[SEQ ID NO:41] LGAsv-A         ACTGTCAGCAATGATTCCAGCATCCAAGGTAACTGTTTCATCTACAATGTCAAGTTCTCT
[SEQ ID NO:43] LGAsv-C         ACTGTCAGCAATGATTCCAGCATCCAAGGCAACTGTTTCACCTACCACGTCAAGTTCTCT
[SEQ ID NO:45] LGAsv-D         ACTGTCAGCAATGATTCCAGCATCCAAGGTAACTGTTTCATCTACAATGTCAAGTTCTCT
[SEQ ID NO:47] LGAsv-E         ACTGTCAGCAATGATTCCAGCATCCAAGGTAACTGTTTCATCTACAATGTCAAGTTCTCT
[SEQ ID NO:49] Misv-A          ACTGTCAGCAATGATTCCAGCATCCAAGGCAACTGTTTCATCTACCATGTCAAGTTCTCT
[SEQ ID NO:51] Misv-B          ACTGTCAGCAATGATTCCAGCATCCAAGGCAACTGTTTCATCTACCATGTCAAGTTCTCT
[SEQ ID NO:53] Misv-F          ACTGTCAGCAATGATTCCAGCATCCAAGGCAACTGTTTCATCTACCATGTCAAGTTCTCT
[SEQ ID NO:55] PM1Asv-rep      ACTGTCAGCAATGATTCCAGCATCCAAGGTAACTGTTTCATCTACAATGTCAAGTTCTCT
[SEQ ID NO:57] PM1Csv-rep      ACTGTCAGCAATGATTCCAGCATGCAAGGCAACTGTTTCATCTACAATGTCAAGTTCTCT
[SEQ ID NO:59] PMsv-4          ACTGTCAGCAATGATTCCAGCATCCAAGGCAACTGTTTCATCTACAATGTCAAGTTCTCT
[SEQ ID NO:61] PMsv-5          ACTGTCAGCAATGATTCCAGCATCCAAGGCAACTGTTTCATCTACAATGTCAAGTTCTCT
[SEQ ID NO:63] PPsv-1          ACTGTCAGCAATGATTCCAGCATCCAAGGCAACTGTTTCACCTACCATGTCAAGTTCTCT
[SEQ ID NO:65] PPsv-2          ACTGTCAGCAATGATTCCAGCATCCAAGGCAACTGTTTCACCTACCATGTCAAGTTCTCT
[SEQ ID NO:67] PPsv-3          ACTGTCAGCAATGATTCCAGCATCCAAGGCAACTGTTTCACCTACCATGTCAAGTTCTCT
[SEQ ID NO:69] PPsv-4          ACTGTCAGCAATGATTCCAGCATCCAAGGCAACTGTTTCACCTACCATGTCAAGTTCTCT
[SEQ ID NO:71] PPsv-5          ACTGTCAGCAATGATTCCAGCATCCAAGGTAACTGTTTCATCTACAATGTCAAGTTCTCT
[SEQ ID NO:73] PPsv-6          ACTGTCAGCAATGATTCCAGCATCCAAGGTAGCTGTTTCATCTACAATGTCAAGTTCTCT
[SEQ ID NO:75] Pavsv-A         ACTGTCAGCAATGATTCCAGCATCCAAGGTAACTGTTTCATCTACAATGTCAAGTTCTCT
[SEQ ID NO:77] Pavsv-B         ACTGTCAGCAATGATTCCAGCATCCAAGGCAACTGTTTCACCTACCATGTCAAGTTCTCT
[SEQ ID NO:79] Pavsv-C         ACTGTCAGCAATGATTCCAGCATCCAAGGCAACTGTTTCATCTACCATGTCAAGTTCTCT
[SEQ ID NO:81] RTsv-1          ACTGTCAGCAATGATTCCAGCATCCAAGGTAACTGTTTCATCTACAATGTCAAGTTCTCT
[SEQ ID NO:83] RTsv-2          ACTGTCAGCAATGATTCCAGCATCCAAGGTAACTGTTTCATCTACAATGTCAAGTTCTCT
[SEQ ID NO:85] RTsv-3          ACTGTCAGCAATGATTCCAGCATCCAAGGTAACTGTTTCATCTACAATGTCAAGTTCTCT
                               ************** ******** ***** * ******** **** * ************
```

Figure 2 continued

```
[SEQ ID NO:19] Aasv-1         GGTTTGAACTTTCCTCCCAATGGACCTGTTATGCAAAAGAAGACACAGGGCTGGGAACCC
[SEQ ID NO:21] Aasv-3         GGTTTGAACTTTCCTCCCAATGGACCTGTTATGCAGAAGAAGACACAGGGCTGGGAACCC
[SEQ ID NO:23] Aasv-P         GGTTTGAACTTTCCTCCCAATGGACCTGTTATGCAGAAGAAGACACAGGGCTGGGAACCC
[SEQ ID NO:25] Acasv-A        GGTTTGAACTTTCCTCCCAATGGACCTGTGATGCAGAAGAAGACACGGGGCTGGGAACCC
[SEQ ID NO:27] Acasv-C        GGTTTGAACTTTCCTCCCAATGGACCTGTTATGCAGAAGAAGACACAGGGCTGGGAACCC
[SEQ ID NO:29] Acasv-D        GGTTTGAACTTTCCTCCCAATGGGCCTGTGATGCAGAAGAAGACACAGGGCTGGGAACCC
[SEQ ID NO:31] Ce61-3sv       GGTTTGAACTTTCCTCCCAATGGACCTGTTATGCAGAAGAAGACACAGGGCTGGGAACCC
[SEQ ID NO:33] Ce61-4sv       GGTTTGAACTTTCCTCCCAATGGGCCTGTTATGCAAAAGAAGACACAGGGCTGGGAACCC
[SEQ ID NO:35] Ce61-5sv-rep   GGTTTGAACTTTCCTCCCAATGGGCCTGTGATGCAGAAGAAGACACAGGGCTGGGAACCC
[SEQ ID NO:37] Ce61-7sv-rep   GGTTTGAACTTTCCTCCCAATGGGCCTGTGATGCAGAAGAAGACACAGGGCTGGGAACCC
[SEQ ID NO:39] GPd58-2sv      GGTTTGAACTTTCCTCCCAATGGACCTGTTATGCAAAAGAAGACACAGGGCTGGGAACCC
[SEQ ID NO:41] LGAsv-A        GGTTTGAACTTTCCTCCCAATGGACCTGTTATGCAAAAGAAGACACAGGGCTGGGAACCC
[SEQ ID NO:43] LGAsv-C        GGTTTGGACTTTCCTCCCAATGGGCCTGTGATGCAGAAGAAGACACAGGGCTGGGAACCC
[SEQ ID NO:45] LGAsv-D        GGTTTGAACTTTCCTCCCAATGGACCTGTTATGCAAAAGAAGACACAGGGCTGGGAACCC
[SEQ ID NO:47] LGAsv-E        GGTTTGAACTTTCCTCCCAATGGACCTGTTATGCAAAAGAAGACACAGGGCTGGGAACCC
[SEQ ID NO:49] Misv-A         GGTTTGAACTTTCCTCCCAATGGACCTGTTATGCAGAAGAAGACACAGGGCTGGGAACCC
[SEQ ID NO:51] Misv-B         GGTTTGAACTTTCCTCCCAATGGACCTGTTATGCAGAAGAAGACACAGGGCTGGGAACCC
[SEQ ID NO:53] Misv-F         GGTTTGAACTTTCCTCCCAATGGACCTGTTATGCAGAAGAAGACACAGGGCTGGGAACCC
[SEQ ID NO:55] PM1Asv-rep     GGTTTGAACTTTCCTCCCAATGGACCTGTTATGCAAAAGAAGACACAGGGCTGGGAACCC
[SEQ ID NO:57] PM1Csv-rep     GGTTTGAACTTTCCTCCCAATGGACCTGTTATGCAGAAGAAGACACAGGGCTGGGAACCC
[SEQ ID NO:59] PMsv-4         GGTTTGAACTTTCCTCCCAATGGACCTGTTATGCAGAAGAAGACACAGGGCTGGGAACCC
[SEQ ID NO:61] PMsv-5         GGTTTGAACTTTCCTCCCAATGGACCTGTTATGCAAAAGAAGACACAGGGCTGGGAACCC
[SEQ ID NO:63] PPsv-1         GGTTTGAACTTTCCTCCCAATGGACCTGTGATGCAGAAGAAGACACAGGGCTGGGAACCC
[SEQ ID NO:65] PPsv-2         GGTTTGAACTTTCCTCCCAATGGACCTGTGATGCAGAAGAAGACACAGGGCTGGGAACCC
[SEQ ID NO:67] PPsv-3         GGTTTGAACTTTCCTCCCAATGGACCTGTGATGCAGAAGAAGACACAGGGCTGGGAACCC
[SEQ ID NO:69] PPsv-4         GGTTTGAACTTTCCTCCCAATGGACCTGTGATGCAGAAGAAGACACGGGGCTGGGAACCC
[SEQ ID NO:71] PPsv-5         GGTTTGAACTTTCCTCCCAATGGACCTGTTATGCAAAAGAAGACACAGGGCTGGGAACCC
[SEQ ID NO:73] PPsv-6         GGTTTGAACTTTCCTCCCAATGGACCTGTTATGCAAAAGAAGACACAGGGCTGGGAACCC
[SEQ ID NO:75] Pavsv-A        GGTTTGAACTTTCCTCCCAATGGACCTGTTATGCAAAAGAAGACACAGGGCTGGTACCC
[SEQ ID NO:77] Pavsv-B        GGTTTGAACTTTCCTCCCAATGGGCCTGTGATGCAGAAGAAGACACAGGGCTGGGAACCC
[SEQ ID NO:79] Pavsv-C        GGTTTGAACTTTCCTCCCAATGGACCTGTTATGCAGAAGAAGACACAGGGCTGGGAACCC
[SEQ ID NO:81] RTsv-1         GGTTTGAACTTTCCTCCCAATGGACCTGTTATGCAAAAGAAGACACAGGGCTGGGAACCC
[SEQ ID NO:83] RTsv-2         GGTTTGAACTTTCCTCCCAATGGACCTGTTATGCAAAAGAAGACACAGGGCTGGGAACCC
[SEQ ID NO:85] RTsv-3         GGTTTGAACTTTCCTCCCAATGGACCTGTTATGCAAAAGAAGACACAGGGCTGGGAACCC
                      ****** **************** ***** ***** ********** ******** ****
```

Figure 2 continued

```
[SEQ ID NO:19]:Aasv-1         AACACTGGGCGTCTCTTTGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCTCTG
[SEQ ID NO:21] Aasv-3         AACACTGAGCGTCTCTTAGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCTCTG
[SEQ ID NO:23] Aasv-P         AACACTGAGCGTCTCTTTGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCTCTG
[SEQ ID NO:25] Acasv-A        CACTCTGAGCGTCTCTTTGCACGGGGTGGAATGCTGATAGGAAACAACTTTATGGCTCTG
[SEQ ID NO:27] Acasv-C        AACACTGAGCGTCTCTCTGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCTCTG
[SEQ ID NO:29] Acasv-D        CACTCTGAGCGTCTCTTTGCACGGGGTGGAATGCTGATAGGAAACAACTTTATGGCTCCG
[SEQ ID NO:31] Ce61-3sv       AACACTGAGCGTCTCTCTGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCTCTG
[SEQ ID NO:33] Ce61-4sv       CACTCTGAGCGTCTCTTTGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCTCTG
[SEQ ID NO:35] Ce61-5sv-rep   CACTCTGAGCGTCTCTTTGCACGGGGTGGAATGCTGATAGGAAACAACTTTATGGCTCTG
[SEQ ID NO:37] Ce61-7sv-rep   CACTCTGAGCGTCTCTTTGCACGGGGTGGAATGCTGATAGGAAACAACTTTATGGCTCTG
[SEQ ID NO:39] GPd58-2sv      AACACTGAGCGTCTCTTTGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCTCTG
[SEQ ID NO:41] LGAsv-A        AACACTGAGCGTCTCTTTGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCTCTG
[SEQ ID NO:43] LGAsv-C        CACTCTGAGCGTCTCTTTGCACGGGGTGGAATGCTGATAGGAAACAACTTTATGGCTCTG
[SEQ ID NO:45] LGAsv-D        AACACTGAGCGTCTCTTTGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCTCTG
[SEQ ID NO:47] LGAsv-E        AACACTGAGCGTCTCTTTGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCTCTG
[SEQ ID NO:49] Misv-A         AACACTGAGCGTCTCTTTGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCTCTG
[SEQ ID NO:51] Misv-B         AACACTGAGCGTCTCTTTGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCTCTG
[SEQ ID NO:53] Misv-F         AACACTGAGCGTCTCTTTGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCTCTG
[SEQ ID NO:55] PM1Asv-rep     AACACTGGGCGTCTCTTTGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCTCTG
[SEQ ID NO:57] PM1Csv-rep     AACACTGAGCGACTTTATGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCTCTG
[SEQ ID NO:59] PMsv-4         AACACTGAGCGTCTTTATGCACGGGATGGAATGCTGATAGGAAACAACTTTATGGCTCTG
[SEQ ID NO:61] PMsv-5         AACACTGAGCGTCTCTTTGCACGAGATGGAGTGCTGATAGGAAACAACTTTATGGCTCTG
[SEQ ID NO:63] PPsv-1         CACTCTGAGCGTCTCTTTGCACGGGGTGGAATGCTGATAGGAAACAACTTTATGGCTCTG
[SEQ ID NO:65] PPsv-2         CACTCTGAGCGTCTCTTTGCACGGGGTGGAATGCTGATAGGAAACAACTTTATGGCTCTG
[SEQ ID NO:67] PPsv-3         CACTCTGAGCGTCTCTTTGCACGGGGTGGAATGCTGATAGGAAACAACTTTATGGCTCTG
[SEQ ID NO:69] PPsv-4         CACTCTGAGCGTCTCTTTGCACGGGGTGGAATGCTGATAGGAAACAACTTTATGGCTCTG
[SEQ ID NO:71] PPsv-5         AACACTGAGCGTCTCTTTGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCTCTG
[SEQ ID NO:73] PPsv-6         AACACTGAGCGTCTCTTTGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCTCTG
[SEQ ID NO:75] Pavsv-A        AACACTGAGCGTCTCTTTGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCTCTG
[SEQ ID NO:77] NO:Pavsv-B     CACTCTGAGCGTCTCTTTGCACGGGGTGGAATGCTGATAGGAAACAACTTTATGGCTCCG
[SEQ ID NO:79] NO:Pavsv-C     AACACTGAGCGTCTCTCTGCACGAGATGGAATGCTAATAGGAAACAACTTTATGGCTCTG
[SEQ ID NO:81] RTsv-1         AACACTGAGCGTCTCTTTGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCTCTG
[SEQ ID NO:83] RTsv-2         AACACTGAGCGTCTCTTTGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCTCTG
[SEQ ID NO:85] RTsv-3         AACACTGAGCGTCTCTTTGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCTCTG
                             ** *** *** ** *  ***** * **** **** *********************** *
```

Figure 2 continued

```
[SEQ ID NO:19]  Aasv-1          AAGTTGGAAGGAGGTGGTCATTATTTGTGTGAATTCAAATCTACTTACAAGGCAAAGAAG
[SEQ ID NO:21]  Aasv-3          AAGTTAGAAGGAGGTGGTCACTATTTGTGTGAATTCAAATCTACTTACAAGGCAAGGAAG
[SEQ ID NO:23]  Aasv-P          AAGTTAGAAGGAGGTGGTCACTATTTGTGTGAATTCAAATCTACTTACAAGGCAAAGAAG
[SEQ ID NO:25]  Acasv-A         AAGTTAGAAGGAGGCGGTCACTATTTGTGTGGATTCAAAACTACTTACAAGGCAAAGAAG
[SEQ ID NO:27]  Acasv-C         AAGTTAGAAGGAGGTGGTCACTATTTGTGTGAATTCAAATCTACTTACAAGGCAAGGAAG
[SEQ ID NO:29]  Acasv-D         AAGTTAGAAGGAGGCGGTCACTATTTGTGTGAATTCAAAACTACTTACAAGGCAAAGAAG
[SEQ ID NO:31]  Ce61-3sv        AAGTTAGAAGGAGGTGGTCACTATTTGTGTGAATTCAAATCTACTTACAAGGCAAGGAAG
[SEQ ID NO:33]  Ce61-4sv        AAGTTNGAAGGAGGNGGTCANTATTTGTGTGAATTCAAATCTACTTACAAGGCAAAGAAG
[SEQ ID NO:35]  Ce61-5sv-rep    AAGTTAGAAGGGGGCGGTCACTATTTGTGTGAATTCAAAACTACTTACAAGGCAAAGAAG
[SEQ ID NO:37]  Ce61-7sv-rep    AAGTTAGAAGGAGGCGGTCACTATTTGTGTGAATTCAAAACTACTTACAAGGCAAAGAAG
[SEQ ID NO:39]  GPd58-2sv       AAGTTGGAAGGAGGTGGTCATTATTTGTGTGAATTCAAATCTACTTACAAGGCAAAGAAG
[SEQ ID NO:41]  LGAsv-A         AAGTTGGAAGGAGGTGGTCATTATTTGTGTGAATTCAAATCTACTTACAAGGCAAAGAAG
[SEQ ID NO:43]  LGAsv-C         AAGTTAGAAGGAGGCGGTCACTATTTGTGTGAATTCAAAACTACTTACAAGGCAAAGAAG
[SEQ ID NO:45]  LGAsv-D         AAGTTGGAAGGAGGTGGTCATTATTTGTGTGAATTCAAATCTACTTACAAGGCAAAGAAG
[SEQ ID NO:47]  LGAsv-E         AAGTTGGAAGGAGGTGGTCATTATTTGTGTGAATTCAAATCTACTTACAAGGCAAAGAAG
[SEQ ID NO:49]  Misv-A          AAGTTAGAAGGAGGTGGTCACTATTTATGTGAATTCAAATCTACTTACAAGGCAAGGAAG
[SEQ ID NO:51]  Misv-B          AAGTTAGAAGGAGGTGGTCACTATTTGTGTGAATTCAAATCTACTTACAAGGCAAGGAAG
[SEQ ID NO:53]  Misv-F          AAGTTAGAAGGAGGTGGCCACTATTTGTGTGAATTCAAATCTACTTACAAGGCAAGGAAG
[SEQ ID NO:55]  PM1Asv-rep      AAGTTGGAAGGAGGTGGTCATTATTTGTGTGAATTCAAATCTACTTACAAGGCAAAGAAG
[SEQ ID NO:57]  PM1Csv-rep      AAGTTGGAAGGAAGTGGTCATTATACCTGTGAATTCAAATCTACTTACAAGGCAAAGAAG
[SEQ ID NO:59]  PMsv-4          AAGTTGGAAGGAGG-------------------------------------GCAAAGAAG
[SEQ ID NO:61]  PMsv-5          AAGTTGGAAGGAGGTGGTCATTATTTGTGTGAATTCAAATCTACTTACAAGGCAAAGAAG
[SEQ ID NO:63]  PPsv-1          AAGTTAGAAGGAGGCGGTCACTATTTGTGTGGATTCAAAACTACTTACAAGGCAAAGAAG
[SEQ ID NO:65]  PPsv-2          AAGTTAGAAGGAGGCGGTCACTATTTGTGTGGATTCAAAACTACTTACAAGGCAAAGAAG
[SEQ ID NO:67]  PPsv-3          AAGTTAGAAGGAGGCGGTCACTATTTGTGTGGATTCAAAACTACTTACAAGGCAAAGAAG
[SEQ ID NO:69]  PPsv-4          AAGTTAGAAGGAGGCGGTCACTATTTGTGTGGATTCAAAACTACTTACAAGGCAAAGAAG
[SEQ ID NO:71]  PPsv-5          AAGTTGGAAGGAGGTGGTCATTATTTGTGTGAATTCAAATCTACTTACAAGGCAAAGAAG
[SEQ ID NO:73]  PPsv-6          AAGTTGGAAGGAGGTGGTCATTATTTGTGTGAATTCAAATCTACTTACAAGGCAAAGAAG
[SEQ ID NO:75]  Pavsv-A         AAGTTGGAAGGAGGTGGTCATTATTTGTGTGAATTCAAATCTACTTACAAGGCAAAGAAG
[SEQ ID NO:77]  Pavsv-B         AAGTTAGAAGGAGGCGGTCACTATTTGTGTGAATTCAAAACTACTTACAAGGCAAAGAAG
[SEQ ID NO:79]  Pavsv-C         AAGTTAGAAGGAGGTGGTCACTATTTGTGTGAATTCAAATCTACTTACAAGGCAAGGAAG
[SEQ ID NO:81]  RTsv-1          AAGTTGGAAGGAGGTGGTCATTATTTGTGTGAATTCAAATCTACTTACAAGGCAAAGAAG
[SEQ ID NO:83]  RTsv-2          AAGTTGGAAGGAGGTGGTCATTATTTGTGTGAATTCAAATCTACTTACAAGGCAAAGAAG
[SEQ ID NO:85]  RTsv-3          AAGTTGGAAGGAGGTGGTCATTATTTGTGTGAATTCAAATCTACTTACAAGGCAAAGAAG
                ***** *****   *                                   **** ****
```

Figure 2 continued

```
[SEQ ID NO:19] Aasv-1          CCTGTGATGATGCCAGGGTATCACTATGTTGACCGCAAGTTGGATGTAACCAATCACAAC
[SEQ ID NO:21] Aasv-3          CCTGTGAAGATGCCAGGGTATCACTATGTTGACCGCAAACTGGATGTAACCAATCACAAC
[SEQ ID NO:23] Aasv-P          CCTGTGAGGATGCCAGGGTATCACTATGTTGACCGCAAACTGGATGTAACCAATCACAAC
[SEQ ID NO:25] Acasv-A         CCTGTGAAGATGCCAGGGTATCATTATGTTGACCGCAAACTGGATGTAACCAATCACAAC
[SEQ ID NO:27] Acasv-C         CCTGTGAAGATGCCAGGGTATCACTGTGTTGACCGCAAACTGGATGTAACCAATCACAAC
[SEQ ID NO:29] Acasv-D         CCTGTGAAGATGCCGGGGTATCATTATGTTGACCGCAAACTGGATGTAACCAATCACAAC
[SEQ ID NO:31] Ce61-3sv        CCTGTGAAGATGCCAGGGTATCACTATGTTGACCGCAAACTGGATGTAACCAATCACAAC
[SEQ ID NO:33] Ce61-4sv        CCTGTGATGATGCCAGGGTATCACTATGTTGACCGCAAATTGGATGTAACCAATCACAAC
[SEQ ID NO:35] Ce61-5sv-rep    CCTGTGAAGATGCCAGGGTATCATTATGTTTACAGCACCATTCATGTAACCAATCACAAC
[SEQ ID NO:37] Ce61-7sv-rep    CCTGTGAAGATGCCAGGGTATCATTATGTTGACCGCAAACTGGATGTAACCAATCACAAC
[SEQ ID NO:39] GPd58-2sv       CCTGTGATGATGCCAGGGTATCACTATGTTGACCGCAAATTGGATGTAACCAATCACAAC
[SEQ ID NO:41] LGAsv-A         CCTGTGATGATGCCAGGGTATCACTATGTTGACCGCAAATTGGATGTAACCAATCACAAC
[SEQ ID NO:43] LGAsv-C         CCTGTGAAGATGCCAGGATATCATTATGTTGACCGCAAACTGGATGTAACCAATCACAAC
[SEQ ID NO:45] LGAsv-D         CCTGTGATGATGCCAGGGTATCACTATGTTGACCGCAAATTGGATGTAACCAATCACAAC
[SEQ ID NO:47] LGAsv-E         CCTGTGATGATGCCAGGGTATCACTATGTTGACCGCAAATTGGATGTAACCAATCACAAC
[SEQ ID NO:49] Misv-A          CCTGTGAAGATGCCAGGGTATCACTATGTTGACCGCAAACTGGATGTAACCAATCACAAC
[SEQ ID NO:51] Misv-B          CCTGTGAAGATGCCAGGGTATCACTATGTTGACCGCAAACTGGATGTAACCAATCACAAC
[SEQ ID NO:53] Misv-F          CCTGTGAAGATGCCAGGGTATCACTATGTTGACCGCAAACTGGATGTAACCAATCACAAC
[SEQ ID NO:55] PM1Asv-rep      CCTGTGATGATGCCAGGGTATCACTATGTTGACCGCAAGTTGGATGTAACCAATCACAAC
[SEQ ID NO:57] PM1Csv-rep      CCTGTGATGATGCCTGGATATCACTATGTTGACCGCAAATTGGATGTAACCAATCACAAC
[SEQ ID NO:59] PMsv-4          CCTGTGATGATGCCAGGGTATCACTATGTTGACCGCGAATTGGATGTAACCAATCACAAC
[SEQ ID NO:61] PMsv-5          CCTGTGATGATGCCAGGGTATCACTATGTTGACCGCAAATTGGATGTAACCAATCACAAC
[SEQ ID NO:63] PPsv-1          CCTGTGAAGATGCCAGGGTATCATTATGTTGACCGCAAACTGGATGTAACCAATCACAAC
[SEQ ID NO:65] PPsv-2          CCTGTGAAGATGCCAGGGTATCATTATGTTGACCGCAAACTGGATGTAACCAATCACAAC
[SEQ ID NO:67] PPsv-3          CCTGTGAAGATGCCAGGGTATCATTATGTTGACCGCAAACTGGATGTAACCAATCACAAC
[SEQ ID NO:69] PPsv-4          CCTGTGAAGATGCCAGGGTATCATTATGTTGACCGCAAACTGGATGTAACCAATCACAAC
[SEQ ID NO:71] PPsv-5          CCTGTGATGATGCCAGGGTATCACTATGTTGACCGCAAATTGGATGTAACCAATCACAAC
[SEQ ID NO:73] PPsv-6          CCTGTGATGATGCCAGGGTATCACTATGTTGACCGCAAATTGGATGTAACCAATCACAAC
[SEQ ID NO:75] Pavsv-A         CCTGTGATGATGCCAGGGTATCACTATGTTGACCGCAAATTGGATGTAACCAATCACAAC
[SEQ ID NO:77] Pavsv-B         CCTGTGAAGATGCCGGGGTATCATTATGTTGACCGCAAACTGGATGTAACCAATCACAAC
[SEQ ID NO:79] Pavsv-C         CCTGTGAAGATGCCAGGGTATCACTATGTTGACCGCAAACTGGATGTAACCAATCACAAC
[SEQ ID NO:81] RTsv-1          CCTGTGATGATGCCAGGGTATCACTATGTTGACCGCAAATTGGATGTAACCAATCACAAC
[SEQ ID NO:83] RTsv-2          CCTGTGATGATGCCAGGGTATCACTATGTTGACCGCAAATTGGATGTAACCAATCACAAC
[SEQ ID NO:85] RTsv-3          CCTGTGATGATGCCAGGGTATCACTATGTTGACCGCAAATTGGATGTAACCAATCACAAC
                               ******* ****** ** ***** * **** ** **    *  *****************
```

Figure 2 continued

```
[SEQ ID NO:19] Aasv-1           AAGGATTACACTTCCGTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:21] Aasv-3           AAGGATTACACTTCCGTTGAGCAGCGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:23] Aasv-P           AAGGATTACACTTCCGTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:25] Acasv-A          AAGGATTACATTTCCGTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:27] Acasv-C          AAGGATTACACTTCCGTTGAGCAGCGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:29] Acasv-D          AAGGATTACACTTCCGTTGAGCAGTGTGAAATCTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:31] Ce61-3sv         AAGGATTACACTTCCGTTGAGCAGCGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:33] Ce61-4sv         AAGGATTACACTTCCGTTGAGCAGTGTGAAATATCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:35] Ce61-5sv-rep     AAGGATTACACTTCCGTTGAGCAGTGTGAAATTTCCNNTNCACGCAAACCTGTGGTCGCC
[SEQ ID NO:37] Ce61-7sv-rep     AAGGATTACACTTCCGTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:39] GPd58-2sv        AAGGATTACACTTCCGTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:41] LGAsv-A          AAGGATTACACTTCCGTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:43] LGAsv-C          AAGGATTACACTTCCGTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:45] LGAsv-D          AAGGATTACACTTCCGTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:47] LGAsv-E          AAGGATTACACTTCCGTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:49] Misv-A           AAGGATTACACTTCCGTTGAGCAGCGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:51] Misv-B           AAGGATTACACTTCCGTTGAGCAGCGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:53] Misv-F           AAGGATTACACTTCCGTTGAGCAGCGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:55] PM1Asv-rep       AAGGATTACACTTCCGTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:57] PM1Csv-rep       AAGGATTACACTTCCGTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:59] PMsv-4           AAGGATTACACTTCCGTTGAGCAGTGTGAGATTTCCATCGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:61] PMsv-5           AAGGATTACACTTCCGTTGAGCAGTGTGAGATTTCCATCGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:63] PPsv-1           AAGGATTACATTTCCGTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:65] PPsv-2           AAGGATTACATTTCCGTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:67] PPsv-3           AAGGATTACATTTCCGTTGAGCAGTGTGAAACTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:69] PPsv-4           AAGGATTACATTTCCGTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:71] PPsv-5           AAGGATTACACTTCCGTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:73] PPsv-6           AAGGATTACACTTCCGTTGAGCAGTGTGGAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:75] Pavsv-A          AAGGATTACACTTCCGTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:77] Pavsv-B          AAGGATTACACTTCCGTTGAGCAGTGTGAAATCTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:79] Pavsv-C          AAGGATTACACTTCCGTTGAGCAGCGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:81] RTsv-1           AAGGATTACACTTCCGTTGAGCAGTGTGAAATTCCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:83] RTsv-2           AAGGATTACACTTCCGTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:85] RTsv-3           AAGGATTACACTTCCGTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
                ********** ************* ***  *   **    ********************
```

Figure 2 continued

```
Aasv-1          ---------------------------------
Aasv-3          ---------------------------------
Aasv-P          TGA------------------------------
Acasv-A         ---------------------------------
Acasv-C         ---------------------------------
Acasv-D         ---------------------------------
Ce61-3sv        ---------------------------------
Ce61-4sv        ---------------------------------
Ce61-5sv-rep    ---------------------------------
Ce61-7sv-rep    ---------------------------------
GPd58-2sv       ---------------------------------
LGAsv-A         ---------------------------------
LGAsv-C         ---------------------------------
LGAsv-D         ---------------------------------
LGAsv-E         ---------------------------------
Misv-A          ---------------------------------
Misv-B          ---------------------------------
Misv-F          ---------------------------------
PM1Asv-rep      ---------------------------------
PM1Csv-rep      ---------------------------------
PMsv-4          TGACGTTTTTTCAGAGTCAAATCAAGGCACAAA
PMsv-5          TGACGTTTTTTCAGAGTCAAATCAAGGCACAAA
PPsv-1          ---------------------------------
PPsv-2          ---------------------------------
PPsv-3          ---------------------------------
PPsv-4          ---------------------------------
PPsv-5          ---------------------------------
PPsv-6          ---------------------------------
Pavsv-A         ---------------------------------
Pavsv-B         ---------------------------------
Pavsv-C         ---------------------------------
RTsv-1          ---------------------------------
RTsv-2          ---------------------------------
RTsv-3          ---------------------------------
```

Figure 2 continued

```
[SEQ ID NO:88]     Aams-2.pep      ATTGLRVMDISISFTEGAT*ETFANRCSALLILNMSVIATQMTYKVYMSGTVNGHYFEVE
[SEQ ID NO:90]     Aams-4.pep      ATTGLRVMDISISFTEGAT*ETFANRCSALLILNMSVIATQMTYKVYMSGTVNGHYFEVE
[SEQ ID NO:92]     Aams-5.pep      -----------------------------------SGIATQMTYKVYMSGTVNGHYFEVE
[SEQ ID NO:94]     Aams-6.pep      -----------------------------------SVIATQMTYKVYMSGTVNGHYFEVE
[SEQ ID NO:96]     Aams-A.pep      SGIATQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC
[SEQ ID NO:98]     Aams-B.pep      SVIATQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC
[SEQ ID NO:100]    Acams-2.pep     ----------------------------------MSVIATQMTYKVYMSGTANGHYFEVE
[SEQ ID NO:102]    Acams-3.pep     ----------------------------------MSVIATQMTYKVYMSGTANGHYFEVE
[SEQ ID NO:104]    Acams-4.pep     ----------------------------------MSVIATQMTYKVYMSGTANGHYFEVE
[SEQ ID NO:106]    Acams-5.pep     -----------------------------------SVIATQMTYKVYMSGTVNGHYFEVE
[SEQ ID NO:108]    Cems-F.pep      ----------------------------------MSVIATQMTYKVYMSGTVNGHYFEVE
[SEQ ID NO:110]    Cems-G.pep      ----------------------------------MSVIATQMTYKVYMSGTVNGHYFEVE
[SEQ ID NO:112]    Cems-H.pep      -----------------------------------SVIATQMTYKVYMSGTVNGHYFEVE
[SEQ ID NO:114]    Cems-I.pep      -----------------------------------SVIATQMTYKVYMSGTVNGHYFEVE
[SEQ ID NO:116]    LGAms-5.pep     ----------------------------------MSVIATQMTYKVYMSGTVNGHYFEVE
[SEQ ID NO:118]    LGAms-6.pep     ----------------------------------MSVIATQMTYKVYMSGTVNGHYLEVE
[SEQ ID NO:120]    Mi68Dms.pep     -----------------------------------SVIATQMTYKVYMSGTVDGHYFEVE
[SEQ ID NO:122]    Mims-A.pep      ----------------------------------MSVIATQMTYKVYMSGTVDGHYFEVE
[SEQ ID NO:124]    Mims-B.pep      ----------------------------------MSVIATQMTYKVYMSGTVDGHYFEVE
[SEQ ID NO:126]    Mims-C.pep      -----------------------------------SVIATQMTYKVYMSGTVDGHYFEVE
[SEQ ID NO:128]    PMms-A.pep      ----------------------------------MSVIATQMTYKVYMPGTVNGHYFEVE
[SEQ ID NO:130]    PMms-B.pep      ----------------------------------MSVIATQMTYKVYMSGTVNGHYFEVE
[SEQ ID NO:132]    PMms-C.pep      -----------------------------------SVIATQMTYKVYMSGTVNGHYFEVQ
[SEQ ID NO:134]    PMms-D.pep      -----------------------------------SVIATQMTYKVYMSGTVNGHYFEVE
[SEQ ID NO:136]    PMms-E.pep      -----------------------------------SVIATQMTYKVYMSGTVNGHYFEVE
[SEQ ID NO:138]    PPd57-1ms.pep   -----------------------------------SVIATQMTYKVYMSGTVNGHYFEVE
[SEQ ID NO:140]    PPd57-2ms.pep   ----------------------------------MSVIATQMTYKVYMSGTVNGHYFEVE
[SEQ ID NO:142]    PPd57-3.pep     ----------------------------------MSVIATQMTYKVYMSGTVNGHYFEVE
[SEQ ID NO:144]    PPd57-4ms.pep   -----------------------------------SVIATQMTYKVYMSGTVNGHYFEVE
[SEQ ID NO:146]    PPms-1.pep      ----------------------------------MSVIATQMTYKVYMSGTVNGHYFEVE
[SEQ ID NO:148]    PPms-2.pep      ----------------------------------MSVIATQMTYKVYMSGTVNGHYFEVE
[SEQ ID NO:150]    PPms-E.pep      -----------------------------------SVIATQMTYKVYMSGTVNGHYFEVE
[SEQ ID NO:152]    PPms-G.pep      -----------------------------------SVIATQMTYKVYMSGTVNGHYFEVE
[SEQ ID NO:154]    Pav5ms.pep      -----------------------------------SVIATQMTYKVYMSGTVNGHYFEVE
[SEQ ID NO:156]    Pavms-2.pep     ----------------------------------MSVIATQMTYKVYMSGTVNGHYFEVE
[SEQ ID NO:158]    Pavms-3.pep     ----------------------------------MSVIATQVTYKVYMSGTVNGHYFEVE
[SEQ ID NO:160]    Pavms-4.pep     -----------------------------------SVIATQMTYKVYMSGTVNGHYFEVE
[SEQ ID NO:162]    RTms-1.pep      ----------------------------------MSVIATQMTYKVYMSGTVNGHYFEVE
[SEQ ID NO:164]    RTms-2.pep      ----------------------------------MSVSATQMTYKVYMSGTVNGHYFEVE
[SEQ ID NO:166]    RTms-5.pep      -----------------------------------SVIATQMTYKVYMSGTVNGHYFEVE
[SEQ ID NO:168]    RTms-6.pep      -----------------------------------SVIVTQMTYKVYMSGTVNGHYFEVE
                                                                      *   **.****** **  *** **.
```

Figure 3

```
[SEQ ID NO:88]       Aams-2.pep        GDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQCQYGSIPFTKYPEDIPDYVKQSFPE
[SEQ ID NO:90]       Aams-4.pep        GDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQCQYGSIPFTKYPEDIPDYVKQSFPE
[SEQ ID NO:92]       Aams-5.pep        GDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQCQYGSIPFTKYPEDIPDYVKQSFPE
[SEQ ID NO:94]       Aams-6.pep        GDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQCQYGSIPFTKYPEDIPDYVKQSFPE
[SEQ ID NO:96]       Aams-A.pep        QYGSIPFTKYPEDIPDYVKQSFPEGFTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKF
[SEQ ID NO:98]       Aams-B.pep        QYGSIPFTKYPEDIPDYVKQSFPEGFTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKF
[SEQ ID NO:100]      Acams-2.pep       GDGKGKPYEGEQTVRLIVTKGGPLPFA*DILSPQYQYGSIPFTKYPEDIPDYVKQSFPE
[SEQ ID NO:102]      Acams-3.pep       GDGKGKPYEGEQTVRLIVTKGGPLPFA*DILSPQYQYGSIPFTKYPEDIPDYVKQSFPE
[SEQ ID NO:104]      Acams-4.pep       GDGKGKPYEGEQTVRLTVTKGGPLPFAWDILSPQYQYGSIPFTKYPEDIPDYVKQSFPE
[SEQ ID NO:106]      Acams-5.pep       GDGKGKPTRGSRR*---------------------------------------------
[SEQ ID NO:108]      Cems-F.pep        GDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQCQYGNIPFTKYPEDVPDYVKRSFPE
[SEQ ID NO:110]      Cems-G.pep        GDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQCQYGNIPFTKYPEDVPDYVKQSFPE
[SEQ ID NO:112]      Cems-H.pep        GDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQCQYGNIPFTKYPEDVPDYVKQSFPE
[SEQ ID NO:114]      Cems-I.pep        GDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQCQYGNIPFTKYPEDVPDYVKQSFPE
[SEQ ID NO:116]      LGAms-5.pep       GDGKGKPYEGEQTVRLTVTKGGPLPFAWDILSPQYQYGSIPFTKYPEDIPDYVKQSFPE
[SEQ ID NO:118]      LGAms-6.pep       GDGKGKPYEGEQTVRLTVTKGGPLPFAWDILSPQYQYGSIPFTKYPEDIPDYVK*SFPE
[SEQ ID NO:120]      Mi68Dms.pep       GDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQCQYGSIPFTKYPEDIPDYVKQSFPE
[SEQ ID NO:122]      Mims-A.pep        GDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQCQYGSIPFTKYPEDIPDYVKQSFPE
[SEQ ID NO:124]      Mims-B.pep        GDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQCQYGSIPFTKYPEDIPDYVKQSFPE
[SEQ ID NO:126]      Mims-C.pep        GDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQCQYGSIPFTKYPEDIPDYVKQSFPE
[SEQ ID NO:128]      PMms-A.pep        GDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQSQYGSIPFTKYPEDIPDYVKQSFPE
[SEQ ID NO:130]      PMms-B.pep        GDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQSQYGSIPFTKYPEDIPDYVKQSFPE
[SEQ ID NO:132]      PMms-C.pep        GDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQTQYGSIPFTKYPDDIPDYVKQSFPE
[SEQ ID NO:134]      PMms-D.pep        GDGQGKPYEGEQTVKLTVTKGGPLPFAWDILSPQSQYGSIPFTKYPEDIPDYVKQSFPE
[SEQ ID NO:136]      PMms-E.pep        GDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQSQYGSIPFTKYPEDIPDYVKQSFPE
[SEQ ID NO:138]      PPd57-1ms.pep     GDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQTQYGSIPFTKYPEDIPDYVKQSFPE
[SEQ ID NO:140]      PPd57-2ms.pep     GDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQCQYGSIPFTKYPEDIPDYVKQSFPE
[SEQ ID NO:142]      PPd57-3.pep       GDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQCQYGSIPFTKYPEDIPDYVKQSFPE
[SEQ ID NO:144]      PPd57-4ms.pep     GDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQSQYGSIPFTKYPEDIPDYVKQSFPE
[SEQ ID NO:146]      PPms-1.pep        GDGKGKPYEGERTVKLTVTKGGPLPFAWDILSPQCQYGNIPFTKYPEDVPDYVKQSFPE
[SEQ ID NO:148]      PPms-2.pep        GDGKGKPYEGEQTVRLTVTKGGPLPFAWDILSPQYQYGSIPFTKYPEDIPDYVK*SFPE
[SEQ ID NO:150]      PPms-E.pep        GDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQSQYGSIPFTKYPEDIPDYVKQSFPE
[SEQ ID NO:152]      PPms-G.pep        GDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQCQYGNIPFTKYPEDVPDYVKQSFPE
[SEQ ID NO:154]      Pav5ms.pep        GDGKGEPYEGEQTVRLTVTKGGPLPFAWDILSPQYQYGSIPFTKYPEDIPDYVKQSFPE
[SEQ ID NO:156]      Pavms-2.pep       GDGKGKPYEGEQTVRLTVTKGGPLPFAWDILSPQYQYGSIPFTKYPEDIPDYV*QSFPE
[SEQ ID NO:158]      Pavms-3.pep       GDGKGKPYEGEQTVRLTVTKGGPLPFAWDILSPQYQYGSIPFTKYPEDIPDYVKQSFPE
[SEQ ID NO:160]      Pavms-4.pep       GDGKGKPYEGEQTVRLTVTKGGPLPFAWDILSPQYQYGSIPFTKYPEDIPDYVKQSFPE
[SEQ ID NO:162]      RTms-1.pep        GDGKGKPYEGEQTVRLTVTKGGPLPFAWDILSPQYQYGSIPFTKYPEDIPDYVKQSFPE
[SEQ ID NO:164]      RTms-2.pep        GDGKGKPYEGEQTVRLTVTKGGPLPFAWDILSPQYQYGSIPFTKYPEDIPGYVKQSFPE
[SEQ ID NO:166]      RTms-5.pep        GDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQCQYGSIPFTKYPEDIPDYVKQSFPE
[SEQ ID NO:168]      RTms-6.pep        GDGKGKPYEGEQTVRLTVTKGGPLPFAWDILSPQYQYGSIPFTKYPEDIPDYVKQSFPE
                ***.*  *  *  .    * ********** ****** *** ******* *.* **   ****
```

Figure 3 continued

```
[SEQ ID NO:88]     Aams-2.pep     GFTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFSGLNFPPNGPVMQKKTQGWEPHS
[SEQ ID NO:90]     Aams-4.pep     GFTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFSGLNFPPNGPVMQKKTQGWEPHS
[SEQ ID NO:92]     Aams-5.pep     GFTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFSGLNFPPNGPVMQKKTQGWEPHS
[SEQ ID NO:94]     Aams-6.pep     GFTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFSGLNFPPNGPVMQKKTQGWEPHS
[SEQ ID NO:96]     Aams-A.pep     SGLNFPPNGPVMQKKTQGWEPHSERLFARDGMLIGNNFMALKLEGGGHYLCEFKTTVK
[SEQ ID NO:98]     Aams-B.pep     SGLNFPPNGPVMQKKTQGWEPHSERLFARDGMLIGNNFMALKLEGGGHYLCEFKTTTK
[SEQ ID NO:100]    Acams-2.pep    GYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFSGLNFPPNGPVMQKKTQGWEPNT
[SEQ ID NO:102]    Acams-3.pep    GYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFSGLNFPPNGPVMQKKTQGWEPNT
[SEQ ID NO:104]    Acams-4.pep    GYTWERIMNFEDGAVCTVSNDSSIQGNCFIHHVKFSGLNFPPNGPVMQKKTQGWEPNT
[SEQ ID NO:106]    Acams-5.pep    ----------------------------------------------------------
[SEQ ID NO:108]    Cems-F.pep     GFTWERIMNFEDGAVCTVSNDSSIQGNCFTYHVKFSGLNFPPNGPVMQKKTQGWEPHS
[SEQ ID NO:110]    Cems-G.pep     GFTWERIMNFEDGAVCTVSNDSSIQGNCFTYHVKFSGLNFPPNGPVMQKKTQGWEPHS
[SEQ ID NO:112]    Cems-H.pep     GFTWERIMNFEDGAVCTVSNDSSIQGNCFTYHVKFSGLNFPPNGPVMQKKTQGWEPHS
[SEQ ID NO:114]    Cems-I.pep     GFTWERIMNFEDGAVCTVSNDSSIQGNCFTYHVKFSGLNFPPNGPVM*KKTQGWEPHS
[SEQ ID NO:116]    LGAms-5.pep    GYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFSGLNFPPNGPVMQKKTQGWEPNT
[SEQ ID NO:118]    LGAms-6.pep    GFTWDRIMDFEDGAVCTVSNDSSIQGNCFIYHVKFSGLNFPPNGPVMQKKTQGWEPNT
[SEQ ID NO:120]    Mi68Dms.pep    GFTWERIMNFENGAVCTVSNDSSIQGNCFTYHVKFSGLNFPPNGPVMQKKTQGWEPHS
[SEQ ID NO:122]    Mims-A.pep     GFTWERIMNFEDGAVCTVSNDSSIQGNCFTYHVKFSGLNFPPNGPVMQKKTQGWEPHS
[SEQ ID NO:124]    Mims-B.pep     GFTWERIMNFEDGAVCTVSNGSSIQGNCFTYHVKFSGLNFPPNGPVMQKKTQGWEPHS
[SEQ ID NO:126]    Mims-C.pep     GFTWERIMNFEDGAVCTVSNDSSIQGNCFTYHVKFSGLNFPPNGPVMQKKTQGWEPHS
[SEQ ID NO:128]    PMms-A.pep     GYTWERIMNFEDGAVCTVSNDSSIQGNCFIYNVKFSGLNFPPNGPVMQKKTQGWEPNT
[SEQ ID NO:130]    PMms-B.pep     GYTWERIMNFEDGAVCTVSNDSSIQGNCFIYNVKFSGLNFPPNGPVMQKKTQGWEPNT
[SEQ ID NO:132]    PMms-C.pep     GYTWERIMKFEDGAVCTVTNDSSMQGNCFIYNVKFSGLNFPPNGPVMQKKTQGWEPNT
[SEQ ID NO:134]    PMms-D.pep     GYTWERIMNFEDGAVCTVSNDSSIQGNCFIYNVKFSGLNFPPNGPVMQKKTQGWEPNT
[SEQ ID NO:136]    PMms-E.pep     GYTWERIMNFEDGAVCTVSNDSSIQGNCFIYNVKFSGLNFPPNGPVMQKKTQGWEPNT
[SEQ ID NO:138]    PPd57-1ms.pep  GYTWERIMKFEDGAVCTVSNDSSMQGNCFIYNVKFSGLNFPPNGPVMQKKTQGWEPNT
[SEQ ID NO:140]    PPd57-2ms.pep  GFTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFSGLNFPPNGPVMQKKTQGWEPHS
[SEQ ID NO:142]    PPd57-3.pep    GFTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFSGLNFPPNGPVMQKKTQGWEPHS
[SEQ ID NO:144]    PPd57-4ms.pep  GYTWERIMNFEDGAVCTVSNDSSIQGNCFIYNVKFSGLNFPPNGPVMQKKTQGWEPNT
[SEQ ID NO:146]    PPms-1.pep     GFTWERIMNFEDGAVCTVSNDSSIQGNCFTYHVKFSGLNFPPNGPVMQKKTQGWEPHS
[SEQ ID NO:148]    PPms-2.pep     GFTWDRIMNFEDGAVCTVSNDSSIQGNCFIYHVKFSGLNFPPNGPVMQKKTQGWEPNT
[SEQ ID NO:150]    PPms-E.pep     GFTWERIMNFEDGAVCTVSNDSSIQGNCFTYHVKFSGLNFPPNGPVMQKKTQGWEPHS
[SEQ ID NO:152]    PPms-G.pep     GFTWEGIMNFEDGAVCTVSNDSSIQGNCFTYHVKFSGLNFPPNGPVMQKKTQGWEPHS
[SEQ ID NO:154]    Pav5ms.pep     GYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFSGLNFPPNGPVTQKKTQGWEPNT
[SEQ ID NO:156]    Pavms-2.pep    GYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFSGLNFPPNGPVMQKKTQGWEPNT
[SEQ ID NO:158]    Pavms-3.pep    GYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFSGLNFPPNGPVMQKKTQGWEPNT
[SEQ ID NO:160]    Pavms-4.pep    GYTWEGIMNFEDGAVCTVSNDSSIQGNCFIYHVKFSGLNFPPNGPVMQKKTQGWEPNT
[SEQ ID NO:162]    RTms-1.pep     GYTWERIMNFEDGAVCAVSNDSSIQGNCFIYHVKFSGLNFPPNGPVMQKKTQGWEPNT
[SEQ ID NO:164]    RTms-2.pep     GYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFSGLNFPPNGPVMQKKTQGWEPNT
[SEQ ID NO:166]    RTms-5.pep     GFTWERIMNFEDGAVCTVSNDSSIQGNCFTYHVKFSGLNFPPNGPVMQKKTQGWEPHS
[SEQ ID NO:168]    RTms-6.pep     GYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFSGLNFPPNGPVMQKKTQGWEPNT
               * **  ** ** **** *.**** *****   **************  ********
```

Figure 3 continued

```
[SEQ ID NO:88]    Aams-2.pep       ERLFARDGMLIGNNFMALKLEGGGHYLCEFKTTYKAKKPVKMPGYHYVDRKLDV
[SEQ ID NO:90]    Aams-4.pep       ERLFARDGMLIGNNFMALKLEGGGHYLCEFKTTYKAKKPVKMPGYHYVDRKLDV
[SEQ ID NO:92]    Aams-5.pep       ERLFARDGMLIGNNFMALKLEGGGHYLCEFKTTYKAKKPVKMPGYHYVDRKLDV
[SEQ ID NO:94]    Aams-6.pep       ERLFARDGMLIGNNFMALKLEGGGHYLCEFKTTYKAKKPVKMPGYHYVDRKLDV
[SEQ ID NO:96]    Aams-A.pep       AKKPVKMPGYHYVDRKLDVINHNKDYTSVEQCEISIARKPVVA-----------
[SEQ ID NO:98]    Aams-B.pep       AKKPVKMPGYHYVDRKLDVINHNKDYTSVEQCEISIARNPVVA-----------
[SEQ ID NO:100]   Acams-2.pep      ERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKKPVKMPGYHYVDRKLDV
[SEQ ID NO:102]   Acams-3.pep      ERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKKPVKMPGYHYVDRKLDV
[SEQ ID NO:104]   Acams-4.pep      ERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKKPVKMPGYHYVDRKLDV
[SEQ ID NO:106]   Acams-5.pep      ------------------------------------------------------
[SEQ ID NO:108]   Cems-F.pep       ERLFARGGMLIGNNFMALKLEGGGHYLCGFKTTYKAKKPVKMPGYHYVDRKLDV
[SEQ ID NO:110]   Cems-G.pep       ERLLARGGMLIGNNFMALKLEGGGHYLCGFKTTYKAKKPVKMPGYHYVDRKLDV
[SEQ ID NO:112]   Cems-H.pep       ERLFARGGMLIGNNFMALKLEGGGHYLCGFKTTYKAKKLVKMPGYHYVDRKLDV
[SEQ ID NO:114]   Cems-I.pep       ERLFARGGMLIGNNFMALKLEGGGHYLCEFKTTYKAKKPVKMPGYHYADRKLDV
[SEQ ID NO:116]   LGAms-5.pep      ERLLARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKKPVKMPGYHYVDRKLDV
[SEQ ID NO:118]   LGAms-6.pep      ERLFARDGMLLGNNFMALKLEGGGHYLCEFKTTYKAKKPVKMPGYHYVDRKLDV
[SEQ ID NO:120]   Mi68Dms.pep      ERLFARGGMLIGNNFMALKLEGGGHYLCEFKTTYKAKKPVKMPGYHYVDRKLDV
[SEQ ID NO:122]   Mims-A.pep       ERLFARGGMLIGNNFMALKLEGGGHYLCEFKTTYKAKKPVKMPGYHYVDRKLDV
[SEQ ID NO:124]   Mims-B.pep       ERLFARGGMLIGNNFMALKLGGGGHYLCEFKTTYRAKKPVKMPGYHYVDRKLDV
[SEQ ID NO:126]   Mims-C.pep       ERLFARGGMLIGNNFMALKLEGGGHYLCEFKTTYKAKKPVKMPGYHYVDRKLDV
[SEQ ID NO:128]   PMms-A.pep       ERLYARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKKPVMMPGYHYVDRKLDV
[SEQ ID NO:130]   PMms-B.pep       ERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKKPVMMPGYHYVDRKLDV
[SEQ ID NO:132]   PMms-C.pep       GRLYARDGMLIGNNFMALKLEGGGHYTCEFKSTYKAKKPVMMPGYHYVDRKLDV
[SEQ ID NO:134]   PMms-D.pep       ERLFARDGMLIGNNFMALKSEGGGHYLCEFKSTYKAKKPVMMPGYHYVDRKLDV
[SEQ ID NO:136]   PMms-E.pep       ERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKKPVMMPGYHYVDRKLDV
[SEQ ID NO:138]   PPd57-1ms.pep    ERLYARDGMLIGNNFMALKLEGGGHYTCEFKSTYKAKKPVMMPGYHYVDRKLDV
[SEQ ID NO:140]   PPd57-2ms.pep    ERLFARDGMLIGNNFMALKLEGGGHYLCEFKTTYKAKKPVKMPGYHYVDRKLDV
[SEQ ID NO:142]   PPd57-3.pep      ERLFARDGMLIGNNFMALKLEGGGHYLCEFKTTYKAKKPVKMPGYHYVDRKLDV
[SEQ ID NO:144]   PPd57-4ms.pep    ERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKKPVMMPGYHYVDRKLDV
[SEQ ID NO:146]   PPms-1.pep       ERLFARGGMLIGNNFMALKLEGGGHYLCGFKTTYKAKKPVKMPGYHYVDRKLDV
[SEQ ID NO:148]   PPms-2.pep       ERLLARDGMLLGNNFMALKLEGGGHYLCEFKTTYKAKKPVKMPGYHYVDRKLDV
[SEQ ID NO:150]   PPms-E.pep       ERLFARGGMLIGNNFMALKLEGGGHYLCGFKTTYKAKKPVKMPGYHYVDRKLDV
[SEQ ID NO:152]   PPms-G.pep       ERLFARGGMLIGNNFMALKLEGGGHYLCGFKTTYKAKKPVKMPGYHYVDRKLDV
[SEQ ID NO:154]   Pav5ms.pep       ERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKKTVKMPGYHYVDRKLDV
[SEQ ID NO:156]   Pavms-2.pep      ERLFARDGLLIGNNFMALKLEEGGHYLCEFKSTYKAKKTAKMPGYHYVDRKLDV
[SEQ ID NO:158]   Pavms-3.pep      ERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKKTVKMPGYHYVDRKLDV
[SEQ ID NO:160]   Pavms-4.pep      ERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKKTVKMPGYHYVDRKLVV
[SEQ ID NO:162]   RTms-1.pep       ERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKKPVKMPGYHYVDRKLDV
[SEQ ID NO:164]   RTms-2.pep       ERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKKPVKMPGYHYVDRKLDV
[SEQ ID NO:166]   RTms-5.pep       ERLFARGGMLIGNNFMALKLEGGGHYLCEFKTTYKAKKPVKMPGYHYVDRKLDV
[SEQ ID NO:168]   RTms-6.pep       ERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKKPVKMPGYHYVDRKLDV
                  ** ** *.***********  ****** ** ******.. ****** **** *
```

Figure 3 continued

```
[SEQ ID NO:88]     Aams-2.pep        TNHNKDYTSVEQCEISITRKPVVA
[SEQ ID NO:90]     Aams-4.pep        TNHNKDYTSVEQCEISITRKPVVA
[SEQ ID NO:92]     Aams-5.pep        INHNKDYTSVEQCEISIARKPVVA
[SEQ ID NO:94]     Aams-6.pep        INHNKDYTSVEQCEISIARNPVVA
[SEQ ID NO:96]     Aams-A.pep
[SEQ ID NO:98]     Aams-B.pep
[SEQ ID NO:100]    Acams-2.pep       TNHNKDYTSVEQCEISIARKPVVA
[SEQ ID NO:102]    Acams-3.pep       TNHNKDYTSVEQCEISIARKPVVA
[SEQ ID NO:104]    Acams-4.pep       TNHNKDYTSVEQCEISIARKPVVA
[SEQ ID NO:106]    Acams-5.pep       ------------------------
[SEQ ID NO:108]    Cems-F.pep        TNHNKDYISVEQCEISIARKPVVA
[SEQ ID NO:110]    Cems-G.pep        TNHNKDYISVEQCEISIARKPVVA
[SEQ ID NO:112]    Cems-H.pep        TNHNKDYISVEQCEISIARKPVVA
[SEQ ID NO:114]    Cems-I.pep        TNHNKDYTSVEQCEISIARKPVVA
[SEQ ID NO:116]    LGAms-5.pep       TNHNKDYTSVEQCEISIARKPVVA
[SEQ ID NO:118]    LGAms-6.pep       TNHNKDYTSVEQCEISIARKPVVA
[SEQ ID NO:120]    Mi68Dms.pep       TNHNKDYTSVEQCEISIARKPVVA
[SEQ ID NO:122]    Mims-A.pep        TNHNKDYTSVEQCEISIARKPVVA
[SEQ ID NO:124]    Mims-B.pep        TNHNKDYTSVEQCEISIARKPVVA
[SEQ ID NO:126]    Mims-C.pep        TNHNKDYTSVEQCEISIARKPVVA
[SEQ ID NO:128]    PMms-A.pep        TNHNKDYTSVEQCEISIARKPVVA
[SEQ ID NO:130]    PMms-B.pep        TNHNKDYTSVEQCEISIARKPVVA
[SEQ ID NO:132]    PMms-C.pep        TNHNKDYTSVEQCEISIARKPVVA
[SEQ ID NO:134]    PMms-D.pep        TNHNKDYTSVEQCEISIARKPVVA
[SEQ ID NO:136]    PMms-E.pep        TNHNKDYTSVEQCEISIARKPVVA
[SEQ ID NO:138]    PPd57-1ms.pep     TNHNKDYTSVEQCEISIARKPVVA
[SEQ ID NO:140]    PPd57-2ms.pep     TNHNKDYTSVEQCEISIARKPVVA
[SEQ ID NO:142]    PPd57-3.pep       TNHNKDYTSVEQCEISIARKPVVA
[SEQ ID NO:144]    PPd57-4ms.pep     TNHNKDYTSVEQCEISIARKPVVA
[SEQ ID NO:146]    PPms-1.pep        TNHNKDYISVEQCEISIARKPVVA
[SEQ ID NO:148]    PPms-2.pep        TNHNKDYTSVERCEISIARKPVVA
[SEQ ID NO:150]    PPms-E.pep        TNHNKDYISVEQCEISIARKPVVA
[SEQ ID NO:152]    PPms-G.pep        TNHNKDYISVEQCEISIARKPVVA
[SEQ ID NO:154]    Pav5ms.pep        TNHNKDYTSVEQCEISIARKPVVA
[SEQ ID NO:156]    Pavms-2.pep       TNHNKDYTSVEQCEISIARKPVVA
[SEQ ID NO:158]    Pavms-3.pep       TNHNKDYTSVEQCEISIARKPVVA
[SEQ ID NO:160]    Pavms-4.pep       TNHNKDYTSVEQCEISIARKPVVA
[SEQ ID NO:162]    RTms-1.pep        TNHNKDYTSVEQCEISIARKPVVA
[SEQ ID NO:164]    RTms-2.pep        TNHNKDYTSVGQCEISIAPKPVVA
[SEQ ID NO:166]    RTms-5.pep        TNHNKDYTSVEQCEISIARKPVVA
[SEQ ID NO:168]    RTms-6.pep        TNHNKDYTSVEQCEISIARKPVVA
                ****** **  *****     ****
```

Figure 3 continued

```
[SEQ ID NO:87]    Aams-2       GCGACCACAGGTTTGCGTGTAATGGACATCAGCATCTCTTTCACGGAAGGAGCTACTTAA
[SEQ ID NO:89]    Aams-4       GCGACCACAGGTTTGCGTGTAATGGACATCAGCATCTCTTTCACGGAAGGAGCTACTTAA
[SEQ ID NO:91]    Aams-5       ------------------------------------------------------------
[SEQ ID NO:93]    Aams-6       ------------------------------------------------------------
[SEQ ID NO:95]    Aams-A       ------------------------------------------------------------
[SEQ ID NO:97]    Aams-B       ------------------------------------------------------------
[SEQ ID NO:99]    Acams-2      ------------------------------------------------------------
[SEQ ID NO:101]   Acams-3      ------------------------------------------------------------
[SEQ ID NO:103]   Acams-4      ------------------------------------------------------------
[SEQ ID NO:105]   Acams-5      ------------------------------------------------------------
[SEQ ID NO:107]   Cems-F       ------------------------------------------------------------
[SEQ ID NO:109]   Cems-G       ------------------------------------------------------------
[SEQ ID NO:111]   Cems-H       ------------------------------------------------------------
[SEQ ID NO:113]   Cems-I       ------------------------------------------------------------
[SEQ ID NO:115]   LGAms-5      ------------------------------------------------------------
[SEQ ID NO:117]   LGAms-6      ------------------------------------------------------------
[SEQ ID NO:119]   Mi68Dms      ------------------------------------------------------------
[SEQ ID NO:121]   Mims-A       ------------------------------------------------------------
[SEQ ID NO:123]   Mims-B       ------------------------------------------------------------
[SEQ ID NO:125]   Mims-C       ------------------------------------------------------------
[SEQ ID NO:127]   PMms-A       ------------------------------------------------------------
[SEQ ID NO:129]   PMms-B       ------------------------------------------------------------
[SEQ ID NO:131]   PMms-C       ------------------------------------------------------------
[SEQ ID NO:133]   PMms-D       ------------------------------------------------------------
[SEQ ID NO:135]   PMms-E       ------------------------------------------------------------
[SEQ ID NO:137]   PPd57-1ms    ------------------------------------------------------------
[SEQ ID NO:139]   PPd57-2ms    ------------------------------------------------------------
[SEQ ID NO:141]   PPd57-3      ------------------------------------------------------------
[SEQ ID NO:143]   PPd57-4ms    ------------------------------------------------------------
[SEQ ID NO:145]   PPms-1       ------------------------------------------------------------
[SEQ ID NO:147]   PPms-2       ------------------------------------------------------------
[SEQ ID NO:149]   PPms-E       ------------------------------------------------------------
[SEQ ID NO:151]   PPms-G       ------------------------------------------------------------
[SEQ ID NO:153]   Pav5ms       ------------------------------------------------------------
[SEQ ID NO:155]   Pavms-2      ------------------------------------------------------------
[SEQ ID NO:157]   Pavms-3      ------------------------------------------------------------
[SEQ ID NO:159]   Pavms-4      ------------------------------------------------------------
[SEQ ID NO:161]   RTms-1       ------------------------------------------------------------
[SEQ ID NO:163]   RTms-2       ------------------------------------------------------------
[SEQ ID NO:165]   RTms-5       ------------------------------------------------------------
[SEQ ID NO:167]   RTms-6       ------------------------------------------------------------
```

Figure 4

```
[SEQ ID NO:87]      Aams-2        GAAACGTTTGCGAATCGTTGTTCTGCGCTACTTATTCTCAATATGAGTGTGATCGCTACA
[SEQ ID NO:89]      Aams-4        GAAACGTTTGCGAATCGTTGTTCTGCGCTACTTATTCTCAATATGAGTGTGATCGCTACA
[SEQ ID NO:91]      Aams-5        ---------------------------------------------AGTGGGATCGCTACA
[SEQ ID NO:93]      Aams-6        ---------------------------------------------AGTGTGATCGCTACA
[SEQ ID NO:95]      Aams-A        ------------------------------------------ATGAGTGTGATCGCTACA
[SEQ ID NO:97]      Aams-B        ------------------------------------------ATGAGTGTGATCGCTACA
[SEQ ID NO:99]      Acams-2       ------------------------------------------ATGAGTGTGATCGCTACA
[SEQ ID NO:101]     Acams-3       ------------------------------------------ATGAGTGTGATCGCTACA
[SEQ ID NO:103]     Acams-4       ------------------------------------------ATGAGTGTGATCGCTACA
[SEQ ID NO:105]     Acams-5       ---------------------------------------------AGTGTGATCGCTACA
[SEQ ID NO:107]     Cems-F        ------------------------------------------ATGAGTGTGATCGCTACA
[SEQ ID NO:109]     Cems-G        ------------------------------------------ATGAGTGTGATCGCTACA
[SEQ ID NO:111]     Cems-H        ---------------------------------------------AGTGTGATCGCTACA
[SEQ ID NO:113]     Cems-I        ---------------------------------------------AGTGTGATCGCTACA
[SEQ ID NO:115]     LGAms-5       ------------------------------------------ATGAGTGTGATCGCTACA
[SEQ ID NO:117]     LGAms-6       ------------------------------------------ATGAGTGTGATCGCTACA
[SEQ ID NO:119]     Mi68Dms       ---------------------------------------------AGTGTGATCGCTACA
[SEQ ID NO:221]     Mims-A        ------------------------------------------ATGAGTGTGATCGCTACA
[SEQ ID NO:123]     Mims-B        ------------------------------------------ATGAGTGTGATCGCTACA
[SEQ ID NO:125]     Mims-C        ---------------------------------------------AGTGTGATCGCTACA
[SEQ ID NO:127]     PMms-A        ------------------------------------------ATGAGTGTGATCGCTACA
[SEQ ID NO:129]     PMms-B        ------------------------------------------ATGAGTGTGATCGCTACA
[SEQ ID NO:131]     PMms-C        ---------------------------------------------AGTGTGATCGCTACA
[SEQ ID NO:133]     PMms-D        ---------------------------------------------AGTGTGATCGCTACA
[SEQ ID NO:135]     PMms-E        ---------------------------------------------AGTGTGATCGCTACA
[SEQ ID NO:137]     PPd57-1ms     ---------------------------------------------AGTGTGATCGCTACA
[SEQ ID NO:139]     PPd57-2ms     ------------------------------------------ATGAGTGTGATCGCTACA
[SEQ ID NO:141]     PPd57-3       ------------------------------------------ATGAGTGTGATCGCTACA
[SEQ ID NO:143]     PPd57-4ms     ---------------------------------------------AGTGTGATCGCTACA
[SEQ ID NO:145]     PPms-1        ------------------------------------------ATGAGTGTGATCGCTACA
[SEQ ID NO:147]     PPms-2        ------------------------------------------ATGAGTGTGATCGCTACA
[SEQ ID NO:149]     PPms-E        ---------------------------------------------AGTGTGATCGCTACA
[SEQ ID NO:151]     PPms-G        ---------------------------------------------AGTGTGATCGCTACA
[SEQ ID NO:153]     Pav5ms        ---------------------------------------------AGTGTGATCGCTACA
[SEQ ID NO:155]     Pavms-2       ------------------------------------------ATGAGTGTGATCGCTACA
[SEQ ID NO:157]     Pavms-3       ------------------------------------------ATGAGTGTGATCGCTACA
[SEQ ID NO:159]     Pavms-4       ---------------------------------------------AGTGTGATCGCTACA
[SEQ ID NO:161]     RTms-1        ------------------------------------------ATGAGTGTGATCGCTACA
[SEQ ID NO:163]     RTms-2        ------------------------------------------ATGAGTGTGAGCGCTACA
[SEQ ID NO:165]     RTms-5        ---------------------------------------------AGTGTGATCGCTACA
[SEQ ID NO:167]     RTms-6        ---------------------------------------------AGTGTGATCGTTACA
                                                           **** ** ** ****
```

Figure 4 continued

```
[SEQ ID NO:87]   Aams-2       CAAATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACACTACTTTGAGGTCGAA
[SEQ ID NO:89]   Aams-4       CAAATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACACTACTTTGAGGTCGAA
[SEQ ID NO:91]   Aams-5       CAAATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACACTACTTTGAGGTCGAA
[SEQ ID NO:93]   Aams-6       CAAATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACACTACTTTGAGGTCGAA
[SEQ ID NO:95]   Aams-A       CAAATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACACTACTTTGAGGTCGAA
[SEQ ID NO:97]   Aams-B       CAAATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACACTACTTTGAGGTCGAA
[SEQ ID NO:99]   Acams-2      CAAATGACCTACAAGGTTTATATGTCAGGCACGGCCAATGGACACTACTTTGAGGTTGAA
[SEQ ID NO:101]  Acams-3      CAAATGACCTACAAGGTTTATATGTCAGGCACGGCCAATGGACACTACTTTGAGGTTGAA
[SEQ ID NO:103]  Acams-4      CAAATGACCTACAAGGTTTATATGTCAGGCACGGCCAATGGACACTACTTTGAGGTTGAA
[SEQ ID NO:105]  Acams-5      CAAATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACACTACTTTGAGGTCGAA
[SEQ ID NO:107]  Cems-F       CAAATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACACTACTTTGAGGTCGAA
[SEQ ID NO:109]  Cems-G       CAAATGACCTACAAGGTTTATATGTCGGGCACGGTCAATGGACACTACTTTGAGGTCGAA
[SEQ ID NO:111]  Cems-H       CAAATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACACTACTTTGAGGTCGAA
[SEQ ID NO:113]  Cems-I       CAAATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACACTACTTTGAGGTCGAA
[SEQ ID NO:115]  LGAms-5      CAAATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACACTACTTTGAGGTTGAA
[SEQ ID NO:117]  LGAms-6      CAAATGACCTACAAGGTTTATATGTCAGGCACAGTCAATGGACACTACCTTGAGGTCGAA
[SEQ ID NO:119]  Mi68Dms      CAAATGACCTACAAGGTTTATATGTCAGGCACGGTCGATGGACACTACTTTGAGGTCGAA
[SEQ ID NO:121]  Mims-A       CAAATGACCTACAAGGTTTATATGTCAGGCACGGTCGATGGACACTACTTTGAGGTCGAA
[SEQ ID NO:123]  Mims-B       CAAATGACCTACAAGGTTTATATGTCAGGCACGGTCGATGGACACTACTTTGAGGTCGAA
[SEQ ID NO:125]  Mims-C       CAAATGACCTACAAGGTTTATATGTCAGGCACGGTCGATGGACACTACTTTGAGGTCGAA
[SEQ ID NO:127]  PMms-A       CAAATGACCTACAAGGTTTATATGCCAGGCACGGTCAATGGACACTACTTTGAGGTTGAA
[SEQ ID NO:129]  PMms-B       CAAATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACACTACTTTGAGGTTGAA
[SEQ ID NO:131]  PMms-C       CAAATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACACTACTTTGAGGTCCAA
[SEQ ID NO:133]  PMms-D       CAAATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACACTACTTTGAGGTTGAA
[SEQ ID NO:135]  PPd57-1ms    CAAATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACACTACTTTGAGGTTGAA
[SEQ ID NO:137]  PPd57-2ms    CAAATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACACTACTTTGAGGTCGAA
[SEQ ID NO:139]  PPd57-3      CAAATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACACTACTTTGAGGTCGAA
[SEQ ID NO:141]  PPd57-4ms    CAAATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACACTACTTTGAGGTTGAA
[SEQ ID NO:143]  PPms-1       CAAATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACACTACTTTGAGGTCGAA
[SEQ ID NO:145]  PPms-2       CAAATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACACTACTTTGAGGTCGAA
[SEQ ID NO:147]  PPms-E       CAAATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACACTACTTTGAGGTCGAA
[SEQ ID NO:149]  PPms-G       CAAATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACACTACTTTGAGGTCGAA
[SEQ ID NO:151]  Pav5ms       CAAATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACACTACTTTGAGGTTGAA
[SEQ ID NO:153]  Pavms-2      CAAATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACACTACTTTGAGGTTGAA
[SEQ ID NO:155]  Pavms-3      CAAGTGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACACTACTTTGAGGTTGAA
[SEQ ID NO:157]  Pavms-4      CAAATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACACTACTTTGAGGTTGAA
[SEQ ID NO:159]  RTms-1       CAAATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACACTACTTTGAGGTTGAA
[SEQ ID NO:161]  RTms-2       CAAATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACACTACTTTGAGGTTGAA
[SEQ ID NO:163]  RTms-5       CAAATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACACTACTTTGAGGTCGAA
[SEQ ID NO:165]  RTms-6       CAAATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACACTACTTTGAGGTTGAA
                              *** ******************** * ***** * * * *********** *******  **
```

Figure 4 continued

```
[SEQ ID NO:87]    Aams-2        GGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAGGCTGGCTGTCACCAAG
[SEQ ID NO:89]    Aams-4        GGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAGGCTGGCTGTCACCAAG
[SEQ ID NO:91]    Aams-5        GGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAGGCTGGCTGTCACCAAG
[SEQ ID NO:93]    Aams-6        GGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAGGCTGGCTGTCACCAAG
[SEQ ID NO:95]    Aams-A        GGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAGGCTGGCTGTCACCAAG
[SEQ ID NO:97]    Aams-B        GGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAGGCTGGCTGTCACCAAG
[SEQ ID NO:99]    Acams-2       GGCGATGGAAAAGGAAAGCCTTACGAAGGGGAGCAGACGGTAAGGCTCATTGTCACAAAG
[SEQ ID NO:101]   Acams-3       GGCGATGGAAAAGGAAAGCCTTACGAAGGGGAGCAGACGGTAAGGCTCATTGTCACAAAG
[SEQ ID NO:103]   Acams-4       GGCGATGGAAAAGGAAAGCCTTACGAAGGGGAGCAGACGGTAAGGCTCACTGTCACAAAG
[SEQ ID NO:105]   Acams-5       GGCGATGGAAAAGGAAAGCCT-ACGAGGGGGAGCAGACGGTAAAGCTCACTGTCACCAAG
[SEQ ID NO:107]   Cems-F        GGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAAGCTCACTGTCACCAAG
[SEQ ID NO:109]   Cems-G        GGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAAGCTCACTGTCACCAAG
[SEQ ID NO:111]   Cems-H        GGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAAGCTCACTGTCACCAAG
[SEQ ID NO:113]   Cems-I        GGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAAGCTCACTGTCACCAAG
[SEQ ID NO:115]   LGAms-5       GGCGATGGAAAAGGAAAGCCTTACGAAGGGGAGCAGACGGTAAGGCTCACTGTCACAAAG
[SEQ ID NO:117]   LGAms-6       GGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAGGCTCACTGTCACCAAG
[SEQ ID NO:119]   Mi68Dms       GGCGATGGAAAAGGAAAGCCTTACGAGGGCGAGCAGACTGTAAAGCTCACTGTCACCAAG
[SEQ ID NO:121]   Mims-A        GGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAAGCTCACTGTCACCAAG
[SEQ ID NO:123]   Mims-B        GGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAAGCTCACTGTCACCAAG
[SEQ ID NO:125]   Mims-C        GGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAAGCTCACTGTCACCAAG
[SEQ ID NO:127]   PMms-A        GGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAAGCTCACTGTCACCAAG
[SEQ ID NO:129]   PMms-B        GGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAAGCTCACTGTCACCAAG
[SEQ ID NO:131]   PMms-C        GGCGATGGAAAAGGAAAGCCTTACGAGGGCGAGCAGACTGTAAAGCTCACTGTCACCAAG
[SEQ ID NO:133]   PMms-D        GGCGATGGACAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAAGCTCACTGTCACCAAG
[SEQ ID NO:135]   PMms-E        GGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAAGCTCACTGTCACCAAG
[SEQ ID NO:137]   PPd57-1ms     GGCGATGGAAAAGGAAAGCCTTACGAGGGCGAGCAGACTGTAAAGCTCACTGTCACCAAG
[SEQ ID NO:139]   PPd57-2ms     GGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAGGCTGGCTGTCACCAAG
[SEQ ID NO:141]   PPd57-3       GGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAGGCTGGCTGTCACCAAG
[SEQ ID NO:143]   PPd57-4ms     GGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAAGCTCACTGTCACCAAG
[SEQ ID NO:145]   PPms-1        GGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCGGACGGTAAAGCTCACTGTCACCAAG
[SEQ ID NO:147]   PPms-2        GGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAGGCTCACTGTCACCAAG
[SEQ ID NO:149]   PPms-E        GGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAAGCTCACTGTCACCAAG
[SEQ ID NO:151]   PPms-G        GGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAAGCTCACTGTCACCAAG
[SEQ ID NO:153]   Pav5ms        GGCGATGGAAAAGGAGAGCCTTACGAGGGGGAGCAGACGGTAAGGCTCACTGTCACAAAG
[SEQ ID NO:155]   Pavms-2       GGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAGGCTCACTGTCACAAAG
[SEQ ID NO:157]   Pavms-3       GGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAAACGGTAAGGCTCACTGTCACAAAG
[SEQ ID NO:159]   Pavms-4       GGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAGGCTCACTGTCACAAAG
[SEQ ID NO:161]   RTms-1        GGCGATGGAAAAGGAAAGCCTTACGAAGGGGAGCAGACGGTAAGGCTCACTGTCACAAAG
[SEQ ID NO:163]   RTms-2        GGCGATGGAAAAGGAAAGCCTTACGAAGGGGAGCAGACGGTAAGGCTCACTGTCACAAAG
[SEQ ID NO:165]   RTms-5        GGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAAGCTCACTGTCACCAAG
[SEQ ID NO:167]   Tms-6         GGCGATGGAAAAGGAAAGCCTTACGAAGGGGAGCAGACGGTAAGGCTCACTGTCACAAAG
                                ********* ***** ***** **** ** ****  ** **** ***   ****** ***
```

Figure 4 continued

```
[SEQ ID NO:87]    Aams-2      GGCGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACAGTGTCAGTACGGAAGCATA
[SEQ ID NO:89]    Aams-4      GGCGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACAGTGTCAGTACGGAAGCATA
[SEQ ID NO:91]    Aams-5      GGCGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACAGTGTCAGTACGGAAGCATA
[SEQ ID NO:93]    Aams-6      GGCGGACCTCTGCCATTTGCCTGGGATATTTTATCACCACAGTGTCAGTACGGAAGCATA
[SEQ ID NO:95]    Aams-A      GGCGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACAGTGTCAGTACGGAAGCATA
[SEQ ID NO:97]    Aams-B      GGCGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACAGTGTCAGTACGGAAGCATA
[SEQ ID NO:99]    Acams-2     GGCGGACCTCTGCCATTTGCTTGAGATATTTTATCACCACAGTATCAGTACGGAAGCATA
[SEQ ID NO:101]   Acams-3     GGCGGACCTCTGCCATTTGCTTGAGATATTTTATCACCACAGTATCAGTACGGAAGCATA
[SEQ ID NO:103]   Acams-4     GGCGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACAGTATCAGTACGGAAGCATA
[SEQ ID NO:105]   Acams-5     GGCGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACAGTGTCAGTACGGAAACATA
[SEQ ID NO:107]   Cems-F      GGCGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACAGTGTCAGTACGGAAATATA
[SEQ ID NO:109]   Cems-G      GGCGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACAGTGTCAGTACGGAAACATA
[SEQ ID NO:111]   Cems-H      GGCGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACAGTGTCAGTACGGAAACATA
[SEQ ID NO:113]   Cems-I      GGCGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACAGTGTCAGTACGGAAACATA
[SEQ ID NO:115]   LGAms-5     GGCGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACAGTATCAGTACGGAAGCATA
[SEQ ID NO:117]   LGAms-6     GGCGGACCTCTGCCATTTGCTTGGGATATTTTGTCACCACAGTATCAGTACGGAAGCATA
[SEQ ID NO:119]   Mi68Dms     GGCGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACAGTGTCAGTACGGAAGCATA
[SEQ ID NO:121]   Mims-A      GGCGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACAGTGTCAGTACGGAAGCATA
[SEQ ID NO:123]   Mims-B      GGCGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACAGTGTCAGTACGGAAGCATA
[SEQ ID NO:125]   Mims-C      GGCGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACAGTGTCAGTACGGAAGCATA
[SEQ ID NO:127]   PMms-A      GGCGGACCTCTGCCATTTGCTTGGGATATTCTATCACCACAGAGTCAGTACGGAAGCATA
[SEQ ID NO:129]   PMms-B      GGCGGACCTCTGCCATTTGCTTGGGATATTCTATCACCACAGAGTCAGTACGGAAGCATA
[SEQ ID NO:131]   PMms-C      GGCGGACCTCTGCCCTTTGCTTGGGATATTTTATCACCTCAGACTCAGTACGGAAGCATA
[SEQ ID NO:133]   PMms-D      GGCGGACCTCTGCCATTTGCTTGGGATATTCTATCACCACAGAGTCAGTACGGAAGCATA
[SEQ ID NO:135]   Mms-E       GGCGGACCTCTGCCATTTGCTTGGGATATTCTATCACCACAGAGTCAGTACGGAAGCATA
[SEQ ID NO:137]   d57-1ms     GGCGGACCTCTGCCGTTTGCTTGGGATATTTTATCACCACAGACTCAGTACGGAAGCATA
[SEQ ID NO:139]   Pd57-2ms    GGCGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACAGTGTCAGTACGGAAGCATA
[SEQ ID NO:141]   PPd57-3     GGCGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACAGTGTCAGTACGGAAGCATA
[SEQ ID NO:143]   PPd57-4ms   GGCGGACCTCTGCCATTTGCTTGGGATATTCTATCACCACAGAGTCAGTACGGAAGCATA
[SEQ ID NO:145]   PPms-1      GGCGGACCTCTGCCGTTTGCTTGGGATATTTTATCACCACAGTGTCAGTACGGAAACATA
[SEQ ID NO:147]   PPms-2      GGCGGACCTCTGCCATTTGCTTGGGATATTTTGTCACCACAGTATCAGTACGGAAGCATA
[SEQ ID NO:149]   PPms-E      GGCGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACAGTGTCAGTACGGAAACATA
[SEQ ID NO:151]   PPms-G      GGCGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACAGTGTCAGTACGGAAACATA
[SEQ ID NO:153]   Pav5ms      GGCGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACAGTATCAGTACGGAAGCATA
[SEQ ID NO:155]   Pavms-2     GGCGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACAGTATCAGTACGGAAGCATA
[SEQ ID NO:157]   Pavms-3     GGCGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACAGTATCAGTACGGAAGCATA
[SEQ ID NO:159]   Pavms-4     GGCGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACAGTATCAGTACGGAAGCATA
[SEQ ID NO:161]   RTms-1      GGCGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACAGTATCAGTACGGAAGCATA
[SEQ ID NO:163]   RTms-2      GGCGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACAGTATCAGTACGGAAGCATA
[SEQ ID NO:165]   RTms-5      GGCGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACAGTGTCAGTACGGAAGCATA
[SEQ ID NO:167]   RTms-6      GGCGGACCCCTGCCATTTGCTTGGGATATTTTATCACCACAGTATCAGTACGGAAGCATA
                ******** ***** ***** ** ****** * ***** ***   ***********   ***
```

Figure 4 continued

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[SEQ ID NO:87]   Aams-2       CCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAGTCATTCCCGGAGGGA
[SEQ ID NO:89]   Aams-4       CCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAGTCATTCCCGGAGGGA
[SEQ ID NO:91]   Aams-5       CCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAGTCATTCCCGGAGGGA
[SEQ ID NO:93]   Aams-6       CCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAGTCATTCCCGGAGGGA
[SEQ ID NO:95]   Aams-A       CCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAGTCATTCCCGGAGGGA
[SEQ ID NO:97]   Aams-B       CCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAGTCATTCCCGGAGGGA
[SEQ ID NO:99]   Acams-2      CCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAGTCATTCCCGGAAGGA
[SEQ ID NO:101]  Acams-3      CCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAGTCATTCCCGGAAGGA
[SEQ ID NO:103]  Acams-4      CCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAGTCATTCCCGGAAGGA
[SEQ ID NO:105]  Acams-5      CCATTCACCAAGTACCCTGAAGACGTCCCTGACTATGTAAAGCAGTCATTCCCGGAGGGA
[SEQ ID NO:107]  Cems-F       CCATTCACCAAGTACCCTGAAGACGTCCCTGACTATGTAAAGCGGTCATTCCCGGAGGGA
[SEQ ID NO:109]  Cems-G       CCATTCACCAAGTACCCTGAAGACGTCCCTGACTATGTAAAGCAGTCATTCCCGGAGGGA
[SEQ ID NO:111]  Cems-H       CCATTCACCAAGTACCCTGAAGACGTCCCTGACTATGTAAAGCAGTCATTCCCGGAGGGA
[SEQ ID NO:113]  Cems-I       CCATTCACCAAGTACCCTGAAGACGTCCCTGACTATGTAAAGCAGTCATTCCCGGAGGGA
[SEQ ID NO:115]  LGAms-5      CCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAGTCATTCCCGGAAGGA
[SEQ ID NO:117]  LGAms-6      CCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGTAGTCATTCCCGGAGGGA
[SEQ ID NO:119]  Mi68Dms      CCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAGTCATTCCCGGAGGGA
[SEQ ID NO:121]  Mims-A       CCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAGTCATTCCCGGAGGGA
[SEQ ID NO:123]  Mims-B       CCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAGTCATTCCCGGAGGGA
[SEQ ID NO:125]  Mims-C       CCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAGTCATTCCCGGAGGGA
[SEQ ID NO:127]  PMms-A       CCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAGTCATTCCCTGAGGGA
[SEQ ID NO:129]  PMms-B       CCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAGTCATTCCCTGAGGGA
[SEQ ID NO:131]  PMms-C       CCATTCACCAAGTACCCTGACGACATCCCTGACTATGTAAAACAGTCATTCCCTGAGGGA
[SEQ ID NO:133]  PMms-D       CCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAGTCATTCCCTGAGGGA
[SEQ ID NO:135]  PMms-E       CCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAGTCATTCCCTGAGGGA
[SEQ ID NO:137]  PPd57-1ms    CCATTCACCAAGTACCCTGAAGACATTCCTGACTATGTAAAACAGTCATTCCCTGAGGGA
[SEQ ID NO:139]  PPd57-2ms    CCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAGTCATTCCCGGAGGGA
[SEQ ID NO:141]  PPd57-3      CCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAGTCATTCCCGGAGGGA
[SEQ ID NO:143]  PPd57-4ms    CCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAGTCATTCCCTGAGGGA
[SEQ ID NO:145]  PPms-1       CCATTCACCAAGTACCCTGAAGACGTCCCTGACTATGTAAAGCAGTCATTCCCGGAGGGA
[SEQ ID NO:147]  PPms-2       CCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGTAGTCATTCCCGGAGGGA
[SEQ ID NO:149]  PPms-E       CCATTCACCAAGTACCCTGAAGACGTCCCTGACTATGTAAAGCAGTCATTCCCGGAGGGA
[SEQ ID NO:151]  PPms-G       CCATTCACCAAGTACCCTGAAGACGTCCCTGACTATGTAAAGCAGTCATTCCCGGAGGGA
[SEQ ID NO:153]  Pav5ms       CCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAGTCATTCCCGGAAGGA
[SEQ ID NO:155]  Pavms-2      CCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTATAGCAGTCATTCCCGGAAGGA
[SEQ ID NO:157]  Pavms-3      CCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAGTCATTCCCGGAAGGA
[SEQ ID NO:159]  Pavms-4      CCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAGTCATTCCCGGAAGGA
[SEQ ID NO:161]  RTms-1       CCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAGTCATTCCCGGAAGGA
[SEQ ID NO:163]  RTms-2       CCATTCACCAAGTACCCTGAAGACATCCCTGGCTATGTAAAGCAGTCATTCCCGGAAGGA
[SEQ ID NO:165]  RTms-5       CCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAGTCATTCCCGGAGGGA
[SEQ ID NO:167]  RTms-6       CCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAGTCATTCCCGGAAGGA
                              ******************** *** * **** ******* *   ********* ** ***
```

Figure 4 continued

```
[SEQ ID NO:87]    Aams-2        TTTACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGTACTGTCAGCAATGAT
[SEQ ID NO:89]    Aams-4        TTTACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGTACTGTCAGCAATGAT
[SEQ ID NO:91]    Aams-5        TTTACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGTACTGTCAGCAATGAT
[SEQ ID NO:93]    Aams-6        TTTACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGTACTGTCAGCAATGAT
[SEQ ID NO:95]    Aams-A        TTTACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGTACTGTCAGCAATGAT
[SEQ ID NO:97]    Aams-B        TTTACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGTACTGTCAGCAATGAT
[SEQ ID NO:99]    Acams-2       TATACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGTACTGTCAGCAATGAT
[SEQ ID NO:101]   Acams-3       TATACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGTACTGTCAGCAATGAT
[SEQ ID NO:103]   Acams-4       TATACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGTACTGTCAGCAATGAT
[SEQ ID NO:105]   Acams-5       TTTACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGTACTGTCAGCAATGAT
[SEQ ID NO:107]   Cems-F        TTTACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGTACTGTCAGCAATGAT
[SEQ ID NO:109]   Cems-G        TTTACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGTACTGTCAGCAATGAT
[SEQ ID NO:111]   Cems-H        TTTACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGTACTGTCAGCAATGAT
[SEQ ID NO:113]   Cems-I        TTTACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGTACTGTCAGCAATGAT
[SEQ ID NO:115]   LGAms-5       TATACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGTACTGTCAGCAATGAT
[SEQ ID NO:117]   LGAms-6       TTTACATGGGACAGGATCATGGACTTTGAAGATGGTGCAGTGTGTACCGTCAGCAATGAT
[SEQ ID NO:119]   Mi68Dms       TTTACATGGGAGAGGATCATGAACTTTGAAAATGGTGCAGTGTGTACTGTCAGCAATGAT
[SEQ ID NO:121]   Mims-A        TTTACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGTACTGTCAGCAATGAT
[SEQ ID NO:123]   Mims-B        TTTACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGTACTGTCAGCAATGGT
[SEQ ID NO:125]   Mims-C        TTTACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGTACTGTCAGCAATGAT
[SEQ ID NO:127]   PMms-A        TATACATGGGAGAGGATCATGAACTTCGAAGATGGTGCAGTGTGTACTGTCAGCAATGAT
[SEQ ID NO:129]   PMms-B        TATACATGGGAGAGGATCATGAACTTCGAAGATGGTGCAGTGTGTACTGTCAGCAATGAT
[SEQ ID NO:131]   PMms-C        TATACATGGGAGAGGATCATGAAGTTTGAAGATGGTGCAGTGTGTACTGTCACCAATGAC
[SEQ ID NO:133]   PMms-D        TATACATGGGAGAGGATCATGAACTTCGAAGATGGTGCAGTGTGTACTGTCAGCAATGAT
[SEQ ID NO:135]   PMms-E        TATACATGGGAGAGGATCATGAACTTCGAAGATGGTGCAGTGTGTACTGTCAGCAATGAT
[SEQ ID NO:137]   PPd57-1ms     TATACATGGGAGAGGATCATGAAGTTTGAAGATGGTGCAGTATGTACTGTCAGCAATGAT
[SEQ ID NO:139]   PPd57-2ms     TTTACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGTACTGTCAGCAATGAT
[SEQ ID NO:141]   PPd57-3       TTTACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGTACTGTCAGCAATGAT
[SEQ ID NO:143]   PPd57-4ms     TATACATGGGAGAGGATCATGAACTTCGAAGATGGTGCAGTGTGTACTGTCAGCAATGAT
[SEQ ID NO:145]   PPms-1        TTTACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGTACTGTCAGCAATGAT
[SEQ ID NO:147]   PPms-2        TTTACATGGGACAGGATCATGAACTTTGAAGATGGTGCAGTGTGTACCGTCAGCAATGAT
[SEQ ID NO:149]   PPms-E        TTTACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGTACTGTCAGCAATGAT
[SEQ ID NO:151]   PPms-G        TTTACATGGGAGGGGATCATGAACTTTGAAGATGGTGCAGTGTGTACTGTCAGCAATGAT
[SEQ ID NO:153]   Pav5ms        TATACATGGGAGAGGATCATGAACTTTGAAGATGGTGCTGTGTGTACTGTCAGCAATGAT
[SEQ ID NO:155]   Pavms-2       TATACATGGGAGAGGATCATGAACTTTGAAGATGGTGCTGTGTGTACTGTCAGCAATGAT
[SEQ ID NO:157]   Pavms-3       TATACATGGGAGAGGATCATGAACTTTGAAGATGGTGCTGTGTGTACTGTCAGCAATGAT
[SEQ ID NO:159]   Pavms-4       TATACATGGGAGGGGATCATGAACTTTGAAGATGGTGCTGTGTGTACTGTCAGCAATGAT
[SEQ ID NO:161]   RTms-1        TATACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGTGCTGTCAGCAATGAT
[SEQ ID NO:163]   RTms-2        TATACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGTACTGTCAGCAATGAT
[SEQ ID NO:165]   RTms-5        TTTACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGTACTGTCAGCAATGAT
[SEQ ID NO:167]   RTms-6        TATACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGTACTGTCAGCAATGAT
                                * *********  ******** * ** *** ******* ** *** * **** *****
```

Figure 4 continued

[SEQ ID NO:87]	Aams-2	TCCAGCATCCAAGGCAACTGTTTCATCTACCATGTCAAGTTCTCTGGTTTGAACTTTCCT
[SEQ ID NO:89]	Aams-4	TCCAGCATCCAAGGCAACTGTTTCATCTACCATGTCAAGTTCTCTGGTTTGAACTTTCCT
[SEQ ID NO:91]	Aams-5	TCCAGCATCCAAGGCAACTGTTTCATCTACCATGTCAAGTTCTCTGGTTTGAACTTTCCT
[SEQ ID NO:93]	Aams-6	TCCAGCATCCAAGGCAACTGTTTCATCTACCATGTCAAGTTCTCTGGTTTGAACTTTCCT
[SEQ ID NO:95]	Aams-A	TCCAGCATCCAAGGCAACTGTTTCATCTACCATGTCAAGTTCTCTGGTTTGAACTTTCCT
[SEQ ID NO:97]	Aams-B	TCCAGCATCCAAGGCAACTGTTTCATCTACCATGTCAAGTTCTCTGGTTTGAACTTTCCT
[SEQ ID NO:99]	Acams-2	TCCAGCATCCAAGGCAACTGTTTCATCTACCATGTCAAGTTCTCTGGTTTGAACTTTCCT
[SEQ ID NO:101]	Acams-3	TCCAGCATCCAAGGCAACTGTTTCATCTACCATGTCAAGTTCTCTGGTTTGAACTTTCCT
[SEQ ID NO:103]	Acams-4	TCCAGCATCCAAGGCAACTGTTTCATCCACCATGTCAAGTTCTCTGGTTTGAACTTTCCT
[SEQ ID NO:105]	Acams-5	TCCAGCATCCAAGGCAACTGTTTCACCTACCATGTCAAGTTCTCTGGTTTGAACTTTCCT
[SEQ ID NO:107]	Cems-F	TCCAGCATCCAAGGCAACTGTTTCACCTACCATGTCAAGTTCTCTGGTTTGAACTTTCCT
[SEQ ID NO:109]	Cems-G	TCCAGCATCCAAGGCAACTGTTTCACCTACCATGTCAAGTTCTCTGGTTTGAACTTTCCT
[SEQ ID NO:111]	Cems-H	TCCAGCATCCAAGGCAACTGTTTCACCTACCATGTCAAGTTCTCTGGTTTGAACTTTCCT
[SEQ ID NO:113]	Cems-I	TCCAGCATCCAAGGCAACTGTTTCACCTACCATGTCAAGTTCTCTGGTTTGAACTTTCCT
[SEQ ID NO:115]	LGAms-5	TCCAGCATCCAAGGCAACTGTTTCATCTACCATGTCAAGTTCTCTGGTTTGAACTTTCCT
[SEQ ID NO:117]	LGAms-6	TCCAGCATCCAAGGCAACTGTTTCATCTACCATGTCAAGTTCTCTGGTTTGAACTTTCCT
[SEQ ID NO:119]	Mi68Dms	TCCAGCATCCAAGGCAACTGTTTCACCTACCATGTCAAGTTCTCTGGTTTGAACTTTCCT
[SEQ ID NO:121]	Mims-A	TCCAGCATCCAAGGCAACTGTTTCACCTACCATGTCAAGTTCTCTGGTTTGAACTTTCCT
[SEQ ID NO:123]	Mims-B	TCCAGCATCCAAGGCAACTGTTTCACCTACCATGTCAAGTTCTCTGGTTTGAACTTTCCT
[SEQ ID NO:125]	Mims-C	TCCAGCATCCAAGGCAACTGTTTCACCTACCATGTCAAGTTCTCTGGTTTGAACTTTCCT
[SEQ ID NO:127]	PMms-A	TCCAGCATCCAAGGTAACTGTTTCATCTACAATGTCAAGTTCTCTGGTTTGAACTTTCCT
[SEQ ID NO:129]	PMms-B	TCCAGCATCCAAGGTAACTGTTTCATCTACAATGTCAAGTTCTCTGGTTTGAACTTTCCT
[SEQ ID NO:131]	PMms-C	TCCAGCATGCAAGGCAACTGTTTCATCTACAATGTCAAGTTCTCTGGTTTGAACTTTCCT
[SEQ ID NO:133]	PMms-D	TCCAGCATCCAAGGCAACTGTTTCATCTACAATGTCAAGTTCTCTGGTTTGAACTTTCCT
[SEQ ID NO:135]	PMms-E	TCCAGCATCCAAGGCAACTGTTTCATCTACAATGTCAAGTTCTCTGGTTTGAACTTTCCT
[SEQ ID NO:137]	PPd57-1ms	TCCAGCATGCAAGGCAACTGTTTCATCTACAATGTCAAGTTCTCTGGTTTGAACTTTCCT
[SEQ ID NO:139]	PPd57-2ms	TCCAGCATCCAAGGCAACTGTTTCATCTACCATGTCAAGTTCTCTGGTTTGAACTTTCCT
[SEQ ID NO:141]	PPd57-3	TCCAGCATCCAAGGCAACTGTTTCATCTACCATGTCAAGTTCTCTGGTTTGAACTTTCCT
[SEQ ID NO:143]	PPd57-4ms	TCCAGCATCCAAGGCAACTGTTTCATCTACAATGTCAAGTTCTCTGGTTTGAACTTTCCT
[SEQ ID NO:145]	PPms-1	TCCAGCATCCAAGGCAACTGTTTCACCTACCATGTCAAGTTCTCTGGTTTGAACTTTCCT
[SEQ ID NO:147]	PPms-2	TCCAGCATCCAAGGCAACTGTTTCATCTACCATGTCAAGTTCTCTGGTTTGAACTTTCCT
[SEQ ID NO:149]	PPms-E	TCCAGCATCCAAGGCAACTGTTTCACCTACCATGTCAAGTTCTCTGGTTTGAACTTTCCT
[SEQ ID NO:151]	PPms-G	TCCAGCATCCAAGGCAACTGTTTCACCTACCATGTCAAGTTCTCTGGTTTGAACTTTCCT
[SEQ ID NO:153]	Pav5ms	TCCAGCATCCAAGGCAACTGTTTCATCTACCATGTCAAGTTCTCTGGTTTGAACTTTCCT
[SEQ ID NO:155]	Pavms-2	TCCAGCATCCAAGGCAACTGTTTCATCTACCATGTCAAGTTTTCTGGTTTGAACTTTCCT
[SEQ ID NO:157]	Pavms-3	TCCAGCATCCAAGGCAACTGTTTCATCTACCATGTCAAGTTTTCTGGTTTGAACTTTCCT
[SEQ ID NO:159]	Pavms-4	TCCAGCATCCAAGGCAACTGTTTCATCTACCATGTCAAGTTCTCTGGTTTGAACTTTCCT
[SEQ ID NO:161]	RTms-1	TCCAGCATCCAAGGCAACTGTTTCATCTACCATGTCAAGTTCTCTGGTTTGAACTTTCCT
[SEQ ID NO:163]	RTms-2	TCCAGCATCCAAGGCAACTGTTTCATCTACCATGTCAAGTTCTCTGGTTTGAACTTTCCT
[SEQ ID NO:165]	RTms-5	TCCAGCATCCAAGGCAACTGTTTCACCTACCATGTCAAGTTCTCTGGTTTGAACTTTCCT
[SEQ ID NO:167]	RTms-6	TCCAGCATCCAAGGCAACTGTTTCATCTACCATGTCAAGTTCTCTGGTTTGAACTTTCCT
		******** ***** ********** * ** ********** ******************

Figure 4 continued

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[SEQ ID NO:87]    Aams-2      CCCAATGGACCTGTTATGCAGAAGAAGACACAGGGCTGGGAACCCCACTCTGAGCGTCTC
[SEQ ID NO:89]    Aams-4      CCCAATGGACCTGTTATGCAGAAGAAGACACAGGGCTGGGAACCCCACTCTGAGCGTCTC
[SEQ ID NO:91]    Aams-5      CCCAATGGACCTGTTATGCAGAAGAAGACACAGGGCTGGGAACCCCACTCTGAGCGTCTC
[SEQ ID NO:93]    Aams-6      CCCAATGGACCTGTTATGCAGAAGAAGACACAGGGCTGGGAACCCCACTCTGAGCGTCTC
[SEQ ID NO:95]    Aams-A      CCCAATGGACCTGTTATGCAGAAGAAGACACAGGGCTGGGAACCCCACTCTGAGCGTCTC
[SEQ ID NO:97]    Aams-B      CCCAATGGACCTGTTATGCAGAAGAAGACACAGGGCTGGGAACCCCACTCTGAGCGTCTC
[SEQ ID NO:99]    Acams-2     CCCAATGGACCTGTGATGCAGAAGAAGACACAGGGCTGGGAACCCAACACTGAGCGTCTC
[SEQ ID NO:101]   Acams-3     CCCAATGGACCTGTGATGCAGAAGAAGACACAGGGCTGGGAACCCAACACTGAGCGTCTC
[SEQ ID NO:103]   Acams-4     CCCAATGGACCTGTGATGCAGAAGAAGACACAGGGCTGGGAACCCAACACTGAGCGTCTC
[SEQ ID NO:105]   Acams-5     CCCAATGGACCTGTGATGCAGAAGGAGACACAGGGCTGGGAACCCCACTCTGAGCGTCTC
[SEQ ID NO:107]   Cems-F      CCCAATGGACCTGTGATGCAGAAGAAGACACAGGGCTGGGAACCCCACTCTGAGCGTCTC
[SEQ ID NO:109]   Cems-G      CCCAATGGACCTGTGATGCAGAAGAAGACACAGGGCTGGGAACCCCACTCTGAGCGTCTC
[SEQ ID NO:111]   Cems-H      CCCAATGGACCTGTGATGCAGAAGAAGACACAGGGCTGGGAACCCCACTCTGAGCGTCTC
[SEQ ID NO:113]   Cems-I      CCCAATGGACCTGTGATGTAGAAGAAGACACAGGGCTGGGAACCCCACTCTGAGCGTCTC
[SEQ ID NO:115]   LGAms-5     CCCAACGGACCTGTGATGCAGAAGAAGACACAGGGCTGGGAACCCAACACTGAGCGTCTC
[SEQ ID NO:117]   LGAms-6     CCCAATGGACCTGTTATGCAGAAGAAGACACAGGGCTGGGAACCCAACACTGAGCGTCTC
[SEQ ID NO:119]   Mi68Dms     CCCAATGGACCTGTGATGCAGAAGAAGACACAGGGCTGGGAACCCCACTCTGAGCGTCTC
[SEQ ID NO:121]   Mims-A      CCCAATGGACCTGTGATGCAGAAGAAGACACAGGGCTGGGAACCCCACTCTGAGCGTCTC
[SEQ ID NO:123]   Mims-B      CCCAATGGACCTGTGATGCAGAAGAAGACACAGGGCTGGGAACCCCACTCTGAGCGTCTC
[SEQ ID NO:125]   Mims-C      CCCAATGGACCTGTGATGCAGAAGAAGACACAGGGCTGGGAACCCCACTCTGAGCGTCTC
[SEQ ID NO:127]   PMms-A      CCCAATGGACCTGTTATGCAAAAGAAGACACAGGGCTGGGAACCCAACACTGAGCGTCTT
[SEQ ID NO:129]   PMms-B      CCCAATGGACCTGTTATGCAAAAGAAGACACAGGGTTGGGAACCCAACACTGAGCGTCTC
[SEQ ID NO:131]   PMms-C      CCCAATGGACCTGTTATGCAGAAGAAGACACAGGGCTGGGAACCCAACACTGGGCGTCTT
[SEQ ID NO:133]   PMms-D      CCCAATGGACCTGTTATGCAAAAGAAGACACAGGGCTGGGAACCCAACACTGAGCGTCTC
[SEQ ID NO:135]   PMms-E      CCCAATGGACCTGTTATGCAAAAGAAGACACAGGGCTGGGAACCCAACACAGAGCGTCTC
[SEQ ID NO:137]   PPd57-1ms   CCCAATGGACCTGTTATGCAGAAGAAGACACAGGGCTGGGAACCCAACACTGAGCGTCTT
[SEQ ID NO:139]   PPd57-2ms   CCCAATGGACCTGTTATGCAGAAGAAGACACAGGGCTGGGAACCCCACTCTGAGCGTCTC
[SEQ ID NO:141]   PPd57-3     CCCAATGGACCTGTTATGCAGAAGAAGACACAGGGCTGGGAACCCCACTCTGAGCGTCTC
[SEQ ID NO:143]   PPd57-4ms   CCCAATGGACCTGTTATGCAAAAGAAGACACAGGGCTGGGAACCCAACACTGAGCGTCTC
[SEQ ID NO:145]   PPms-1      CCCAATGGACCTGTGATGCAGAAGAAGACACAGGGCTGGGAACCCCACTCTGAGCGTCTC
[SEQ ID NO:147]   PPms-2      CCCAATGGACCTGTTATGCAGAAGAAGACACAGGGCTGGGAACCCAACACTGAGCGTCTC
[SEQ ID NO:149]   PPms-E      CCCAATGGACCTGTGATGCAGAAGAAGACACAGGGCTGGGAACCCCACTCTGAGCGTCTC
[SEQ ID NO:151]   PPms-G      CCCAATGGACCTGTGATGCAGAAGAAGACACAGGGCTGGGAACCCCACTCTGAGCGTCTC
[SEQ ID NO:153]   Pav5ms      CCCAATGGACCTGTGACGCAGAAGAAGACACAGGGCTGGGAACCCAACACTGAGCGTCTC
[SEQ ID NO:155]   Pavms-2     CCCAATGGACCTGTGATGCAGAAGAAGACACAGGGCTGGGAACCCAACACTGAGCGTCTC
[SEQ ID NO:157]   Pavms-3     CCCAATGGACCTGTGATGCAGAAGAAGACACAGGGCTGGGAACCCAACACTGAGCGTCTC
[SEQ ID NO:159]   Pavms-4     CCCAATGGACCTGTGATGCAGAAGAAGACACAGGGCTGGGAACCCAACACTGAGCGTCTC
[SEQ ID NO:161]   RTms-1      CCCAATGGACCTGTGATGCAAAAGAAGACACAGGGCTGGGAACCCAACACTGAGCGTCTC
[SEQ ID NO:163]   RTms-2      CCCAATGGACCTGTGATGCAAAAAAAGACACAAGGCTGGGAACCCAACACTGAGCGTCTC
[SEQ ID NO:165]   RTms-5      CCTAATGGACCTGTGATGCAGAAGAAGACACAGGGCTGGGAACCCCACTCTGAGCGTCTC
[SEQ ID NO:167]   RTms-6      CCCAATGGACCTGTGATGCAGAAGAAGACACAGGGCTGGGAACCCAACACTGAGCGTCTC
                              ** ** ******** * * * **  ******* ** ********* ** * * ******
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Figure 4 continued

```
[SEQ ID NO:87]   Aams-2        TTTGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCTCTGAAGTTAGAAGGAGGC
[SEQ ID NO:89]   Aams-4        TTTGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCTCTGAAGTTAGAAGGAGGC
[SEQ ID NO:91]   Aams-5        TTTGCACGAGACGGAATGCTGATAGGAAACAACTTTATGGCTCTGAAGTTAGAAGGAGGC
[SEQ ID NO:93]   Aams-6        TTTGCACGAGACGGAATGCTGATAGGAAACAACTTTATGGCTCTGAAGTTAGAAGGAGGC
[SEQ ID NO:95]   Aams-A        TTTGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCTCTGAAGTTAGAAGGAGGC
[SEQ ID NO:97]   Aams-B        TTTGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCTCTGAAGTTAGAAGGAGGC
[SEQ ID NO:99]   Acams-2       TTTGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCTCTGAAGTTAGAAGGAGGC
[SEQ ID NO:101]  Acams-3       TTTGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCTCTGAAGTTAGAAGGAGGC
[SEQ ID NO:103]  Acams-4       TTTGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCTCTGAAGTTAGAAGGAGGC
[SEQ ID NO:105]  Acams-5       TTTGCACGGGGTGGAATGCTGATAGGAAACAACTTTGTGGCTCTGAAGTTAGAAGGAGGC
[SEQ ID NO:107]  Cems-F        TTTGCACGGGGTGGAATGCTGATAGGAAACAACTTTATGGCTCTGAAGTTAGAAGGAGGC
[SEQ ID NO:109]  Cems-G        CTTGCACGGGGTGGAATGCTGATAGGAAACAACTTTATGGCTCTGAAGTTAGAAGGAGGC
[SEQ ID NO:111   Cems-H        TTTGCACGGGGTGGAATGCTGATAGGAAACAACTTTATGGCTCTGAAGTTAGAAGGAGGC
[SEQ ID NO:113]  Cems-I        TTTGCACGGGGTGGAATGCTGATAGGAAACAACTTTATGGCTCTGAAGTTAGAAGGAGGT
[SEQ ID NO:115]  LGAms-5       TTAGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCTCTGAAGTTAGAAGGAGGC
[SEQ ID NO:117]  LGAms-6       TTTGCACGAGATGGAATGCTGCTAGGAAACAACTTTATGGCTCTGAAGTTAGAAGGAGGT
[SEQ ID NO:119]  Mi68Dms       TTTGCACGGGGTGGAATGCTGATAGGAAACAACTTTATGGCTCTGAAGTTAGAAGGAGGC
[SEQ ID NO:121]  Mims-A        TTTGCACGGGGTGGAATGCTGATAGGAAACAACTTTATGGCTCTGAAGTTAGAAGGAGGC
[SEQ ID NO:123]  Mims-B        TTTGCACGGGGTGGAATGCTGATAGGAAACAACTTTATGGCTCTGAAGTTAGGAGGAGGC
[SEQ ID NO:125]  Mims-C        TTTGCACGGGGTGGAATGCTGATAGGAAACAACTTTATGGCTCTGAAGTTAGAAGGAGGC
[SEQ ID NO:127]  PMms-A        TATGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCTCTGAAGTTGGAAGGAGGT
[SEQ ID NO:129]  PMms-B        TTTGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCTCTGAAGTTGGAAGGAGGT
[SEQ ID NO:131]  PMms-C        TATGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCTCTGAAGTTGGAAGGAGGT
[SEQ ID NO:133]  PMms-D        TTTGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCTCTGAAGTCGGAAGGAGGT
[SEQ ID NO:135]  PMms-E        TTTGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCTCTGAAGTTGGAAGGAGGT
[SEQ ID NO:137]  PPd57-1ms     TATGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCTCTGAAGTTGGAAGGAGGT
[SEQ ID NO:139]  PPd57-2ms     TTTGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCTCTGAAGTTAGAAGGAGGC
[SEQ ID NO:141]  PPd57-3       TTTGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCTCTGAAGTTAGAAGGAGGC
[SEQ ID NO:143]  PPd57-4ms     TTTGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCTCTGAAGTTGGAAGGAGGT
[SEQ ID NO:145]  PPms-1        TTTGCACGGGGTGGAATGCTGATAGGAAACAACTTTATGGCTCTGAAGTTAGAAGGAGGC
[SEQ ID NO:147]  PPms-2        CTTGCACGAGATGGAATGCTGCTAGGAAACAACTTTATGGCTCTGAAGTTAGAAGGAGGT
[SEQ ID NO:149]  PPms-E        TTTGCACGGGGTGGAATGCTGATAGGAAACAACTTTATGGCTCTGAAGTTAGAAGGAGGC
[SEQ ID NO:151]  PPms-G        TTTGCACGGGGTGGAATGCTGATAGGAAACAACTTTATGGCTCTGAAGTTAGAAGGAGGC
[SEQ ID NO:153]  Pav5ms        TTTGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCTCTGAAGTTAGAAGGAGGC
[SEQ ID NO:155]  Pavms-2       TTTGCACGAGATGGATTGCTGATAGGAAACAACTTTATGGCTCTGAAGTTAGAAGAAGGC
[SEQ ID NO:157]  Pavms-3       TTTGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCTCTGAAGTTAGAAGGAGGC
[SEQ ID NO:159]  Pavms-4       TTTGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCTCTGAAGTTAGAAGGAGGC
[SEQ ID NO:161]  RTms-1        TTTGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCTCTGAAGTTAGAAGGAGGC
[SEQ ID NO:163]  RTms-2        TTTGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCTCTGAAGTTAGAAGGAGGC
[SEQ ID NO:165]  RTms-5        TTTGCACGGGGTGGAATGCTGATAGGAAACAACTTTATGGCTCTGAAGTTAGAAGGAGGC
[SEQ ID NO:167]  RTms-6        TTTGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCTCTGAAGTTAGAAGGAGGC
                                  ***** *  *** ***** ************** ************  * ** ***
```

Figure 4 continued

```
[SEQ ID NO:87]    Aams-2       GGTCACTATTTGTGTGAATTCAAAACTACTTACAAGGCAAAGAAGCCTGTGAAGATGCCA
[SEQ ID NO:89]    Aams-4       GGTCACTATTTGTGTGAATTCAAAACTACTTACAAGGCAAAGAAGCCTGTGAAGATGCCA
[SEQ ID NO:91]    Aams-5       GGTCACTATTTGTGTGAATTCAAAACTACTTACAAGGCAAAGAAGCCTGTGAAGATGCCA
[SEQ ID NO:93]    Aams-6       GGTCACTATTTGTGTGAATTCAAAACTACTTACAAGGCAAAGAAGCCTGTGAAGATGCCA
[SEQ ID NO:95]    Aams-A       GGTCACTATTTGTGTGAATTCAAAACTACTTACAAGGCAAAGAAGCCTGTGAAGATGCCA
[SEQ ID NO:97]    Aams-B       GGTCACTATTTGTGTGAATTCAAAACTACTTACAAGGCAAAGAAGCCTGTGAAGATGCCA
[SEQ ID NO:99]    Acams-2      GGTCACTATTTGTGTGAATTCAAATCTACTTACAAGGCAAAGAAGCCTGTGAAGATGCCA
[SEQ ID NO:101]   Acams-3      GGTCACTATTTGTGTGAATTCAAATCTACTTACAAGGCAAAGAAGCCTGTGAAGATGCCA
[SEQ ID NO:103]   Acams-4      GGTCACTATTTGTGTGAATTCAAATCTACTTACAAGGCAAAGAAGCCTGTGAAGATGCCA
[SEQ ID NO:105]   Acams-5      GGTCACTATTTGTGTGGATTCAAAACTACTTACAAGGCAAAGAAACCTGTGAAGATGCCA
[SEQ ID NO:107]   Cems-F       GGTCACTATTTGTGTGGATTCAAAACTACTTACAAGGCAAAGAAGCCTGTGAAGATGCCA
[SEQ ID NO:109]   Cems-G       GGTCACTATTTGTGTGGATTCAAAACTACTTACAAGGCAAAGAAGCCTGTGAAGATGCCA
[SEQ ID NO:111]   Cems-H       GGTCACTATTTGTGTGGATTCAAAACTACTTACAAGGCAAAGAAGCTTGTGAAGATGCCA
[SEQ ID NO:113]   Cems-I       GGTCACTATTTGTGTGAATTCAAAACTACTTACAAGGCAAAGAAGCCTGTGAAGATGCCA
[SEQ ID NO:115]   LGAms-5      GGTCACTATTTGTGTGAATTCAAATCTACTTACAAGGCAAAGAAGCCTGTGAAGATGCCA
[SEQ ID NO:117]   LGAms-6      GGTCACTATTTGTGTGAATTCAAAACTACTTACAAGGCAAAGAAGCCTGTGAAGATGCCA
[SEQ ID NO:119]   Mi68Dms      GGTCACTATTTGTGTGAATTCAAAACTACTTACAAGGCAAAGAAGCCTGTGAAGATGCCA
[SEQ ID NO:121]   Mims-A       GGTCACTATTTGTGTGAATTCAAAACTACTTACAAGGCAAAGAAGCCTGTGAAGATGCCA
[SEQ ID NO:123]   Mims-B       GGTCACTATTTGTGTGAATTCAAAACTACTTACAGGGCAAAGAAGCCTGTGAAGATGCCA
[SEQ ID NO:125]   Mims-C       GGTCACTATTTGTGTGAATTCAAAACTACTTACAAGGCAAAGAAGCCTGTGAAGATGCCA
[SEQ ID NO:127]   PMms-A       GGTCATTATTTGTGTGAATTCAAATCTACTTACAAGGCAAAGAAGCCTGTGATGATGCCT
[SEQ ID NO:129]   PMms-B       GGTCATTATTTGTGTGAATTCAAATCTACTTACAAGGCAAAGAAGCCTGTGATGATGCCA
[SEQ ID NO:131]   PMms-C       GGTCATTATACCTGTGAATTCAAATCTACTTACAAGGCAAAGAAGCCTGTGATGATGCCT
[SEQ ID NO:133]   PMms-D       GGTCATTATTTGTGTGAATTCAAATCTACTTACAAGGCAAAGAAGCCTGTGATGATGCCA
[SEQ ID NO:135]   PMms-E       GGTCATTATTTGTGTGAATTCAAATCTACTTACAAGGCAAAGAAGCCTGTGATGATGCCA
[SEQ ID NO:137]   PPd57-1ms    GGTCATTATACCTGTGAATTCAAATCTACTTACAAGGCAAAGAAGCCTGTGATGATGCCT
[SEQ ID NO:139]   PPd57-2ms    GGTCACTATTTGTGTGAATTCAAAACTACTTACAAGGCAAAGAAGCCTGTGAAGATGCCA
[SEQ ID NO:141]   PPd57-3      GGTCACTATTTGTGTGAATTCAAAACTACTTACAAGGCAAAGAAGCCTGTGAAGATGCCA
[SEQ ID NO:143]   PPd57-4ms    GGTCATTATTTGTGTGAATTCAAATCTACTTACAAGGCAAAGAAGCCTGTGATGATGCCA
[SEQ ID NO:145]   PPms-1       GGTCACTATTTGTGTGGATTCAAAACTACTTACAAGGCAAAGAAGCCTGTGAAGATGCCA
[SEQ ID NO:147]   PPms-2       GGTCACTATTTGTGTGAATTCAAAACTACTTACAAGGCAAAGAAGCCTGTGAAGATGCCA
[SEQ ID NO:149]   PPms-E       GGTCACTATTTGTGTGGATTCAAAACTACTTACAAGGCAAAGAAGCCCGTGAAGATGCCA
[SEQ ID NO:151]   PPms-G       GGTCACTATTTGTGTGGATTCAAAACTACTTACAAGGCAAAGAAGCCTGTGAAGATGCCA
[SEQ ID NO:153]   Pav5ms       GGTCACTATTTGTGTGAATTCAAATCGACTTACAAGGCAAAGAAGACTGTGAAGATGCCA
[SEQ ID NO:155]   Pavms-2      GGTCACTATTTGTGTGAATTCAAATCGACTTACAAGGCAAAGAAGACTGCGAAGATGCCA
[SEQ ID NO:157]   Pavms-3      GGTCACTATTTGTGTGAATTCAAATCGACTTACAAGGCAAAGAAGACTGTGAAGATGCCA
[SEQ ID NO:159]   Pavms-4      GGTCACTATTTGTGTGAATTCAAATCGACTTACAAGGCAAAGAAGACTGTGAAGATGCCA
[SEQ ID NO:161]   RTms-1       GGTCACTATTTGTGTGAATTCAAATCTACTTACAAGGCAAAGAAGCCTGTGAAGATGCCA
[SEQ ID NO:163]   RTms-2       GGTCACTATTTGTGTGAATTCAAATCTACTTACAAGGCAAAGAAGCCTGTGAAGATGCCA
[SEQ ID NO:165]   RTms-5       GGTCACTATTTGTGTGAATTCAAAACTACTTACAAGGCAAAGAAGCCTGTGAAGATGCCA
[SEQ ID NO:167]   RTms-6       GGTCACTATTTGTGTGAATTCAAATCTACTTACAAGGCAAAGAAGCCTGTGAAGATGCCA
                               ***** ***   **** ******* * ******* *********    * ** ******
```

Figure 4 continued

```
[SEQ ID NO:87]    Aams-2        GGGTATCATTATGTTGACCGCAAACTGGATGTAACCAATCACAACAAGGATTACACTTCC
[SEQ ID NO:89]    Aams-4        GGGTATCATTATGTTGACCGCAAACTGGATGTAACCAATCACAACAAGGATTACACTTCC
[SEQ ID NO:91]    Aams-5        GGGTATCATTATGTTGACCGCAAACTGGATGTAATCAATCACAACAAGGATTACACTTCC
[SEQ ID NO:93]    Aams-6        GGGTATCATTATGTTGACCGCAAACTGGATGTAATCAATCACAACAAGGATTACACTTCC
[SEQ ID NO:95]    Aams-A        GGGTATCATTATGTTGACCGCAAACTGGATGTAACCAATCACAACAAGGATTACACTTCC
[SEQ ID NO:97]    Aams-B        GGGTATCATTATGTTGACCGCAAACTGGATGTAACCAATCACAACAAGGATTACACTTCC
[SEQ ID NO:99]    Acams-2       GGGTATCACTATGTTGACCGCAAACTGGATGTAACCAATCACAACAAGGATTACACTTCC
[SEQ ID NO:101]   Acams-3       GGGTATCACTATGTTGACCGCAAACTGGATGTAACCAATCACAACAAGGATTACACTTCC
[SEQ ID NO:103]   Acams-4       GGGTATCACTATGTTGACCGCAAACTGGATGTAACCAATCACAACAAGGATTACACTTCC
[SEQ ID NO:105]   Acams-5       GGGTATCATTATGTTGACCGCAAACTGGATGTAACCAATCACAACAAGGATTACATTTCC
[SEQ ID NO:107]   Cems-F        GGGTATCATTATGTTGACCGCAAACTGGATGTAACCAATCACAACAAGGATTACATTTCC
[SEQ ID NO:109]   Cems-G        GGGTATCATTATGTTGACCGCAAACTGGATGTAACCAATCACAACAAGGATTACATTTCC
[SEQ ID NO:111]   Cems-H        GGGTATCATTATGTTGACCGCAAACTGGATGTAACCAATCACAACAAGGATTACATTTCC
[SEQ ID NO:113]   Cems-I        GGGTATCACTATGCTGACCGCAAACTGGATGTAACCAATCACAACAAGGATTACACCTCC
[SEQ ID NO:115]   LGAms-5       GGGTATCACTATGTTGACCGCAAACTGGATGTAACCAATCACAACAAGGATTACACTTCC
[SEQ ID NO:117]   LGAms-6       GGGTATCACTATGTTGACCGCAAACTGGATGTAACCAATCACAACAAGGATTACACTTCC
[SEQ ID NO:119]   M168Dms       GGGTATCATTATGTTGACCGCAAACTGGATGTAACCAATCACAACAAGGATTACACTTCC
[SEQ ID NO:121]   Mims-A        GGGTATCATTATGTTGACCGCAAACTGGATGTAACCAATCACAACAAGGATTACACTTCC
[SEQ ID NO:123]   Mims-B        GGGTATCATTATGTTGACCGCAAACTGGATGTAACCAATCACAACAAGGATTACACTTCC
[SEQ ID NO:125]   Mims-C        GGGTATCATTATGTTGACCGCAAACTGGATGTAACCAATCACAACAAGGATTACACTTCC
[SEQ ID NO:127]   PMms-A        GGATATCACTATGTTGACCGCAAATTGGATGTAACCAATCACAACAAGGATTACACTTCC
[SEQ ID NO:129]   PMms-B        GGGTATCACTATGTTGACCGCAAATTGGATGTAACCAATCACAACAAGGATTACACTTCC
[SEQ ID NO:131]   PMms-C        GGATATCACTATGTTGACCGCAAATTGGATGTAACCAATCACAACAAGGATTACACTTCC
[SEQ ID NO:133]   PMms-D        GGGTATCACTATGTTGACCGCAAATTGGATGTAACCAATCACAACAAGGATTACACTTCC
[SEQ ID NO:135]   PMms-E        GGGTATCACTATGTTGACCGCAAATTGGATGTAACCAATCACAACAAGGATTACACTTCC
[SEQ ID NO:137]   PPd57-1ms     GGATATCACTATGTTGACCGCAAATTGGATGTAACCAATCACAACAAGGATTACACTTCC
[SEQ ID NO:139]   PPd57-2ms     GGGTATCATTATGTTGACCGCAAACTGGATGTAACCAATCACAACAAGGATTACACTTCC
[SEQ ID NO:141]   PPd57-3       GGGTATCATTATGTTGACCGCAAACTGGATGTAACCAATCACAACAAGGATTACACTTCC
[SEQ ID NO:143]   PPd57-4ms     GGGTATCACTATGTTGACCGCAAATTGGATGTAACCAATCACAACAAGGATTACACTTCC
[SEQ ID NO:145]   PPms-1        GGGTATCATTATGTTGACCGCAAACTGGATGTAACCAATCACAACAAGGATTACATTTCC
[SEQ ID NO:147]   PPms-2        GGGTATCACTATGTTGACCGCAAACTGGATGTAACCAATCACAACAAGGATTACACTTCC
[SEQ ID NO:149]   PPms-E        GGGTATCATTATGTTGACCGCAAACTGGATGTAACCAATCACAACAAGGATTACATTTCC
[SEQ ID NO:151]   PPms-G        GGGTATCATTATGTTGACCGCAAACTGGATGTAACCAATCACAACAAGGATTACATTTCC
[SEQ ID NO:153]   Pav5ms        GGGTATCACTATGTTGACCGCAAACTGGATGTAACCAATCACAACAAGGATTACACTTCC
[SEQ ID NO:155]   Pavms-2       GGGTATCACTATGTTGACCGCAAACTGGATGTAACCAATCACAACAAGGATTACACTTCC
[SEQ ID NO:157]   Pavms-3       GGGTATCACTATGTTGACCGCAAACTGGATGTAACCAATCACAACAAGGATTACACTTCC
[SEQ ID NO:159]   Pavms-4       GGGTATCACTATGTTGACCGCAAACTGGTTGTAACCAATCACAACAAGGATTACACTTCC
[SEQ ID NO:161]   RTms-1        GGGTATCACTATGTTGACCGCAAACTGGATGTAACCAATCACAACAAGGATTACACTTCC
[SEQ ID NO:163]   RTms-2        GGGTATCACTATGTTGACCGCAAACTGGATGTAACCAATCACAACAAGGATTACACTTCC
[SEQ ID NO:165]   RTms-5        GGGTATCATTATGTTGACCGCAAACTGGATGTAACCAATCACAACAAGGATTACACTTCC
[SEQ ID NO:167]   RTms-6        GGGTATCACTATGTTGACCGCAAACTGGATGTAACCAATCACAACAAGGATTACACCTCC
                                ** ***** **** ********** *** ***** ********************  ***
```

Figure 4 continued

```
[SEQ ID NO:87]    Aams-2       GTTGAGCAGTGTGAAATTTCCATTACACGCAAACCTGTGGTCGCC
[SEQ ID NO:89]    Aams-4       GTTGAGCAGTGTGAAATTTCCATTACACGCAAACCTGTGGTCGCC
[SEQ ID NO:91]    Aams-5       GTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:93]    Aams-6       GTTGAGCAGTGTGAAATTTCCATTGCACGCAACCCTGTGGTCGCC
[SEQ ID NO:95]    Aams-A       GTTGAGCAGTGTGAAATTTCCATTACACGCAAACCTGTGGTCGCC
[SEQ ID NO:97]    Aams-B       GTTGAGCAGTGTGAAATTTCCATTACACGCAAACCTGTGGTCGCC
[SEQ ID NO:99]    Acams-2      GTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:101]   Acams-3      GTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:103]   Acams-4      GTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:105]   Acams-5      GTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:107]   Cems-F       GTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:109]   Cems-G       GTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:111]   Cems-H       GTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:113]   Cems-I       GTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:115]   LGAms-5      GTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:117]   LGAms-6      GTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:119]   Mi68Dms      GTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:121]   Mims-A       GTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:123]   Mims-B       GTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:125]   Mims-C       GTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:127]   PMms-A       GTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:129]   PMms-B       GTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:131]   PMms-C       GTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:133]   PMms-D       GTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:135]   PMms-E       GTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:137]   PPd57-1ms    GTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:139]   PPd57-2ms    GTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:141]   PPd57-3      GTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:143]   PPd57-4ms    GTTGAGCAGTGTGAGATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:145]   PPms-1       GTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:147]   PPms-2       GTTGAGCGGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:149]   PPms-E       GTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:151]   PPms-G       GTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:153]   Pav5ms       GTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:155]   Pavms-2      GTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:157]   Pavms-3      GTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:159]   Pavms-4      GTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:161]   RTms-1       GTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:163]   RTms-2       GTTGGGCAGTGTGAAATTTCCATTGCCCCCAAACCTGTGGTCGCC
[SEQ ID NO:165]   RTms-5       GTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:167]   RTms-6       GTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
                               **** ** ****** ********* * * *** ************
```

Figure 4 continued

```
[SEQ ID NO:170]   Acasv-B.pep       SVIAKQMTASTLS*QQEARRRLQSRTRERDTWDLSREQISRRQMEPGMTRYLWLALLKKP
[SEQ ID NO:172]   GPd58-1sv.pep     SVIAKQMTASTLS*QQEARRRLQSRTRERDTWDLSREQISRRQMEPGMTRYLWLALLKKP
[SEQ ID NO:174]   GPd58-3sv.pep     SVIAKQMTASTLS*QQEARRRLQSRTRERDTWDLSREQISRRQMEPGMTRYLWLALLKKP
[SEQ ID NO:176]   GPd58-4sv.pep     SVIAKQMTASPLS*QQEARRRLQSRTRERDTWDLSREQISRRQVEPGMTRYLWLALLKKP
[SEQ ID NO:178]   Misv-D.pep        SVIAKQMTASTLS*QQEARRRLQSRTRERDTWDLSREQISRRQVEPGMTRYLWLALLKKP
[SEQ ID NO:180]   Pavsv-D.pep       SVIAKQMTASTLS*QQEARRRLQSRTRERDTWDLSREQISRRQMEPGMTRYLWLALLKKP
                                    ********** ** *****************************.****************

[SEQ ID NO:170]   Acasv-B.pep       *YCVV*GITR*ISRTQ*RDVIDQSVKVRSSR*QTYLW*QWSLMQMNARHLTWFRW*RHPY
[SEQ ID NO:172]   GPd58-1sv.pep     *YCVV*GITR*ISRTQ*RDVIDQSVKVRSSR*QTYLW*QWSLMQMNARHLTWFRW*RHPY
[SEQ ID NO:174]   GPd58-3sv.pep     *YCVV*GITR*ISRTQ*RDVIDQSVKVRSSR*QTYLW*QWSLMQMNARHLTWFRW*RHPY
[SEQ ID NO:176]   GPd58-4sv.pep     *YCVV*GITR*ISRTQ*RDVIDQSVKVRSSR*QTYLW*QWSLMQMNARHLTWFRW*RHPY
[SEQ ID NO:178]   Misv-D.pep        *YCVV*GITR*ISRTQ*RDVIDQSVKVRSSR*QTYLW*QWSLMQMNARHLTWFRW*RHPY
[SEQ ID NO:180]   Pavsv-D.pep       *YCVV*GITR*ISRTQ*RDVIDQSVKVRSSR*QTYLW*QWSLMQMNARHLTWFRW*RHPY
                                     **** **** ***** ************** ***** ***************** ****

[SEQ ID NO:170]   Acasv-B.pep       -MNSNLS*GWW*WLTLA*SRSILAERNNGCI*GTGSWGTSWILSTWRIICRHLTA*FRN*
[SEQ ID NO:172]   GPd58-1sv.pep     -MNSNLS*GWW*WLTLV*SRSILAERNNGCI*GTGSWGTSWILSTWRIICRHLTA*FS-*
[SEQ ID NO:174]   GPd58-3sv.pep     -MNSNLS*GWW*WLTLA*SRSILAERNNGCI*GTGSWGTSWILSTWRIICRHLTA*FRN*
[SEQ ID NO:176]   GPd58-4sv.pep     -MNSNLS*GWW*WLTLV*SRSILAERNNGCI*GTGSWGTSWILSTWRIICRHLTA*FRN*
[SEQ ID NO:178]   Misv-D.pep        CMNSNLS*GWW*WLTLV*SRSILAERNNGCI*GTGSWGTSWILSTWRIICRHLTA*FRN*
[SEQ ID NO:180]   Pavsv-D.pep       -MNSNLS*GWW*WLTLA*SRSILAERNNGCI*GTGSWGTSWILSTWRIICRHLTA*FRN*
                                     ****** *** ****  ************* *********************** *

[SEQ ID NO:170]   Acasv-B.pep       IVS-FF-MTINRQV-*N*L*R*V*V*TSVW*GNYDRNYCHA*RETVTLHANLWS
[SEQ ID NO:172]   GPd58-1sv.pep     LNCVVVFLNDN--TV*N*L*R*V*V*TSVW*GNYDRNYCHA*RETVTLHANLWS
[SEQ ID NO:174]   GPd58-3sv.pep     IVS-FF-MTINRQV-*N*L*R*V*V*TSVW*GXYXRNYC---------------
[SEQ ID NO:176]   GPd58-4sv.pep     IVS-FF-MTINRQV-*N*L*R*V*V*TSVW*GNYDRNYCHA*RETVTSHANLWS
[SEQ ID NO:178]   Misv-D.pep        IVS-FF-MTINRQV-*N*L*R*V*V*TSVW*GNYDRNYCHA*RETVTSHANLWS
[SEQ ID NO:180]   Pavsv-D.pep       IVS-FF-MTINRQV-*N*L*R*V*V*TSVW*GNYDRNYCHA*RETVTLHANLWS
                                    . .    .. *     * * * * * **** ********
```

Figure 5

```
[SEQ ID NO:169]   Acasv-B      TCCGTTATCGCTAAACAGATGACCGCTTCAACGTTAAGTTGACAACAGGAAGCACGACGG
[SEQ ID NO:171]   GPd58-1sv    TCCGTTATCGCTAAACAGATGACCGCTTCAACGTTAAGTTGACAACAGGAAGCACGACGG
[SEQ ID NO:173]   GPd58-3sv    TCCGTTATCGCTAAACAGATGACCGCTTCAACGTTAAGTTGACAACAGGAAGCACGACGG
[SEQ ID NO:175]   GPd58-4sv    TCCGTTATCGCTAAACAGATGACCGCTTCACCGTTAAGTTGACAACAGGAAGCACGACGG
[SEQ ID NO:177]   Misv-D       TCCGTTATCGCTAAACAGATGACCGCTTCAACGTTAAGTTGACAACAGGAAGCACGACGG
[SEQ ID NO:179]   Pavsv-D      TCCGTTATCGCTAAACAGATGACCGCTTCAACGTTAAGTTGACAACAGGAAGCACGACGG
                               ****************************** *****************************

[SEQ ID NO:169]   Acasv-B      AGACTGCAGTCCCGTACGCGCGAACGGGATACCTGGGATTTATCAAGAGAACAGATTTCA
[SEQ ID NO:171]   GPd58-1sv    AGACTGCAGTCCCGTACGCGCGAACGGGATACCTGGGATTTATCAAGAGAACAGATTTCA
[SEQ ID NO:173]   GPd58-3sv    AGACTGCAGTCCCGTACGCGCGAACGGGATACCTGGGATTTATCAAGAGAACAGATTTCA
[SEQ ID NO:175]   GPd58-4sv    AGACTGCAGTCCCGTACGCGCGAACGGGATACCTGGGATTTATCAAGAGAACAGATTTCA
[SEQ ID NO:177]   Misv-D       AGACTGCAGTCCCGTACGCGCGAACGGGATACCTGGGATTTATCAAGAGAACAGATTTCA
[SEQ ID NO:179]   Pavsv-D      AGACTGCAGTCCCGTACGCGCGAACGGGATACCTGGGATTTATCAAGAGAACAGATTTCA
                               ************************************************************

[SEQ ID NO:169]   Acasv-B      CGCAGACAGATGGAGCCCGGCATGACGCGTTATTTGTGGTTGGCCCTCTTGAAGAAACCA
[SEQ ID NO:171]   GPd58-1sv    CGCAGACAGATGGAGCCCGGCATGACGCGTTATTTGTGGTTGGCCCTCTTGAAGAAACCA
[SEQ ID NO:173]   GPd58-3sv    CGCAGACAGATGGAGCCCGGCATGACGCGTTATTTGTGGTTGGCCCTCTTGAAGAAACCA
[SEQ ID NO:175]   GPd58-4sv    CGCAGACAGGTGGAGCCCGGCATGACGCGTTATTTGTGGTTGGCCCTCTTGAAGAAACCA
[SEQ ID NO:177]   Misv-D       CGCAGACAGGTGGAGCCCGGCATGACGCGTTATTTGTGGTTGGCCCTCTTGAAGAAACCA
[SEQ ID NO:179]   Pavsv-D      CGCAGACAGATGGAGCCCGGCATGACGCGTTATTTGTGGTTGGCCCTCTTGAAGAAACCA
                               ********* **************************************************

[SEQ ID NO:169]   Acasv-B      TGATATTGCGTGGTATGAGGTATCACCCGGTAGATATCGAGAACACAGTGACGAGATGTC
[SEQ ID NO:171]   GPd58-1sv    TGATATTGCGTGGTATGAGGTATCACCCGGTAGATATCGAGAACACAGTGACGAGATGTC
[SEQ ID NO:173]   GPd58-3sv    TGATATTGCGTGGTATGAGGTATCACCCGGTAGATATCGAGAACACAGTGACGAGATGTC
[SEQ ID NO:175]   GPd58-4sv    TGATATTGCGTGGTATGAGGTATCACCCGGTAGATATCGAGAACACAGTGACGAGATGTC
[SEQ ID NO:177]   Misv-D       TGATATTGCGTGGTATGAGGTATCACCCGGTAGATATCGAGAACACAGTGACGAGATGTC
[SEQ ID NO:179]   Pavsv-D      TGATATTGCGTGGTATGAGGTATCACCCGGTAGATATCGAGAACACAGTGACGAGATGTC
                               ************************************************************
```

Figure 6

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[SEQ ID NO:169]   Acasv-B      ATCGATCAATCTGTGAAAGTGCGGTCTTCACGATGACAAACCTACTTGTGGTAGCAGTGG
[SEQ ID NO:171]   GPd58-1sv    ATCGATCAATCTGTGAAAGTGCGGTCTTCACGATGACAAACCTACTTGTGGTAGCAGTGG
[SEQ ID NO:173]   GPd58-3sv    ATCGATCAATCTGTGAAAGTGCGGTCTTCACGATGACAAACCTACTTGTGGTAGCAGTGG
[SEQ ID NO:175]   GPd58-4sv    ATCGATCAATCTGTGAAAGTGCGGTCTTCACGATGACAAACCTACTTGTGGTAGCAGTGG
[SEQ ID NO:177]   Misv-D       ATCGATCAATCTGTGAAAGTGCGGTCTTCACGATGACAAACCTACTTGTGGTAGCAGTGG
[SEQ ID NO:179]   Pavsv-D      ATCGATCAATCTGTGAAAGTGCGGTCTTCACGATGACAAACCTACTTGTGGTAGCAGTGG
                               ************************************************************

[SEQ ID NO:169]   Acasv-B      AGCTTGATGCAGATGAACGCGAGGCACTTGACGTGGTTCCGCTGGTGACGACATCCGTAC
[SEQ ID NO:171]   GPd58-1sv    AGCTTGATGCAGATGAACGCGAGGCACTTGACGTGGTTCCGCTGGTGACGACATCCGTAC
[SEQ ID NO:173]   GPd58-3sv    AGCTTGATGCAGATGAACGCGAGGCACTTGACGTGGTTCCGCTGGTGACGACATCCGTAC
[SEQ ID NO:175]   GPd58-4sv    AGCTTGATGCAGATGAACGCGAGGCACTTGACGTGGTTCCGCTGGTGACGACATCCGTAC
[SEQ ID NO:177]   Misv-D       AGCTTGATGCAGATGAACGCGAGGCACTTGACGTGGTTCCGCTGGTGACGACATCCGTAC
[SEQ ID NO:179]   Pavsv-D      AGCTTGATGCAGATGAACGCGAGGCACTTGACGTGGTTCCGCTGGTGACGACATCCGTAC
                               ************************************************************

[SEQ ID NO:169]   Acasv-B      TGAATGAACAGCAACTTGTCGTAGGGGTGGTGGTAGTGGTTGACCCTGGCGTAGTCCCGA
[SEQ ID NO:171]   GPd58-1sv    TGAATGAACAGCAACTTGTCGTAGGGGTGGTGGTAGTGGTTGACCCTGGTGTAGTCCCGA
[SEQ ID NO:173]   GPd58-3sv    TGAATGAACAGCAACTTGTCGTAGGGGTGGTGGTAGTGGTTGACCCTGGCGTAGTCCCGA
[SEQ ID NO:175]   GPd58-4sv    TGAATGAACAGCAACTTGTCGTAGGGGTGGTGGTAGTGGTTGACCCTGGTGTAGTCCCGA
[SEQ ID NO:177]   Misv-D       TGTATGAACAGCAACTTGTCGTAGGGGTGGTGGTAGTGGTTGACCCTGGTGTAGTCCCGA
[SEQ ID NO:179]   Pavsv-D      TGAATGAACAGCAACTTGTCGTAGGGGTGGTGGTAGTGGTTGACCCTGGCGTAGTCCCGA
                               ** ********************************************** **********

[SEQ ID NO:169]   Acasv-B      TCAATTCTCGCGGAGAGAAACAACGGATGCATCTGAGGGACGGGTTCCTGGGGGACCAGT
[SEQ ID NO:171]   GPd58-1sv    TCAATTCTCGCGGAGAGAAACAACGGATGCATCTGAGGGACGGGTTCCTGGGGGACCAGT
[SEQ ID NO:173]   GPd58-3sv    TCAATTCTCGCGGAGAGAAACAACGGATGCATCTGAGGGACGGGTTCCTGGGGGACCAGT
[SEQ ID NO:175]   GPd58-4sv    TCAATTCTCGCGGAGAGAAACAACGGATGCATCTGAGGGACGGGTTCCTGGGGGACCAGT
[SEQ ID NO:177]   Misv-D       TCAATTCTCGCGGAGAGAAACAACGGATGCATCTGAGGGACGGGTTCCTGGGGGACCAGT
[SEQ ID NO:179]   Pavsv-D      TCAATTCTCGCGGAGAGAAACAACGGATGCATCTGAGGGACGGGTTCCTGGGGGACCAGT
                               ************************************************************
```

Figure 6 continued

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[SEQ ID NO:169]   Acasv-B      TGGATCCTATCTACGTGGCGTATAATATGTAGACACCTCACTGCTTAGTTT-CGTAATTG
[SEQ ID NO:171]   GPd58-1sv    TGGATCCTATCTACGTGGCGTATAATATGTAGACACCTCACTGCTTAATTTTCGTAATTG
[SEQ ID NO:173]   GPd58-3sv    TGGATCCTATCTACGTGGCGTATAATATGTAGACACCTCACTGCTTAGTTT-CGTAATTG
[SEQ ID NO:175]   GPd58-4sv    TGGATCCTATCTACGTGGCGTATAATATGTAGACACCTCACTGCTTAGTTT-CGTAATTG
[SEQ ID NO:177]   Misv-D       TGGATCCTATCTACGTGGCGTATAATATGTAGACACCTCACTGCTTAGTTT-CGTAATTG
[SEQ ID NO:179]   Pavsv-D      TGGATCCTATCTACGTGGCGTATAATATGTAGACACCTCACTGCTTAGTTT-CGTAATTG
                               *********************************************** *** ********

[SEQ ID NO:169]   Acasv-B      AATTGTGTCGTAGTTTTTTTAAATGACAATTAATAGACAAGTTTGAAATTGACTGTAGCG
[SEQ ID NO:171]   GPd58-1sv    AATTGTGTCGTAGTTTTTTTAAATGACAACTAATAGACA-GTTTGAAATTGACTGTAGCG
[SEQ ID NO:173]   GPd58-3sv    AATTGTGTCGTAGTTTTTTTAAATGACAATTAATAGACAAGTTTGAAATTGACTGTAGCG
[SEQ ID NO:175]   GPd58-4sv    AATTGTGTCGTAGTTTTTTTAAATGACAATTAATAGACAAGTTTGAAATTGACTGTAGCG
[SEQ ID NO:177]   Misv-D       AATTGTGTCGTAGTTTTTTTAAATGACAATTAATAGACAAGTTTGAAATTGACTGTAGCG
[SEQ ID NO:179]   Pavsv-D      AATTGTGTCGTAGTTTTTTTAAATGACAATTAATAGACAAGTTTGAAATTGACTGTAGCG
                               ***************************** ********* ********************

[SEQ ID NO:169]   Acasv-B      CTAGGTTTAGGTATAAACTAGCGTTTGGTAAGGCAATTATGACAGGAACTACTGTCACGC
[SEQ ID NO:171]   GPd58-1sv    CTAGGTTTAGGTATAAACTAGCGTTTGGTAAGGCAATTATGACAGGAATTACTGTCACGC
[SEQ ID NO:173]   GPd58-3sv    CTAGGTTTAGGTATAAACTAGCGTTTGGTAAGGCNATTATNACAGGAACTACTGTCACGC
[SEQ ID NO:175]   GPd58-4sv    CTAGGTTTAGGTATAAACTAGCGTTTGGTAAGGCAATTATGACAGGAATTACTGTCACGC
[SEQ ID NO:177]   Misv-D       CTAGGTTTAGGTATAAACTAGCGTTTGGTAAGGCAATTATGACAGGAATTACTGTCACGC
[SEQ ID NO:179]   Pavsv-D      CTAGGTTTAGGTATAAACTAGCGTTTGGTAAGGCAATTATGACAGGAACTACTGTCACGC
                               ********************************** ***** ******* ***********

[SEQ ID NO:169]   Acasv-B      GTGACGCGAGACCGTCACTTTACACGCAAACCTGTGGTCGCC
[SEQ ID NO:171]   GPd58-1sv    GTGACGCGAGACCGTCACTTTACACGCAAACCTGTGGTCGCC
[SEQ ID NO:173]   GPd58-3sv    GTGACGCGAGACCGTCACTTTACACGCAAACCTGTGGTCGCC
[SEQ ID NO:175]   GPd58-4sv    GTGACGCGAGACCGTCACTTCACACGCAAACCTGTGGTCGCC
[SEQ ID NO:177]   Misv-D       GTGACGCGAGACCGTCACTTCACACGCAAACCTGTGGTCGCC
[SEQ ID NO:179]   Pavsv-D      GTGACGCGAGACCGTCACTTTACACGCAAACCTGTGGTCGCC
                               ******************** *********************
```

Figure 6 continued

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[SEQ ID NO:19]    Aasv-1          TCCGTTATCGCTAAACAGATGACC--TACAAGGTTTATATGTCAG--ACACGGTCAATGG
[SEQ ID NO:169]   Acasv-B         TCCGTTATCGCTAAACAGATGACCGCTTCAACGTTAAGTTGACAACAGGAAGCACGACGG
                                  ************************  * *** *** *  ** **     * *  * * **

[SEQ ID NO:19]    Aasv-1          ACACTACTTTGAGGTTGAAGGCGATGGAAAAGGAAAGCCTTACGAGGGGGA---------
[SEQ ID NO:169]   Acasv-B         AGACTGCAGTCCCGTACGCGCGAACGGGATACCTGGGATTTATCAAGAGAACAGATTTCA
                                  * *** *  *   **    *   * ** * *     *  ***  * * * *

[SEQ ID NO:19]    Aasv-1          -GCAGACGG-TAAAGCTCACT-------GTCACCAAGGGCGGACCTCTGCCATTTGCTTG
[SEQ ID NO:169]   Acasv-B         CGCAGACAGATGGAGCCCGGCATGACGCGTTATTTGTGGTTGGCCCTCTTGAAGAAACCA
                                   ****** * *  *** *          ** *     **  * **      *

[SEQ ID NO:19]    Aasv-1          GGATATTCTATCACCACAGAGTCAGTACGGAAGCATACCATTCACCAAGTACCCTGAAGA
[SEQ ID NO:169]   Acasv-B         TGATATTGCGTGGTATGAGGTATCACCCGGTAG-ATATCGAGAACACAGTGACGAGATGT
                                  ******   *      **        *** ** *** *    **  ***  *  ** *

[SEQ ID NO:19]    Aasv-1          CATCCCTGACTATGTAAAGCAGTCATTCCCTGAGGGATATACATGGGAGAGG--ATCATG
[SEQ ID NO:169]   Acasv-B         CATCGATCAATCTGTGAAAGTGCGGTCTTCACGATGACAAACCTACTTGTGGTAGCAGTG
                                  ****  * * * *** **   *   *   *     ** * ** *    * **      **

[SEQ ID NO:19]    Aasv-1          AACTTCGAAGATGGTGCAGTGTGTACTGTCAGCAATGATTCCAGCATCCAAGGTAACTGT
[SEQ ID NO:169]   Acasv-B         GAGCTTGATGCAGATG-AACGCGAGGCACTTGACGTGGTTCCGCTGGTGACGACATCCGT
                                   *  * ** *  * ** *  * *        *   ** ****       * *  * * **

[SEQ ID NO:19]    Aasv-1          TTCATCTACAATGTCAAGTTCTC----------TGGTTTGAACTTTCCTCCCAATGGACC
[SEQ ID NO:169]   Acasv-B         ACTGAATG-AACAGCAACTTGTCGTAGGGGTGGTGGTAGTGGTTGACCCTGGCGTAGTCC
                                  *  **   *** ** **          ****      *  **      * * **

[SEQ ID NO:19]    Aasv-1          TGTT--ATGCAAAAGAAGACACAGGGCTGGGAACCCAACACTGGGCGTCTCTTTGCACGA
[SEQ ID NO:169]   Acasv-B         CGATCAATTCTCGCGGAGAGAAACAACGGATGCATCTGAGGGACGGGTTCCTGGGGGACC
                                   * *  ** *    * *** * *   * *      *        * **  **  *
```

Figure 7

```
[SEQ ID NO:19]    Aasv-1     GATGGAATGCTGATAGGAAACAACTTTATGGCTCTGAAGTTGGAAGGAGGTGGTCATTAT
[SEQ ID NO:169]   Acasv-B    AGTTGGATCCTATCTACGTGGCGTATAATATGTAGACACCTCACTGCTTAGTTTCGTAAT
                               * * ** **              * **   *    *  *    *       ** * **

[SEQ ID NO:19]    Aasv-1     TTGTGTGAATTCAAATCTACTTACAAGGCAA---AGAAGCCTGTGATGATGCCAGGGTAT
[SEQ ID NO:169]   Acasv-B    TGAATTGTGTCGTAGTTTTTTTAAATGACAATTAATAGACAAGTTTGAAATTGACTGTAG
                             *    **  *   * * *  *** * * ***   * *  *  **    *    *  ***

[SEQ ID NO:19]    Aasv-1     CACTATGTTGAC-CGCAAGTTGGATGT-----AACCAATCACAACAAGGATTACACTTCC
[SEQ ID NO:169]   Acasv-B    CGCTAGGTTTAGGTATAAACTAGCGTTTGGTAAGGCAATTATGACAGGAACTACTGTCAC
                             * *** *** *     **  * *   *     *  **** *  *** * * ***  *  *

[SEQ ID NO:19]    Aasv-1     GTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
[SEQ ID NO:169]   Acasv-B    GC-GTGACGCGAGACCGTCACTTTACACGCAAACCTGTGGTCGCC
                             *  * *  * * **   *  * ** ********************
```

Figure 7 continued

```
[SEQ ID NO:181]   Aapat1            SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC
[SEQ ID NO:182]   Aapat2            SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGLPYEGGQTVRLAVTKGGPLPFAWDILSPQC
[SEQ ID NO:20]    Aasv-1.pep        SVIAKQMTYKVYMSDTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQS
[SEQ ID NO:22]    Aasv-3.pep        SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLTVTKGGPLPFAWDILSPQS
[SEQ ID NO:24]    Aasv-P.pep        SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQS
[SEQ ID NO:26]    Acasv-A.pep       SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPRC
[SEQ ID NO:28]    Acasv-C.pep       SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLTVTKGGPLPFAWDILSPQS
[SEQ ID NO:30]    Acasv-D.pep       SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQC
[SEQ ID NO:32]    Ce61-3sv.pep      SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLTVTKGGPLPFAWDILSPQS
[SEQ ID NO:34]    Ce61-4sv.pep      SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTXGGPLPFAWDIXSPQS
[SEQ ID NO:36]    Ce61-5sv.pep      SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQC
[SEQ ID NO:38]    Ce61-7sv.pep      SVIAKQMTYXXYXSGTVXGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQC
[SEQ ID NO:40]    GPd58-2sv.pep     SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQS
[SEQ ID NO:42]    LGAsv-A.pep       SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQS
[SEQ ID NO:44]    LGAsv-C.pep       SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQC
[SEQ ID NO:46]    LGAsv-D.pep       SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQS
[SEQ ID NO:48]    LGAsv-E.pep       SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTEGGPLPFAWDILSPQS
[SEQ ID NO:50]    Misv-A.pep        SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQS
[SEQ ID NO:52]    Misv-B.pep        SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLTVTKGGPLPFAWDILSPQS
[SEQ ID NO:54]    Misv-F.pep        SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLTVTKGGPLPFAWDILSPQS
[SEQ ID NO:56]    PM1Asv-rep.pep    SVIAKQMTYKVYMSDTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQS
[SEQ ID NO:58]    PM1Csv-rep.pep    SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGRPYEGEQTVKLTVTKGGPLPFAWDILSPQS
[SEQ ID NO:60]    PMsv-4.pep        SVIAKQMTYKVYMSGTVNGHYFXVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQS
[SEQ ID NO:62]    PMsv-5.pep        SVIAKQMTYKVYMSGTVNGHYFEVQGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQS
[SEQ ID NO:64]    PPsv-1.pep        SVIAKQMTYKVYMSGTVNGHYFEVEGDRKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQC
[SEQ ID NO:66]    PPsv-2.pep        SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQC
[SEQ ID NO:68]    PPsv-3.pep        SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQC
[SEQ ID NO:70]    PPsv-4.pep        SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPRC
[SEQ ID NO:72]    PPsv-5.pep        SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQS
[SEQ ID NO:74]    PPsv-6.pep        SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQS
[SEQ ID NO:76]    Pavsv-A.pep       SVIAKQMTYKVNMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTEGGPLPFAWDILSPQS
[SEQ ID NO:78]    Pavsv-B.pep       SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQC
[SEQ ID NO:80]    Pavsv-C.pep       SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTEGGPLPFAWDILSPQS
[SEQ ID NO:82]    RTsv-1.pep        SVIAKQMTYKVYMSGTVNGHYFEAEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQS
[SEQ ID NO:84]    RTsv-2.pep        SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQS
[SEQ ID NO:86]    RTsv-3.pep        SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQS
                                    *********    * ** ****  .** ** **** ***.*.** ********** **..
```

Figure 8

```
Aapat1            QYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS
Aapat2            QYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKRS
Aasv-1.pep        QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYNVKFS
Aasv-3.pep        QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS
Aasv-P.pep        QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIVNFEDGAVCTVSNDSSIQGNCFIYNVKFS
Acasv-A.pep       QYGNIPFTKYPEDVPDYVKQSFPEGFTWERIMNFEDGAVCTVSNDSSIQGNCFTYHVKFS
Acasv-C.pep       QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS
Acasv-D.pep       QYGSIPFTKYPEDIPDYVKQSFPEGFTWERIMNFEDGAVCTVSNDSSIQGNCFTYHVKFS
Ce61-3sv.pep      QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS
Ce61-4sv.pep      QYGSXPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS
Ce61-5sv.pep      QYGSIPFTKYPEDIPDYVKQSFPEGFTWERIMNFEDGAVCTVSNDSSIQGNCFTYHVKFS
Ce61-7sv.pep      QYGSIPFTKYPEDIPDYVKQSFPEGFTWERIMNFEDGAVCTVSNDSSIQGNCFTYHVKFS
GPd58-2sv.pep     QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYNVKFS
LGAsv-A.pep       QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYNVKFS
LGAsv-C.pep       QYGSIPFTKYPEDIPDYVKQSFPEGFTWERIMNFEDGAVCTVSNDSSIQGNCFTYHVKFS
LGAsv-D.pep       QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYNVKFS
LGAsv-E.pep       QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYNVKFS
Misv-A.pep        QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS
Misv-B.pep        QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS
Misv-F.pep        QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS
PM1Asv-rep.pep    QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYNVKFS
PM1Csv-rep.pep    QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMKFEDGAVCTVSNDSSMQGNCFIYNVKFS
PMsv-4.pep        QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIVNFEDGAVCTVSNDSSIQGNCFIYNVKFS
PMsv-5.pep        QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFKDGAVCTVSNDSSIQGNCFIYNVKFS
PPsv-1.pep        QYGNIPFTKYPEDVPDYVKQSFPEGFTWERIMNFEDGAVCTVSNDSSIQGNCFTYHVKFS
PPsv-2.pep        QYGNIPFTKYPEDVPDYVKQSFPEGFTWERIMNFEDGAVCTVSNDSSIQGNCFTYHVKFS
PPsv-3.pep        QYGNIPFTKYPEDVPDYVKQSFPEGFTWERIMNFEDGAVCTVSNDSSIQGNCFTYHVKFS
PPsv-4.pep        QYGNIPFTKYPEDVPDYVKQSFPEGFTWERIMNFEDGAVCTVSNDSSIQGNCFTYHVKFS
PPsv-5.pep        QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYNVKFS
PPsv-6.pep        QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGSCFIYNVKFS
Pavsv-A.pep       QYGSVPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYNVKFS
Pavsv-B.pep       QYGSIPFTKYPEDIPDYVKQSFPEGFTWERIMNFEDGAVCTVSNDSSIQGNCFTYHVKFS
Pavsv-C.pep       QYGSVPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS
RTsv-1.pep        QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYNVKFS
RTsv-2.pep        QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYNVKFS
RTsv-3.pep        QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYNVKFS
                  *** ********.*********  .*****. * ***********.** ** *.** *
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Figure 8 continued

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Aapat1             GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKARK
Aapat2             GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKK
Aasv-1.pep         GLNFPPNGPVMQKKTQGWEPNTGRLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKK
Aasv-3.pep         GLNFPPNGPVMQKKTQGWEPNTERLLARDGMLIGNNFMALKLEGGGHYLCEFKSTYKARK
Aasv-P.pep         GLNFPPNGPVMQKKTQGWEPNTERLYARDGMLIGNNFMALKLEGGQRSL*----------
Acasv-A.pep        GLNFPPNGPVMQKKTRGWEPHSERLFARGGMLIGNNFMALKLEGGGHYLCGFKTTYKAKK
Acasv-C.pep        GLNFPPNGPVMQKKTQGWEPNTERLSARDGMLIGNNFMALKLEGGGHYLCEFKSTYKARK
Acasv-D.pep        GLNFPPNGPVMQKKTQGWEPHSERLFARGGMLIGNNFMAPKLEGGGHYLCEFKTTYKAKK
Ce61-3sv.pep       GLNFPPNGPVMQKKTQGWEPNTERLSARDGMLIGNNFMALKLEGGGHYLCEFKSTYKARK
Ce61-4sv.pep       GLNFPPNGPVMQKKTQGWEPHSERLFARDGMLIGNNFMALKXEGGGXYLCEFKSTYKAKK
Ce61-5sv.pep       GLNFPPNGPVMQKKTQGWEPHSERLFARGGMLIGNNFMALKLEGGGHYLCEFKTTYKAKK
Ce61-7sv.pep       GLNFPPNGPVMQKKTQGWEPHSERLFARGGMLIGNNFMALKLEGGGHYLCEFKTTYKAKK
GPd58-2sv.pep      GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKK
LGAsv-A.pep        GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKK
LGAsv-C.pep        GLDFPPNGPVMQKKTQGWEPHSERLFARGGMLIGNNFMALKLEGGGHYLCEFKTTYKAKK
LGAsv-D.pep        GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKK
LGAsv-E.pep        GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKK
Misv-A.pep         GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKARK
Misv-B.pep         GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKARK
Misv-F.pep         GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKARK
PM1Asv-rep.pep     GLNFPPNGPVMQKKTQGWEPNTGRLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKK
PM1Csv-rep.pep     GLNFPPNGPVMQKKTQGWEPNTERLYARDGMLIGNNFMALKLEGSGHYTCEFKSTYKAKK
PMsv-4.pep         GLNFPPNGPVMQKKTQGWEPNTERLYARDGMLIGNNFMALKLEGGQRSL--CQGITMLTA
PMsv-5.pep         GLNFPPNGPVMQKKTQGWEPNTERLFARDGVLIGNNFMALKLEGGGHYLCEFKSTYKAKK
PPsv-1.pep         GLNFPPNGPVMQKKTQGWEPHSERLFARGGMLIGNNFMALKLEGGGHYLCGFKTTYKAKK
PPsv-2.pep         GLNFPPNGPVMQKKTQGWEPHSERLFARGGMLIGNNFMALKLEGGGHYLCGFKTTYKAKK
PPsv-3.pep         GLNFPPNGPVMQKKTQGWEPHSERLFARGGMLIGNNFMALKLEGGGHYLCGFKTTYKAKK
PPsv-4.pep         GLNFPPNGPVMQKKTRGWEPHSERLFARGGMLIGNNFMALKLEGGGHYLCGFKTTYKAKK
PPsv-5.pep         GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKK
PPsv-6.pep         GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKK
Pavsv-A.pep        GLNFPPNGPVMQKKTQGWVPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKK
Pavsv-B.pep        GLNFPPNGPVMQKKTQGWEPHSERLFARGGMLIGNNFMAPKLEGGGHYLCEFKTTYKAKK
Pavsv-C.pep        GLNFPPNGPVMQKKTQGWEPNTERLSARDGMLIGNNFMALKLEGGGHYLCEFKSTYKARK
RTsv-1.pep         GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKK
RTsv-2.pep         GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKK
RTsv-3.pep         GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKK
                   ** ************.** *.. ** ** *.******** * **
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Figure 8 continued

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Aapat1             PVKMPGYHYVDRKLDVTNHNKDYTSVEQREISIARKPLVACCFFRVKSRHK----
Aapat2             PVKMPGYHYVDRKLDVTNHNLDYTSVEQCEISIARKPVVACRFFRVKSRHKYAVA
Aasv-1.pep         PVMMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA---------------
Aasv-3.pep         PVKMPGYHYVDRKLDVTNHNKDYTSVEQREISIARKPVVA---------------
Aasv-P.pep         -------------------------------------------------------
Acasv-A.pep        PVKMPGYHYVDRKLDVTNHNKDYISVEQCEISIARKPVVA---------------
Acasv-C.pep        PVKMPGYHCVDRKLDVTNHNKDYTSVEQREISIARKPVVA---------------
Acasv-D.pep        PVKMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA---------------
Ce61-3sv.pep       PVKMPGYHYVDRKLDVTNHNKDYTSVEQREISIARKPVVA---------------
Ce61-4sv.pep       PVMMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA---------------
Ce61-5sv.pep       PVKMPGYHYVYSTIHVTNHNKDYTSVEQCEISXXRKPVVA---------------
Ce61-7sv.pep       PVKMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA---------------
GPd58-2sv.pep      PVMMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA---------------
LGAsv-A.pep        PVMMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA---------------
LGAsv-C.pep        PVKMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA---------------
LGAsv-D.pep        PVMMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA---------------
LGAsv-E.pep        PVMMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA---------------
Misv-A.pep         PVKMPGYHYVDRKLDVTNHNKDYTSVEQREISIARKPVVA---------------
Misv-B.pep         PVKMPGYHYVDRKLDVTNHNKDYTSVEQREISIARKPVVA---------------
Misv-F.pep         PVKMPGYHYVDRKLDVTNHNKDYTSVEQREISIARKPVVA---------------
PM1Asv-rep.pep     PVMMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA---------------
PM1Csv-rep.pep     PVMMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA---------------
PMsv-4.pep         NWM-PITTRITLPLSSVRFPSHANLWSPDVFSESNQGT-----------------
PMsv-5.pep         PVMMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA-RFFRVKSRHK----
PPsv-1.pep         PVKMPGYHYVDRKLDVTNHNKDYISVEQCEISIARKPVVA---------------
PPsv-2.pep         PVKMPGYHYVDRKLDVTNHNKDYISVEQCEISIARKPVVA---------------
PPsv-3.pep         PVKMPGYHYVDRKLDVTNHNKDYISVEQCETSIARKPVVA---------------
PPsv-4.pep         PVKMPGYHYVDRKLDVTNHNKDYISVEQCEISIARKPVVA---------------
PPsv-5.pep         PVMMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA---------------
PPsv-6.pep         PVMMPGYHYVDRKLDVTNHNKDYTSVEQCGISIARKPVVA---------------
Pavsv-A.pep        PVMMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA---------------
Pavsv-B.pep        PVKMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA---------------
Pavsv-C.pep        PVKMPGYHYVDRKLDVTNHNKDYTSVEQREISIARKPVVA---------------
RTsv-1.pep         PVMMPGYHYVDRKLDVTNHNKDYTSVEQCEIPIARKPVVA---------------
RTsv-2.pep         PVMMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA---------------
RTsv-3.pep         PVMMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA---------------
                       *    .   .                     .
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Figure 8 continued

SEQ ID NO	N-terminus	name	extra bases	stop codon at AA14
SEQ ID NO:170	sviak	Acasv-B.pep	701 bases	SVIAKQMTASTLS*
SEQ ID NO:171	sviak	GPd58-1sv.pep	701 bases	SVIAKQMTASTLS*
SEQ ID NO:172	sviak	GPd58-3sv.pep	701 bases	SVIAKQMTASTLS*
SEQ ID NO:173	sviak	GPd58-4sv.pep	701 bases	SVIAKQMTASPLS*
SEQ ID NO:174	sviak	Misv-D.pep	701 bases	SVIAKQMTASTLS*
SEQ ID NO:180	sviak	Pavsv-D.pep	701 bases	SVIAKQMTASTLS*

	N-terminus	name	type	"QYG" fluorophore and 26 aa within 5A
SEQ ID NO:64	sviak	PPsv-1.pep	5	QVLSPQCQYGNIFWRNSYEHENMGRLQCE
SEQ ID NO:65	sviak	PPsv-2.pep	5	QVLSPQCQYGNIFWRNSYEHENMGRLQCE
SEQ ID NO:66	sviak	PPsv-3.pep	5	QVLSPQCQYGNIFWRNSYEHENMGRLQCE
SEQ ID NO:67	sviak	Acasv-A.pep	4	QVLSPRCQYGNIFWRNSYEHENMGRLQCE
SEQ ID NO:68	sviak	PPsv-4.pep	4	QVLSPRCQYGNIFWRNSYEHENMGRLQCE
SEQ ID NO:69	sviak	Acasv-D.pep	1	QVLSPQCQYGSIFWRNSYEHENMERLQCE
SEQ ID NO:70	sviak	LGAsv-C.pep	1	QVLSPQCQYGSIFWRNSYEHENMERLQCE
SEQ ID NO:71	sviak	Pavsv-B.pep	1	QVLSPQCQYGSIFWRNSYEHENMERLQCE
SEQ ID NO:72	sviak	Ce61-7sv-rep.pe	RES 1?	QVLSPQCQYGSIFWRNSYEHENMERLQCE
SEQ ID NO:73	sviak	Ce61-5sv-rep.pe	RES 18	QVLSPQCQYGSIFWRNSYEHENMESIQCE
SEQ ID NO:74	sviak	Ce61-4sv.pep	20	QVXSPQSQYGSXYWRNSYEHENMERLQCE
SEQ ID NO:75	sviak	PMsv-4.pep	2*	QVLSPQSQYGSIYWRNSYENENM*
SEQ ID NO:76	sviak	LGAsv-E.pep	2	QVLSPQSQYGSIYWRNSYENENMERLQCE
SEQ ID NO:77	sviak	RTsv-1.pep	2	QVLSPQSQYGSIYWRNSYENENMERLQCE
SEQ ID NO:78	sviak	GPd58-2sv.pep	2	QVLSPQSQYGSIYWRNSYENENMERLQCE
SEQ ID NO:79	sviak	LGAsv-A.pep	2	QVLSPQSQYGSIYWRNSYENENMERLQCE
SEQ ID NO:80	sviak	LGAsv-D.pep	2	QVLSPQSQYGSIYWRNSYENENMERLQCE
SEQ ID NO:81	sviak	PPsv-5.pep	2	QVLSPQSQYGSIYWRNSYENENMERLQCE
SEQ ID NO:82	sviak	RTsv-2.pep	2	QVLSPQSQYGSIYWRNSYENENMERLQCE
SEQ ID NO:83	sviak	RTsv-3.pep	2	QVLSPQSQYGSIYWRNSYENENMERLQCE
SEQ ID NO:84	sviak	Aasv-P.pep	2	QVLSPQSQYGSIYWRNSYENENMERLQCE
SEQ ID NO:85	sviak	PMsv-5.pep	2	QVLSPQSQYGSIYWRNSYENENMERLQCE
SEQ ID NO:86	sviak	PM1Csv-rep.pep	2	QVLSPQSQYGSIYWRNSYENENMERLQCE
SEQ ID NO:87	sviak	Aasv-1.pep	15	QVLSPQSQYGSIYWRNSYENGNMERLQCE
SEQ ID NO:88	sviak	PM1Asv-rep.pep	15	QVLSPQSQYGSIYWRNSYENGNMERLQCE
SEQ ID NO:89	sviak	PPsv-6.pep	10	QVLSPQSQYGSIYWRNSYENENMERLQCG
SEQ ID NO:90	sviak	Misv-A.pep	14	QVLSPQSQYGSIYWRNSYENENMERLQRE
SEQ ID NO:91	sviak	Aasv-3.pep	14	QVLSPQSQYGSIYWRNSYENENMERLQRE
SEQ ID NO:92	sviak	Acasv-C.pep	14	QVLSPQSQYGSIYWRNSYENENMERLQRE
SEQ ID NO:93	sviak	Ce61-3sv.pep	14	QVLSPQSQYGSIYWRNSYENENMERLQRE
SEQ ID NO:94	sviak	Misv-B.pep	14	QVLSPQSQYGSIYWRNSYENENMERLQRE
SEQ ID NO:95	sviak	Misv-F.pep	14	QVLSPQSQYGSIYWRNSYENENMERLQRE
SEQ ID NO:96	sviak	Pavsv-C.pep	17	QVLSPQSQYGSVYWRNSYENENMERLQRE
SEQ ID NO:97	sviak	Pavsv-A.pep	7	QVLSPQSQYGSVYWRNSYVNENMERLQCE

Figure 9

SEQ ID NO	variable amino acids across sequence				
SEQ ID NO:64	VIAKMKVYMSGVNFEVE	GKKYQVKTKWLSPQCQYGNIEVDKC	FWERMNEDTSNDSINTYHNMQQE	HSEFGGMLINMLLEGGLGTKKPVKYVDRKL	DTIEQCEISIARK
SEQ ID NO:65	VIAKMKVYMSGVNFEVE	GKKYQVKTKWLSPQCQYGNIEVDKC	FWERMNEDTSNDSINTYHNMQQE	HSEFGGMLINMLLEGGLGTKKPVKYVDRKL	DTIEQCEISIARK
SEQ ID NO:66	VIAKMKVYMSGVNFEVE	GKKYQVKTKWLSPQCQYGNIEVDKC	FWERMNEDTSNDSINTYHNMQQE	HSEFGGMLINMLLEGGLGTKKPVKYVDRKL	DTIEQCETSIARK
SEQ ID NO:67	VIAKMKVYMSGVNFEVE	GKKYQVKTKWLSPRCQYGNIEVDKC	FWERMNEDTSNDSINTYHNMQRE	HSEFGGMLINMLLEGGLGTKKPVKYVDRKL	DTIEQCEISIARK
SEQ ID NO:68	VIAKMKVYMSGVNFEVE	GKKYQVKTKWLSPRCQYGNIEVDKC	FWERMNEDTSNDSINTYHNMQRE	HSEFGGMLINMLLEGGLGTKKPVKYVDRKL	DTIEQCEISIARK
SEQ ID NO:69	VIAKMKVYMSGVNFEVE	GKKYQVKTKWLSPQCQYGSIEIDKQ	FWERMNEDTSNDSINTYHNMQQE	HSEFGGMLINMPLEGGLETKKPVKYVDRKL	DTTEQCEISIARK
SEQ ID NO:70	VIAKMKVYMSGVNFEVE	GKKYQVKTKWLSPQCQYGSIEIDKQ	FWERMNEDTSNDSINTYHDMQQE	HSEFGGMLINMLLEGGLETKKPVKYVDRKL	DTTEQCEISIARK
SEQ ID NO:71	VIAKMKVYMSGVNFEVE	GKKYQVKTKWLSPQCQYGSIEIDKQ	FWERMNEDTSNDSINTYHNMQQE	HSEFGGMLINMPLEGGLETKKPVKYVDRKL	DTTEQCEISIARK
SEQ ID NO:72	VIAKMXXYXSGVXFEVE	GKKYQVKTKWLSPQCQYGSIEIDKQ	FWERMNEDTSNDSINTYHNMQQE	HSEFGGMLINMLLEGGLETKKPVKYVDRKL	DTTEQCEISIARK
SEQ ID NO:73	VIAKMKVYMSGVNFEVE	GKKYQVKTKWLSPQCQYGSIEIDKQ	FWERMNEDTSNDSINTYHNMQQE	HSEFGGMLINMLLEGGLETKKPVKYVYSTI	HTTEQCEISXXRK
SEQ ID NO:74	VIAKMKVYMSGVNFEVE	GKKYQVKTXWXSPQSQYGSXEIDKC	YWERMNEDTSNDSINIYHNMQQE	HSEFDGMLINMLXEGGLESKKPVMYVDRKL	DTTEQCEISIARK
SEQ ID NO:75	VIAKMKVYMSGVNFXVE	GKKYQVKTKWLSPQSQYGSIEIDKQ	YWERVNEDTSNDSINIYNNMQQE	NTEYDGMLINMLLEGG?-	
SEQ ID NO:76	VIAKMKVYMSGVNFEVE	GKKYQVKTEWLSPQSQYGSIEIDKQ	YWERMNEDTSNDSINIYNNMQQE	NTEFDGMLINMLLEGGLESKKPVMYVDRKL	DTTEQCEISIARK
SEQ ID NO:77	VIAKMKVYMSGVNFEAE	GKKYQVKTKWLSPQSQYGSIEIDKQ	YWERMNEDTSNDSINIYNNMQQE	NTEFDGMLINMLLEGGLESKKPVMYVDRKL	DTTEQCEIPIARK
SEQ ID NO:78	VIAKMKVYMSGVNFEVE	GKKYQVKTKWLSPQSQYGSIEIDKQ	YWERMNEDTSNDSINIYNNMQQE	NTEFDGMLINMLLEGGLESKKPVMYVDRKL	DTTEQCEISIARK
SEQ ID NO:79	VIAKMKVYMSGVNFEVE	GKKYQVKTKWLSPQSQYGSIEIDKQ	YWERMNEDTSNDSINIYNNMQQE	NTEFDGMLINMLLEGGLESKKPVMYVDRKL	DTTEQCEISIARK
SEQ ID NO:80	VIAKMKVYMSGVNFEVE	GKKYQVKTKWLSPQSQYGSIEIDKQ	YWERMNEDTSNDSINIYNNMQQE	NTEFDGMLINMLLEGGLESKKPVMYVDRKL	DTTEQCEISIARK
SEQ ID NO:81	VIAKMKVYMSGVNFEVE	GKKYQVKTKWLSPQSQYGSIEIDKQ	YWERMNEDTSNDSINIYNNMQQE	NTEFDGMLINMLLEGGLESKKPVMYVDRKL	DTTEQCEISIARK
SEQ ID NO:82	VIAKMKVYMSGVNFEVE	GKKYQVKTKWLSPQSQYGSIEIDKQ	YWERMNEDTSNDSINIYNNMQQE	NTEFDGMLINMLLEGGLESKKPVMYVDRKL	DTTEQCEISIARK
SEQ ID NO:83	VIAKMKVYMSGVNFEVE	GKKYQVKTKWLSPQSQYGSIEIDKQ	YWERMNEDTSNDSINIYNNMQQE	NTEFDGMLINMLLEGGLESKKPVMYVDRKL	DTTEQCEISIARK
SEQ ID NO:84	VIAKMKVYMSGVNFEVE	GKKYQVRTKWLSPQSQYGSIEIDKQ	YWERMNEDTSNDSINIYHNMQQE	NTEFDGMLINMLLEGGLESKKPVRYVDRKL	DTTEQCEISIARK
SEQ ID NO:85	VIAKMKVYMSGVNFEVQ	GKKYQVKTKWLSPQSQYGSIEIDKQ	YWERMNKDTSNDSINIYNNMQQE	NTEFDGVLINMLLEGGLESKKPVMYVDRKL	DTTEQCEISIARK*RFFRVKSR
SEQ ID NO:86	VIAKMKVYMSGVNFEVE	GKRYQVKTKWLSPQSQYGSIEIDKQ	YWERMKEDTSNDSMNIYNNMQQE	NTEYDGMLINMLLEGSTESKKPVMYVDRKL	DTTEQCEISIARK
SEQ ID NO:87	VIAKMKVYMSDVNFEVE	GKKYQVKTKWLSPQSQYGSIEIDKQ	YWERMNEDTSNDSINIYNNMQQE	NTGFDGMLINMLLEGGLESKKPVMYVDRKL	DTTEQCEISIARK
SEQ ID NO:88	VIAKMKVYMSDVNFEVE	GKKYQVKTKWLSPQSQYGSIEIDKQ	YWERMNEDTSNDSINIYNNMQQE	NTGFDGMLINMLLEGGLESKKPVMYVDRKL	DTTEQCEISIARK
SEQ ID NO:89	VIAKMKVYMSGVNFEVE	GKKYQVKTKWLSPQSQYGSIEIDKQ	YWERMNEDTSNDSISIYNNMQQE	NTEFDGMLINMLLEGGLESKKPVMYVDRKL	DTTEQCGISIARK
SEQ ID NO:90	VIAKMKVYMSGVNFEVE	GKKYQVKTKWLSPQSQYGSIEIDKQ	YWERMNEDTSNDSINIYHNMQQE	NTEFDGMLINMLLEGGLESKRPVKYVDRKL	DTTEQREISIARK
SEQ ID NO:91	VIAKMKVYMSGVNFEVE	GKKYQVRTKWLSPQSQYGSIEIDKQ	YWERMNEDTSNDSINIYHNMQQE	NTELDGMLINMLLEGGLESKRPVKYVDRKL	DTTEQREISIARK
SEQ ID NO:92	VIAKMKVYMSGVNFEVE	GKKYQVRTKWLSPQSQYGSIEIDKQ	YWERMNEDTSNDSINIYHNMQQE	NTESDGMLINMLLEGGLESKRPVKCVDRKL	DTTEQREISIARK
SEQ ID NO:93	VIAKMKVYMSGVNFEVE	GKKYQVRTKWLSPQSQYGSIEIDKQ	YWERMNEDTSNDSINIYHNMQQE	NTESDGMLINMLLEGGLESKRPVKYVDRKL	DTTEQREISIARK
SEQ ID NO:94	VIAKMKVYMSGVNFEVE	GKKYQVRTKWLSPQSQYGSIEIDKQ	YWERMNEDTSNDSINIYHNMQQE	NTEFDGMLINMLLEGGLESKRPVKYVDRKL	DTTEQREISIARK
SEQ ID NO:95	VIAKMKVYMSGVNFEVE	GKKYQVRTKWLSPQSQYGSIEIDKQ	YWERMNEDTSNDSINIYHNMQQE	NTEFDGMLINMLLEGGLESKRPVKYVDRKL	DTTEQREISIARK
SEQ ID NO:96	VIAKMKVYMSGVNFEVE	GKKYQVKTEWLSPQSQYGSVEIDKC	YWERMNEDTSNDSINIYHNMQQE	NTESDGMLINMLLEGGLESKRPVKYVDRKL	DTTEQREISIARK
SEQ ID NO:97	VIAKMKVYMSGVNFEVE	GKKYQVKTEWLSPQSQYGSVEIDKC	YWERMNEDTSNDSINIYNNMQQV	NTEFDGMLINMLLEGGLESKKPVMYVDRKL	DTTEQCEISIARK

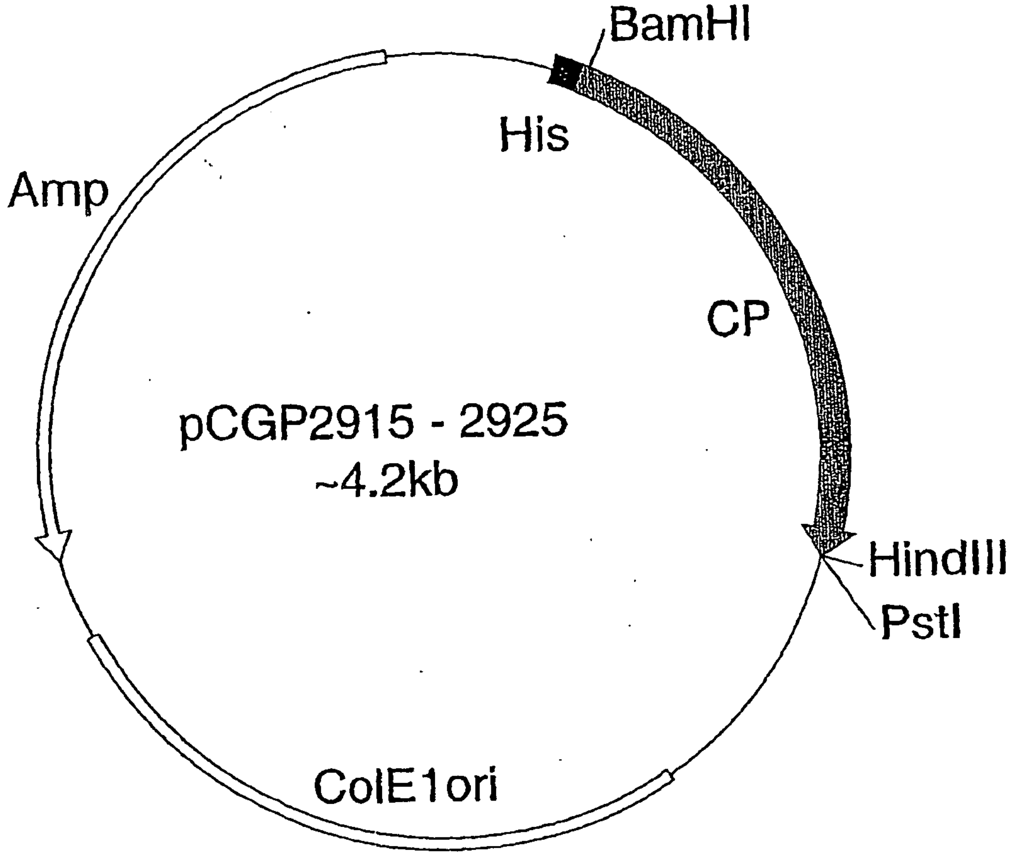
Figure 9 continued

SEQ ID NO	N-terminus	name	type	"QYG" fluorophore and 26 aa within 5A
SEQ ID NO:92	sgiat	Aams-5.pep	1	QVLSPQCQYGSIFWRNSYEHENMERLQCE
SEQ ID NO:93	sviat	PPms-G.pep	13	QVLSPQCQYGNIFWGNSYEHENMGRLQCE
SEQ ID NO:94	sviat	Cems-G.pep	5	QVLSPQCQYGNIFWRNSYEHENMGRLQCE
SEQ ID NO:95	sviat	Cems-H.pep	5	QVLSPQCQYGNIFWRNSYEHENMGRLQCE
SEQ ID NO:96	sviat	PPms-E.pep	5	QVLSPQCQYGNIFWRNSYEHENMGRLQCE
SEQ ID NO:97	sviat	Cems-F.pep	5	QVLSPQCQYGNIFWRNSYEHENMGRLQCE
SEQ ID NO:98	sviat	PPms-1.pep	8	RVLSPQCQYGNIFWRNSYEHENMGRLQCE
SEQ ID NO:99	sviat	Cems-I.pep	16*	QVLSPQCQYGNIFWRNSYEHENMERLQCE
SEQ ID NO:100	sviat	MI68Dms.pep	1	QVLSPQCQYGSIFWRNSYEHENMERLQCE
SEQ ID NO:101	sviat	MIms-A.pep	1	QVLSPQCQYGSIFWRNSYEHENMERLQCE
SEQ ID NO:102	sviat	Mims-B.pep	1	QVLSPQCQYGSIFWRNSYEHENMERLQCE
SEQ ID NO:103	sviat	Mims-C.pep	1	QVLSPQCQYGSIFWRNSYEHENMERLQCE
SEQ ID NO:104	sviat	RTms-5.pep	1	QVLSPQCQYGSIFWRNSYEHENMERLQCE
SEQ ID NO:105	sviat	Aams-2.pep	1	QVLSPQCQYGSIFWRNSYEHENMERLQCE
SEQ ID NO:106	sviat	Aams-4.pep	1	QVLSPQCQYGSIFWRNSYEHENMERLQCE
SEQ ID NO:107	sviat	Aams-6.pep	1	QVLSPQCQYGSIFWRNSYEHENMERLQCE
SEQ ID NO:108	sviat	PPd57-2ms.pep	1	QVLSPQCQYGSIFWRNSYEHENMERLQCE
SEQ ID NO:109	sviat	PPd57-3.pep	1	QVLSPQCQYGSIFWRNSYEHENMERLQCE
SEQ ID NO:110	sviat	PMms-A.pep	2	QVLSPQSQYGSIYWRNSYENENMERLQCE
SEQ ID NO:111	sviat	PMms-B.pep	2	QVLSPQSQYGSIYWRNSYENENMERLQCE
SEQ ID NO:112	sviat	PMms-E.pep	2	QVLSPQSQYGSIYWRNSYENENMERLQCE
SEQ ID NO:113	sviat	PPd57-4ms.pep	2	QVLSPQSQYGSIYWRNSYENENMERLQCE
SEQ ID NO:114	sviat	PMms-D.pep	2	QVLSPQSQYGSIYWRNSYENENMERLQCE
SEQ ID NO:115	sviat	PPd57-1ms.pep	12	QVLSPQTQYGSIYWRNSYENENMERLQCE
SEQ ID NO:116	sviat	PMms-C.pep	9	QVLSPQTQYGSIYWRNSYENGNMERLQCE
SEQ ID NO:117	sviat	LGAms-6.pep	18*	QVLSPQYQYGSIFWRNSYENENMERLQCE
SEQ ID NO:118	sviat	PPms-2.pep	19*	QVLSPQYQYGSIFWRNSYENENMERLRCE
SEQ ID NO:119	sviat	Pavms-4.pep	11	QVLSPQYQYGSIYWGNSYENENMERLQCE
SEQ ID NO:120	sviat	Acams-4.pep	3	QVLSPQYQYGSIYWRNSHENENMERLQCE
SEQ ID NO:121	sviat	Acams-2.pep	6*	QVLSPQYQYGSIYWRNSYENENMERLQCE
SEQ ID NO:122	sviat	Pavms-2.pep	6*	QVLSPQYQYGSIYWRNSYENENMERLQCE
SEQ ID NO:123	sviat	Pav5ms.pep	6	QVLSPQYQYGSIYWRNSYENENMERLQCE
SEQ ID NO:124	sviat	LGAms-5.pep	6	QVLSPQYQYGSIYWRNSYENENMERLQCE
SEQ ID NO:125	sviat	RTms-1.pep	6	QVLSPQYQYGSIYWRNSYENENMERLQCE
SEQ ID NO:126	sviat	Pavms-3.pep	6	QVLSPQYQYGSIYWRNSYENENMERLQCE
SEQ ID NO:127	sviat	Acams-3?.pep	6	QVLSPQYQYGSIYWRNSYENENMERLQCE
SEQ ID NO:128	sviat	Acams-5.pep		
SEQ ID NO:129	svivt	RTms-6.pep	6	QVLSPQYQYGSIYWRNSYENENMERLQCE
SEQ ID NO:130	svsat	RTms-2.pep	6	QVLSPQYQYGSIYWRNSYENENMERLQCE

Figure 9 continued

SEQ ID NO	variable amino acids across sequence
SEQ ID NO:92	GIATMKVYMSGVNFEVE GKKYQVRAKWLSPQCQYGSIEIDKQ FWERMNEDTSNDSINIYHNMQQE HSEFDGMLINMLLEGGLETKKPVKYVDRKL DITEQCEISIARK
SEQ ID NO:93	VIATMKVYMSGVNFEVE GKKYQVKTKWLSPQCQYGNIEVDK(FWEGMNEDTSNDSINTYHNMQQE HSEFGGMLINMLLEGGLGTKKPVKYVDRKL DTIEQCEISIARK
.SEQ ID NO:94	VIATMKVYMSGVNFEVE GKKYQVKTKWLSPQCQYGNIEVDK(FWERMNEDTSNDSINTYHNMQQE HSELGGMLINMLLEGGLGTKKPVKYVDRKL DTIEQCEISIARK
SEQ ID NO:95	VIATMKVYMSGVNFEVE GKKYQVKTKWLSPQCQYGNIEVDK(FWERMNEDTSNDSINTYHNMQQE HSEFGGMLINMLLEGGLGTKKLVKYVDRKL DTIEQCEISIARK
SEQ ID NO:96	VIATMKVYMSGVNFEVE GKKYQVKTKWLSPQCQYGNIEVDK(FWERMNEDTSNDSINTYHNMQQE HSEFGGMLINMLLEGGLGTKKPVKYVDRKL DTIEQCEISIARK
SEQ ID NO:97	VIATMKVYMSGVNFEVE GKKYQVKTKWLSPQCQYGNIEVDKF FWERMNEDTSNDSINTYHNMQQE HSEFGGMLINMLLEGGLGTKKPVKYVDRKL DTIEQCEISIARK
SEQ ID NO:98	VIATMKVYMSGVNFEVE GKKYRVKTKWLSPQCQYGNIEVDK(FWERMNEDTSNDSINTYHNMQQE HSEFGGMLINMLLEGGLGTKKPVKYVDRKL DTIEQCEISIARK
SEQ ID NO:99	VIATMKVYMSGVNFEVE GKKYQVKTKWLSPQCQYGNIEVDK(FWERMNEDTSNDSINTYHNM*QE HSEFGGMLINMLLEGGLETKKPVKYADRKL DTTEQCEISIARK
SEQ ID NO:100	VIATMKVYMSGVDFEVE GKKYQVKTKWLSPQCQYGSIEIDKQ FWERMNENTSNDSINTYHNMQQE HSEFGGMLINMLLEGGLETKKPVKYVDRKL DTTEQCEISIARK
SEQ ID NO:101	VIATMKVYMSGVDFEVE GKKYQVKTKWLSPQCQYGSIEIDKQ FWERMNEDTSNDSINTYHNMQQE HSEFGGMLINMLLEGGLETKKPVKYVDRKL DTTEQCEISIARK
SEQ ID NO:102	VIATMKVYMSGVDFEVE GKKYQVKTKWLSPQCQYGSIEIDKQ FWERMNEDTSNGSINTYHNMQQE HSEFGGMLINMLLGGGLETRKPVKYVDRKL DTTEQCEISIARK
SEQ ID NO:103	VIATMKVYMSGVDFEVE GKKYQVKTKWLSPQCQYGSIEIDKQ FWERMNEDTSNDSINTYHNMQQE HSEFGGMLINMLLEGGLETKKPVKYVDRKL DTTEQCEISIARK
SEQ ID NO:104	VIATMKVYMSGVNFEVE GKKYQVKTKWLSPQCQYGSIEIDKQ FWERMNEDTSNDSINTYHNMQQE HSEFGGMLINMLLEGGLETKKPVKYVDRKL DTTEQCEISIARK
SEQ ID NO:105	VIATMKVYMSGVNFEVE GKKYQVRAKWLSPQCQYGSIEIDKQ FWERMNEDTSNDSINIYHNMQQE HSEFDGMLINMLLEGGLETKKPVKYVDRKL DTTEQCEISITRK
SEQ ID NO:106	VIATMKVYMSGVNFEVE GKKYQVRAKWLSPQCQYGSIEIDKQ FWERMNEDTSNDSINIYHNMQQE HSEFDGMLINMLLEGGLETKKPVKYVDRKL DTTEQCEISITRK
SEQ ID NO:107	VIATMKVYMSGVNFEVE GKKYQVRAKWLSPQCQYGSIEIDKQ FWERMNEDTSNDSINIYHNMQQE HSEFDGMLINMLLEGGLETKKPVKYVDRKL DITEQCEISIARN
SEQ ID NO:108	VIATMKVYMSGVNFEVE GKKYQVRAKWLSPQCQYGSIEIDKQ FWERMNEDTSNDSINIYHNMQQE HSEFDGMLINMLLEGGLETKKPVKYVDRKL DTTEQCEISIARK
SEQ ID NO:109	VIATMKVYMSGVNFEVE GKKYQVRAKWLSPQCQYGSIEIDKQ FWERMNEDTSNDSINIYHNMQQE HSEFDGMLINMLLEGGLETKKPVKYVDRKL DTTEQCEISIARK
SEQ ID NO:110	VIATMKVYMPGVNFEVE GKKYQVKTKWLSPQSQYGSIEIDKQ YWERMNEDTSNDSINIYNNMQQE NTEYDGMLINMLLEGGLESKKPVMYVDRKL DTTEQCEISIARK
SEQ ID NO:111	VIATMKVYMSGVNFEVE GKKYQVKTKWLSPQSQYGSIEIDKQ YWERMNEDTSNDSINIYNNMQQE NTEFDGMLINMLLEGGLESKKPVMYVDRKL DTTEQCEISIARK
SEQ ID NO:112	VIATMKVYMSGVNFEVE GKKYQVKTKWLSPQSQYGSIEIDKQ YWERMNEDTSNDSINIYNNMQQE NTEFDGMLINMLLEGGLESKKPVMYVDRKL DTTEQCEISIARK
SEQ ID NO:113	VIATMKVYMSGVNFEVE GKKYQVKTKWLSPQSQYGSIEIDKQ YWERMNEDTSNDSINIYNNMQQE NTEFDGMLINMLLEGGLESKKPVMYVDRKL DTTEQCEISIARK
SEQ ID NO:114	VIATMKVYMSGVNFEVE GQKYQVKTKWLSPQSQYGSIEIDKQ YWERMNEDTSNDSINIYNNMQQE NTEFDGMLINMLSEGGLESKKPVMYVDRKL DTTEQCEISIARK
SEQ ID NO:115	VIATMKVYMSGVNFEVE GKKYQVKTKWLSPQTQYGSIEIDKQ YWERMKEDTSNDSMNIYNNMQQE NTEYDGMLINMLLEGGTESKKPVMYVDRKL DTTEQCEISIARK
SEQ ID NO:116	VIATMKVYMSGVNFEVQ GKKYQVKTKWLSPQTQYGSIDIDKQ YWERMKEDTTNDSMNIYNNMQQE NTGYDGMLINMLLEGGTESKKPVMYVDRKL DTTEQCEISIARK
SEQ ID NO:117	VIATMKVYMSGVNLEVE GKKYQVRTKWLSPQYQYGSIEIDK* FWDRMDEDTSNDSINIYHNMQQE NTEFDGMLLNMLLEGGLETKKPVKYVDRKL DTTEQCEISIARK
SEQ ID NO:118	VIATMKVYMSGVNFEVE GKKYQVRTKWLSPQYQYGSIEIDK* FWDRMNEDTSNDSINIYHNMQQE NTELDGMLLNMLLEGGLETKKPVKYVDRKL DTTERCEISIARK
SEQ ID NO:119	VIATMKVYMSGVNFEVE GKKYQVRTKWLSPQYQYGSIEIDKQ YWEGMNEDTSNDSINIYHNMQQE NTEFDGMLINMLLEGGLESKKTVKYVDRKL VTTEQCEISIARK
SEQ ID NO:120	VIATMKVYMSGANFEVE GKKYQVRTKWLSPQYQYGSIEIDKQ YWERMNEDTSNDSINIHHNMQQE NTEFDGMLINMLLEGGLESKKPVKYVDRKL DTTEQCEISIARK
SEQ ID NO:121	VIATMKVYMSGANFEVE GKKYQVRIK*LSPQYQYGSIEIDKQ YWERMNEDTSNDSINIYHNMQQE NTEFDGMLINMLLEGGLESKKPVKYVDRKL DTTEQCEISIARK
SEQ ID NO:122	VIATMKVYMSGVNFEVE GKKYQVRTKWLSPQYQYGSIEID*Q YWERMNEDTSNDSINIYHNMQQE NTEFDGLLINMLLEEGLESKKTAKYVDRKL DTTEQCEISIARK
SEQ ID NO:123	VIATMKVYMSGVNFEVE GKEYQVRTKWLSPQYQYGSIEIDKQ YWERMNEDTSNDSINIYHNTQQE NTEFDGMLINMLLEGGLESKKTVKYVDRKL DTTEQCEISIARK
SEQ ID NO:124	VIATMKVYMSGVNFEVE GKKYQVRTKWLSPQYQYGSIEIDKQ YWERMNEDTSNDSINIYHNMQQE NTELDGMLINMLLEGGLESKKPVKYVDRKL DTTEQCEISIARK
SEQ ID NO:125	VIATMKVYMSGVNFEVE GKKYQVRTKWLSPQYQYGSIEIDKQ YWERMNEDASNDSINIYHNMQQE NTEFDGMLINMLLEGGLESKKPVKYVDRKL DTTEQCEISIARK
SEQ ID NO:126	VIATVKVYMSGVNFEVE GKKYQVRTKWLSPQYQYGSIEIDKQ YWERMNEDTSNDSINIYHNMQQE NTEFDGMLINMLLEGGLESKKTVKYVDRKL DTTEQCEISIARK
SEQ ID NO:127	
SEQ ID NO:128	VIATMKVYMSGVNFEVE GKKTRSR*
SEQ ID NO:129	VIVTMKVYMSGVNFEVE GKKYQVRTKWLSPQYQYGSIEIDKQ YWERMNEDTSNDSINIYHNMQQE NTEFDGMLINMLLEGGLESKKPVKYVDRKL DTTEQCEISIARK
SEQ ID NO:130	VSATMKVYMSGVNFEVE GKKYQVRTKWLSPQYQYGSIEIDKQ YWERMNEDTSNDSINIYHNMQQE NTEFDGMLINMLLEGGLESKKPVKYVDRKL DTTGQCEISIAPK

Figure 9 continued



Replicon: pQE30 BamHI/PstI ~3.5kb vector

Insert: ~0.7kb BamHI/PstI PCR products generated using visproF1 and visproR1 primers and cDNA prepared from RNA isolated from various marine organisms

Figure 10

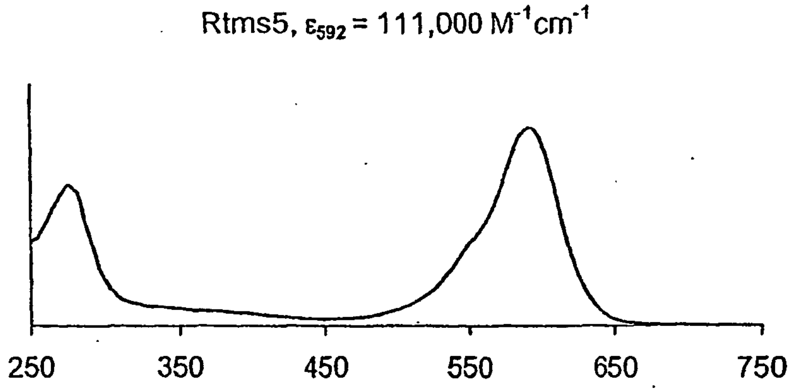


Figure 11(a)

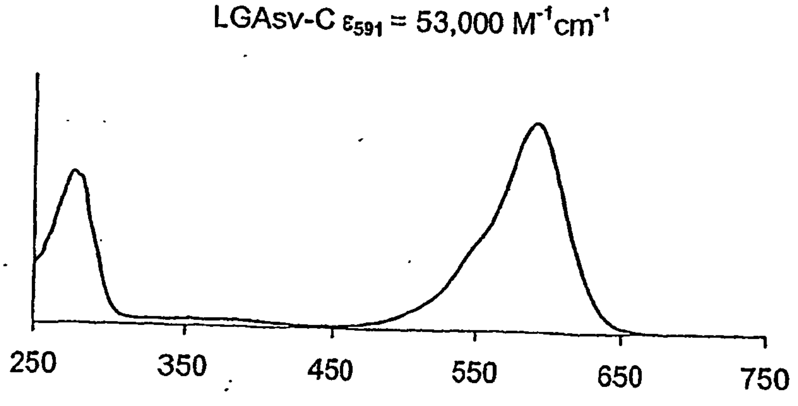


Figure 11(b)

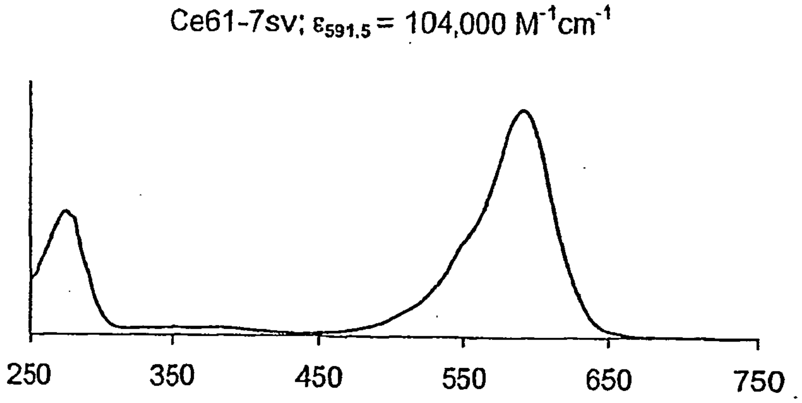


Figure 11(c)

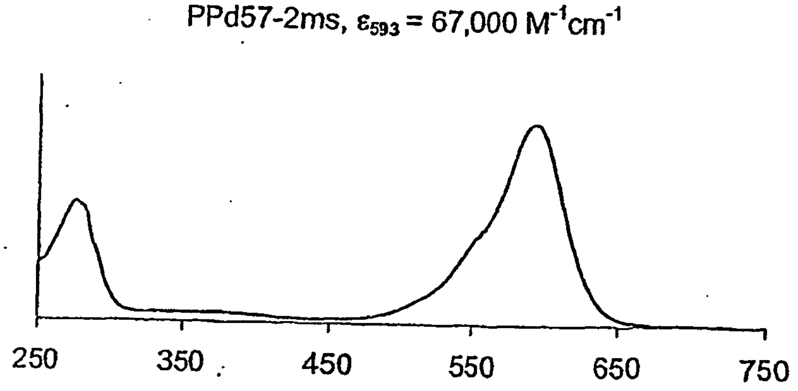


Figure 11(d)

MimsC, $\varepsilon_{589} = 48{,}000\ M^{-1}cm^{-1}$

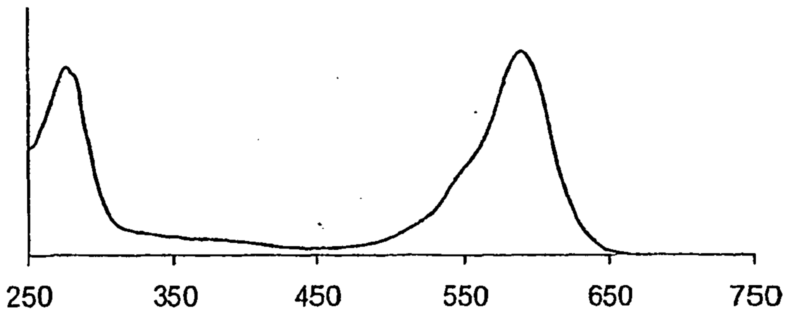
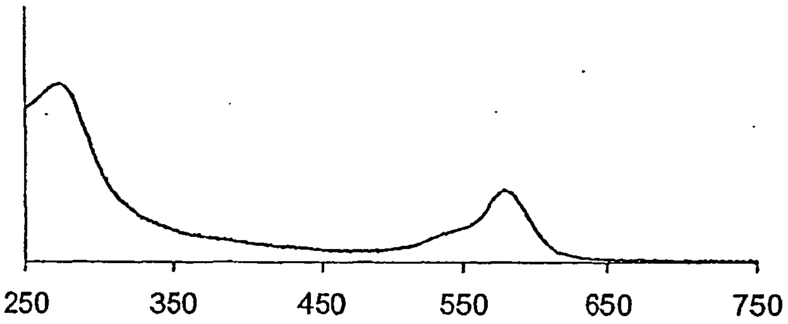


Figure 11(e)

PMms-B, $\varepsilon_{579.5}$ = 39,000 M^{-1}cm^{-1}



rtsv2 $\varepsilon_{579.5}$ = 75,000 M^{-1}cm^{-1}

Figure 12A(a)

LGAsv-D, ε_{579} = 72,400 M^{-1}cm^{-1}

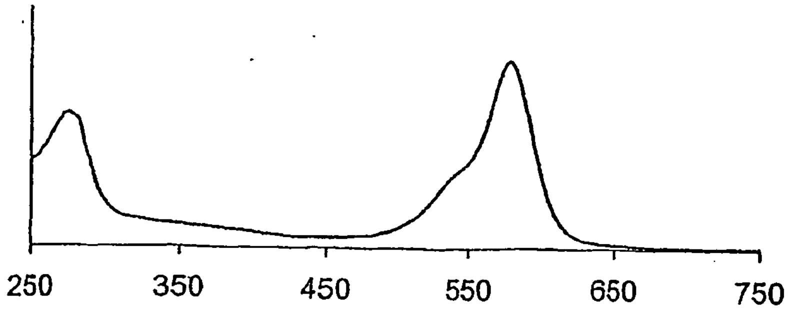


Figure 12A(b)

rtsv2 $\varepsilon_{579.5}$ = 75,000 $M^{-1}cm^{-1}$

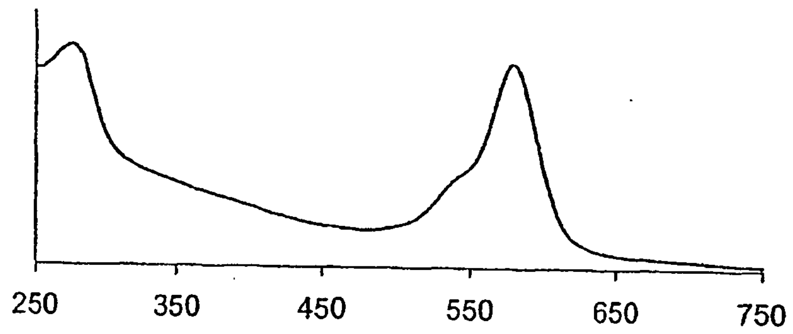


Figure 12A(c)

MisvF ε_{579} = 111,000 $M^{-1}cm^{-1}$

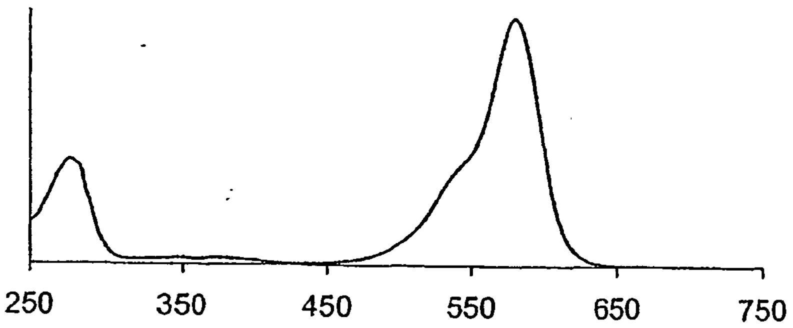


Figure 12B(d)

AcasvC $\varepsilon_{579.5}$ = 32,300 $M^{-1}cm^{-1}$

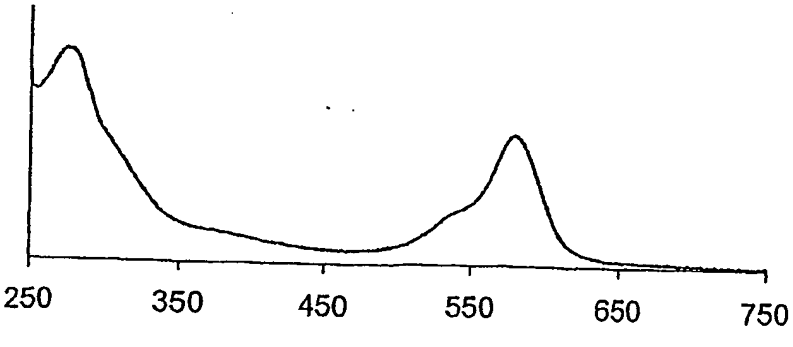


Figure 12B(e)

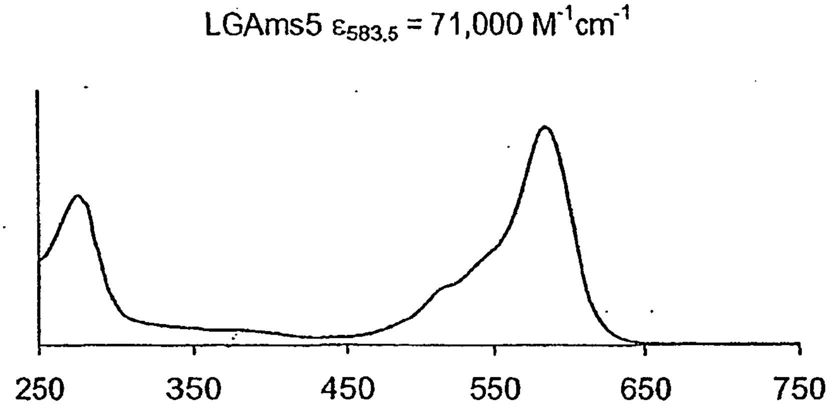


Figure 13(a)

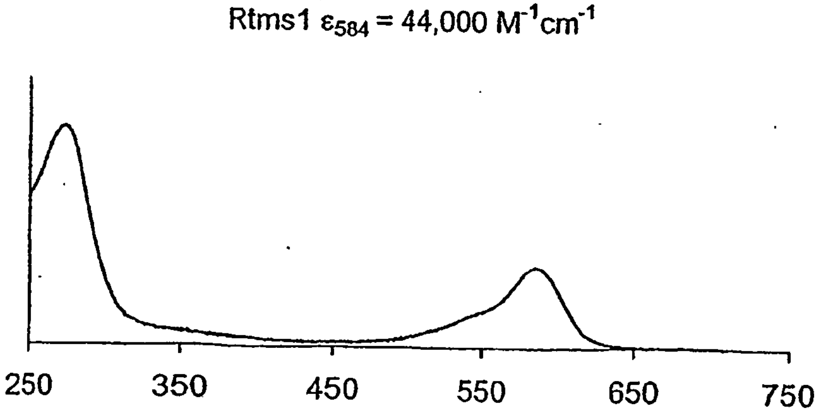


Figure 13(b)

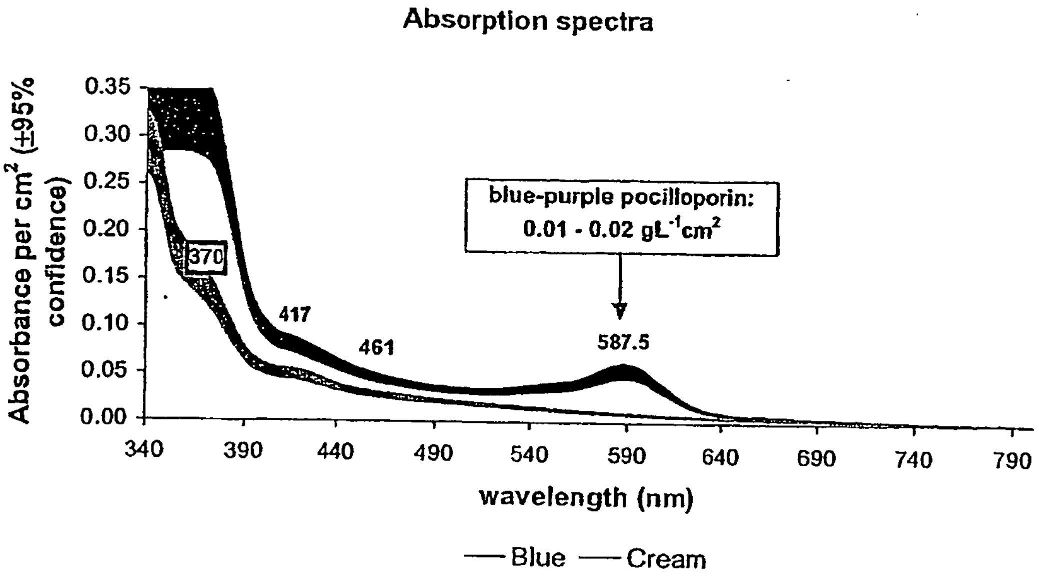


Figure 14(a)

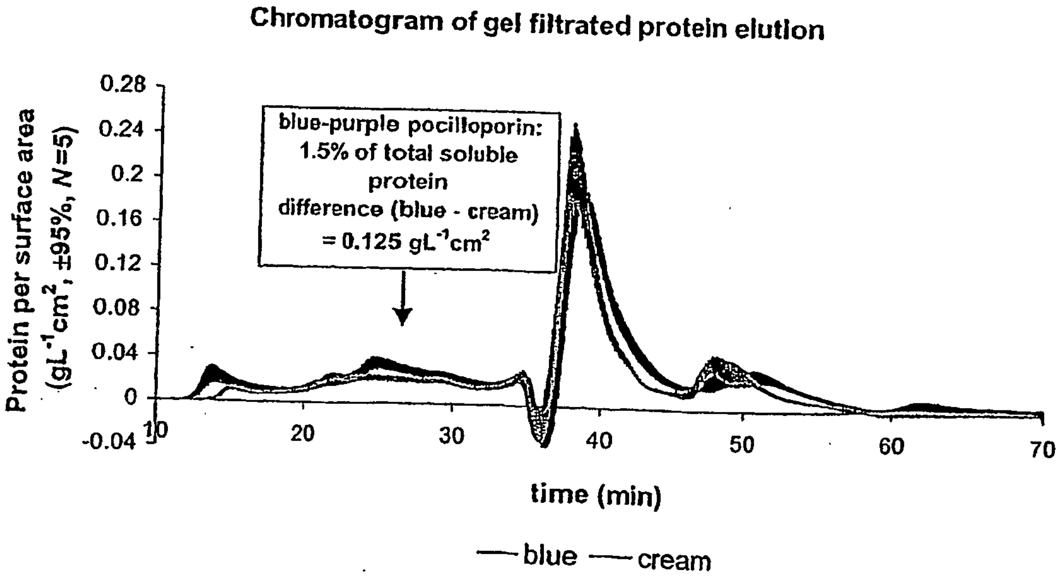


Figure 14(b)

```
T1-aa      1 GSVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPL  50
D1-aa      1 GSVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPL  50
S1-aa      1 GSVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPL  50
T3-aa      1 GSVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPL  50
D10-aa     1 GSVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLTVTKGGPL  50
S3-aa      1 GSVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPL  50
A8-aa      1 GSVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPL  50
             ****************************************.*.*******

T1-aa     51 PFAWDILSPQCQYGSIPFTKYPEDIPDYVKRSFPEGFTWERIMNFEDGAV 100
D1-aa     51 PFAWDILSPQCQYGSIPFTKYPEDIPDYVKQSFPEGFTWERIMNFEDGAV 100
S1-aa     51 PFAWDILSPQCQYGSIPFTKYLEDIPDYVKQSFPEGFTWERIMNFEDGAV 100
T3-aa     51 PFAWDILSPQSQYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAV 100
D10-aa    51 PFAWDILSPQSQYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAV 100
S3-aa     51 PFAWDILSPQSQYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAV 100
A8-aa     51 PFAWDILSPQSQYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAV 100
             **********.********** ********.*****.*************

T1-aa    101 CTVSNDSSIQGNCFIYHVKFSGLNFPPNGPVMQKKTQGWEPHSERLFARD 150
D1-aa    101 CPVSNDSSIQGNCFIYHVKFSGLNFPPNGPVMQKKTQGWEPHSERLFARD 150
S1-aa    101 CTVSNDSSIQGNCFIYHVKFSGLNFPPNGPVMQKKTQGWEPNTERLFARD 150
T3-aa    101 CTVSNDSSIQGNCFIYHVKFSGLNFPPNGPVMQKKTQGWEPNTERLFARD 150
D10-aa   101 CTVSNDSSIQGNCFIYHVKFSGLNFPPNGPVMQKKTQGWEPNTERLLARD 150
S3-aa    101 CTVSNDSSIQGNCFIYHVKFSGLNFPSNGPVMQKKTQGWEPNTERLFARD 150
A8-aa    101 CTVSNDSSIQGNCFIYHVKFSGLNFPPNGPVMQKKTQGWEPNTERLFARD 150
             * ************************ **************..*** ***

T1-aa    151 GMLIGNNFMALKLEGGGHYLCEFKTTYKAKKPVKMPGYHYVDRKLDVINH 200
D1-aa    151 GMLIGNTFMALKLEGGGHYLCEFKTTYKAKKPVKMPGYHYVDRKLDVINH 200
S1-aa    151 GMLIGNNFMALKLEGGGHYLCEFKSTYKAKKPVKMPGYHYVDRKLDVTNH 200
T3-aa    151 GMLIGNNFMALKLEGGGHYLCEFKSTYKAKKPVKMPGYHYVDRKLDVTNH 200
D10-aa   151 GMLIGNNFMALKLEGGGHYLCEFKSTYKARKPVKMPGYHYVDRKLDVTNH 200
S3-aa    151 GMLIGNNFMALKLEGGGHYLCEFKSTYKAKKPVKMPGYHYVDRKLDVTNH 200
A8-aa    151 GMLIGNNFMALKLEGGGHYLCEFKSTYKAKKPVKMPGYHYVDRKLDVTNH 200
             ******.****************.****.****************** **

T1-aa    201 NKDYTSVEQCEISIARKPVVALQ 223
D1-aa    201 NKDYTSVEQCEISIARKPVVALQ 223
S1-aa    201 NKDYTSVEQCEISIARKPLVALQ 223
T3-aa    201 NKDYTSVEQCEISIARKPVVALQ 223
D10-aa   201 NKDYTSVEQREISIARKPVVALQ 223
S3-aa    201 NKDYTSVEQCEISIARKPLVALQ 223
A8-aa    201 NKDYTSVEQCEISIARKPVVALQ 223
             ********* ********.****
```

Figure 15

```
[SEQIDNO:20]Aasv-1.p  1  -SVIAKQMTYKVYMSETVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQ 59
[SEQIDNO:22]Aasv-3.p  1  -SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLTVTKGGPLPFAWDILSPQ 59
[SEQIDNO:24]Aasv-P.p  1  -SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQ 59
[SEQIDNO:26]Acasv-A.  1  -SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPR 59
[SEQIDNO:28]Acasv-C.  1  -SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLTVTKGGPLPFAWDILSPQ 59
[SEQIDNO:30]Acasv-D.  1  -SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQ 59
[SEQIDNO:32]Ce61-3sv  1  -SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLTVTKGGPLPFAWDILSPQ 59
[SEQIDNO:34]Ce61-4sv  1  -SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTXGGPLPFAWDIXSPQ 59
[SEQIDNO:36]Ce61-5sv  1  -SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQ 59
[SEQIDNO:38]Ce61-7sv  1  -SVIAKQMTYXXYXSGTVXGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQ 59
[SEQIDNO:40]GPd58-2s  1  -SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQ 59
[SEQIDNO:42]LGAsv-A.  1  -SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQ 59
[SEQIDNO:44]LGAsv-C.  1  -SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQ 59
[SEQIDNO:46]LGAsv-D.  1  -SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQ 59
[SEQIDNO:48]LGAsv-E.  1  -SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTEGGPLPFAWDILSPQ 59
[SEQIDNO:50]Misv-A.p  1  -SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQ 59
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[SEQIDNO:54]Misv-F.p  1  -SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLTVTKGGPLPFAWDILSPQ 59
[SEQIDNO:56]PM1Asv-r  1  -SVIAKQMTYKVYMSETVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQ 59
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[SEQIDNO:60]PMsv-4.p  1  -SVIAKQMTYKVYMSGTVNGHYFXVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQ 59
[SEQIDNO:62]PMsv-5.p  1  -SVIAKQMTYKVYMSGTVNGHYFEVQGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQ 59
[SEQIDNO:64]PPsv-1.p  1  -SVIAKQMTYKVYMSGTVNGHYFEVEGDRKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQ 59
[SEQIDNO:66]PPsv-2.p  1  -SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQ 59
[SEQIDNO:68]PPsv-3.p  1  -SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQ 59
[SEQIDNO:70]PPsv-4.p  1  -SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPR 59
[SEQIDNO:72]PPsv-5.p  1  -SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQ 59
[SEQIDNO:74]PPsv-6.p  1  -SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQ 59
[SEQIDNO:76]Pavsv-A.  1  -SVIAKQMTYKVNMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTEGGPLPFAWDILSPQ 59
[SEQIDNO:78]Pavsv-B.  1  -SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQ 59
[SEQIDNO:80]Pavsv-C.  1  -SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTEGGPLPFAWDILSPQ 59
[SEQIDNO:82]RTsv-1.p  1  -SVIAKQMTYKVYMSGTVNGHYFEAEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQ 59
[SEQIDNO:84]RTsv-2.p  1  -SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQ 59
[SEQIDNO:86]RTsv-3.p  1  -SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQ 59
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[SEQIDNO:15]D-aa      1  GSVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQ 60
[SEQIDNO:17]S-aa      1  GSVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQ 60
[SEQIDNO:13]T-aa      1  GSVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQ 60
[SEQIDNO:9]D-aa       1  GSVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLTVTKGGPLPFAWDILSPQ 60
[SEQIDNO:11]S-aa      1  GSVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQ 60
[SEQIDNO:7]A-aa       1  GSVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQ 60
```

Figure 16

```
[SEQIDNO:20]Aasv-1.p    60   SQYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYNVKF  119
[SEQIDNO:22]Aasv-3.p    60   SQYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKF  119
[SEQIDNO:24]Aasv-P.p    60   SQYGSIPFTKYPEDIPDYVKQSFPEGYTWERIVNFEDGAVCTVSNDSSIQGNCFIYNVKF  119
[SEQIDNO:26]Acasv-A.    60   CQYGNIPFTKYPEDVPDYVKQSFPEGFTWERIMNFEDGAVCTVSNDSSIQGNCFTYHVKF  119
[SEQIDNO:28]Acasv-C.    60   SQYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKF  119
[SEQIDNO:30]Acasv-D.    60   CQYGSIPFTKYPEDIPDYVKQSFPEGFTWERIMNFEDGAVCTVSNDSSIQGNCFTYHVKF  119
[SEQIDNO:32]Ce61-3sv    60   SQYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKF  119
[SEQIDNO:34]Ce61-4sv    60   SQYGSKPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKF  119
[SEQIDNO:36]Ce61-5sv    60   CQYGSIPFTKYPEDIPDYVKQSFPEGFTWERIMNFEDGAVCTVSNDSSIQGNCFTYHVKF  119
[SEQIDNO:38]Ce61-7sv    60   CQYGSIPFTKYPEDIPDYVKQSFPEGFTWERIMNFEDGAVCTVSNDSSIQGNCFTYHVKF  119
[SEQIDNO:40]GPd58-2s    60   SQYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYNVKF  119
[SEQIDNO:42]LGAsv-A.    60   SQYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYNVKF  119
[SEQIDNO:44]LGAsv-C.    60   CQYGSIPFTKYPEDIPDYVKQSFPEGFTWERIMNFEDGAVCTVSNDSSIQGNCFTYHVKF  119
[SEQIDNO:46]LGAsv-D.    60   SQYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYNVKF  119
[SEQIDNO:48]LGAsv-E.    60   SQYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYNVKF  119
[SEQIDNO:50]Misv-A.p    60   SQYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKF  119
[SEQIDNO:52]Misv-B.p    60   SQYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKF  119
[SEQIDNO:54]Misv-F.p    60   SQYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKF  119
[SEQIDNO:56]PM1Asv-r    60   SQYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYNVKF  119
[SEQIDNO:58]PM1Csv-r    60   SQYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMKFEDGAVCTVSNDSSVQGNCFIYNVKF  119
[SEQIDNO:60]PMsv-4.p    60   SQYGSIPFTKYPEDIPDYVKQSFPEGYTWERIVNFEDGAVCTVSNDSSIQGNCFIYNVKF  119
[SEQIDNO:62]PMsv-5.p    60   SQYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFKDGAVCTVSNDSSIQGNCFIYNVKF  119
[SEQIDNO:64]PPsv-1.p    60   CQYGNIPFTKYPEDVPDYVKQSFPEGFTWERIMNFEDGAVCTVSNDSSIQGNCFTYHVKF  119
[SEQIDNO:66]PPsv-2.p    60   CQYGNIPFTKYPEDVPDYVKQSFPEGFTWERIMNFEDGAVCTVSNDSSIQGNCFTYHVKF  119
[SEQIDNO:68]PPsv-3.p    60   CQYGNIPFTKYPEDVPDYVKQSFPEGFTWERIMNFEDGAVCTVSNDSSIQGNCFTYHVKF  119
[SEQIDNO:70]PPsv-4.p    60   CQYGNIPFTKYPEDVPDYVKQSFPEGFTWERIMNFEDGAVCTVSNDSSIQGNCFTYHVKF  119
[SEQIDNO:72]PPsv-5.p    60   SQYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYNVKF  119
[SEQIDNO:74]PPsv-6.p    60   SQYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGSCFIYNVKF  119
[SEQIDNO:76]Pavsv-A.    60   SQYGSVPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYNVKF  119
[SEQIDNO:78]Pavsv-B.    60   CQYGSIPFTKYPEDIPDYVKQSFPEGFTWERIMNFEDGAVCTVSNDSSIQGNCFTYHVKF  119
[SEQIDNO:80]Pavsv-C.    60   SQYGSVPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKF  119
[SEQIDNO:82]RTsv-1.p    60   SQYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYNVKF  119
[SEQIDNO:84]RTsv-2.p    60   SQYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYNVKF  119
[SEQIDNO:86]RTsv-3.p    60   SQYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYNVKF  119
[SEQIDNO:19]T-aa        61   CQYGSIPFTKYPEDIPDYVKRSFPEGFTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKF  120
[SEQIDNO:15]D-aa        61   CQYGSIPFTKYPEDIPDYVKQSFPEGFTWERIMNFEDGAVCPVSNDSSIQGNCFIYHVKF  120
[SEQIDNO:17]S-aa        61   CQYGSIPFTKYLEDIPDYVKQSFPEGFTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKF  120
[SEQIDNO:13]T-aa        61   SQYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKF  120
[SEQIDNO:9]D-aa         61   SQYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKF  120
[SEQIDNO:11]S-aa        61   SQYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKF  120
[SEQIDNO:7]A-aa         61   SQYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKF  120
```

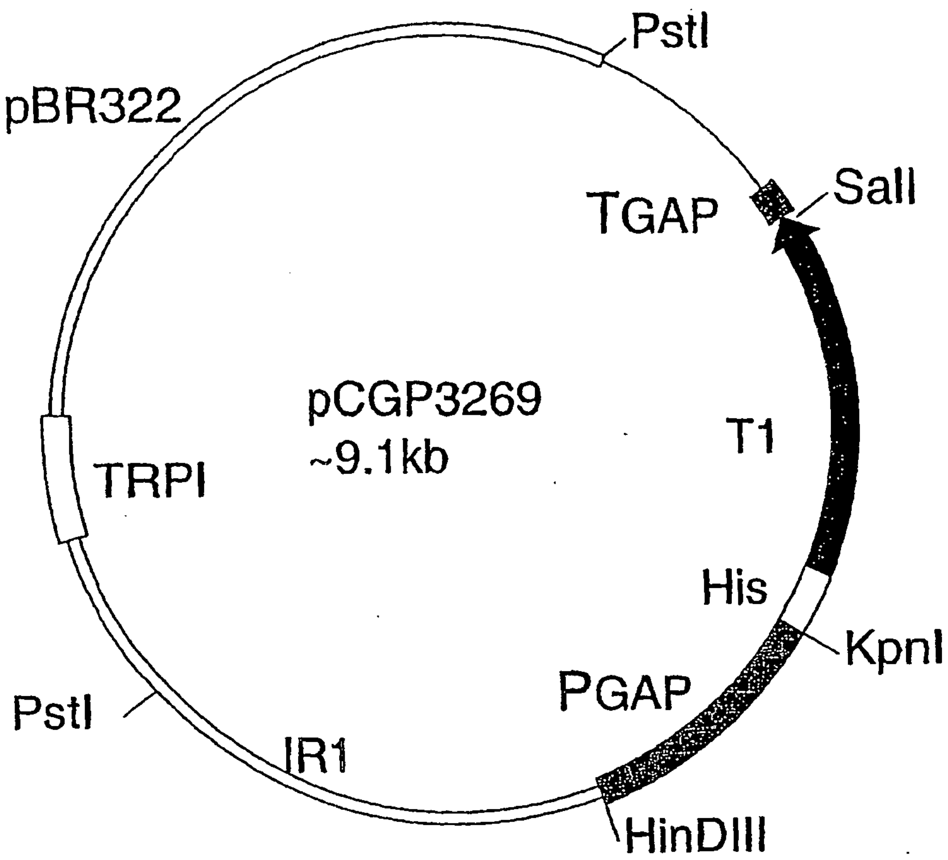
Figure 16 continued

```
[SEQIDNO:20]Aasv-1.p  120 SGLNFPPNGPVMQKKTQGWEPNTGRLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAK 179
[SEQIDNO:22]Aasv-3.p  120 SGLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAR 179
[SEQIDNO:24]Aasv-P.p  120 SGLNFPPNGPVMQKKTQGWEPNTERLYARDGMLIGNNFMALKLEGG-------------- 165
[SEQIDNO:26]Acasv-A.  120 SGLNFPPNGPVMQKKTRGWEPHSERLFARCGMLIGNNFMALKLEGGGHYLCGFKTTYKAK 179
[SEQIDNO:28]Acasv-C.  120 SGLNFPPNGPVMQKKTQGWEPNTERLSARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAR 179
[SEQIDNO:30]Acasv-D.  120 SGLNFPPNGPVMQKKTQGWEPHSERLFARCGMLIGNNFMAPKLEGGGHYLCEFKTTYKAK 179
[SEQIDNO:32]Ce61-3sv  120 SGLNFPPNGPVMQKKTQGWEPNTERLSARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAR 179
[SEQIDNO:34]Ce61-4sv  120 SGLNFPPNGPVMQKKTQGWEPHSERLFARDGMLIGNNFMALKXEGGGXYLCEFKSTYKAK 179
[SEQIDNO:36]Ce61-5sv  120 SGLNFPPNGPVMQKKTQGWEPHSERLFARCGMLIGNNFMALKLEGGGHYLCEFKTTYKAK 179
[SEQIDNO:38]Ce61-7sv  120 SGLNFPPNGPVMQKKTQGWEPHSERLFARCGMLIGNNFMALKLEGGGHYLCEFKTTYKAK 179
[SEQIDNO:40]GPd58-2s  120 SGLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAK 179
[SEQIDNO:42]LGAsv-A.  120 SGLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAK 179
[SEQIDNO:44]LGAsv-C.  120 SGLDFPPNGPVMQKKTQGWEPHSERLFARCGMLIGNNFMALKLEGGGHYLCEFKTTYKAK 179
[SEQIDNO:46]LGAsv-D.  120 SGLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAK 179
[SEQIDNO:48]LGAsv-E.  120 SGLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAK 179
[SEQIDNO:50]Misv-A.p  120 SGLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAR 179
[SEQIDNO:52]Misv-B.p  120 SGLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAR 179
[SEQIDNO:54]Misv-F.p  120 SGLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAR 179
[SEQIDNO:56]PM1Asv-r  120 SGLNFPPNGPVMQKKTQGWEPNTGRLFARDGMLIGNNFMALKLEGGGHYLCEFKTTYKAK 179
[SEQIDNO:58]PM1Csv-r  120 SGLNFPPNGPVMQKKTQGWEPNTERLYARDGMLIGNNFMALKLEGSGHYTCEFKSTYKAK 179
[SEQIDNO:60]PMsv-4.p  120 SGLNFPPNGPVMQKKTQGWEPNTERLYARDGMLIGNNFMALKLEGG-------------- 165
[SEQIDNO:62]PMsv-5.p  120 SGLNFPPNGPVMQKKTQGWEPNTERLFARDGVLIGNNFMALKLEGGGHYLCEFKSTYKAK 179
[SEQIDNO:64]PPsv-1.p  120 SGLNFPPNGPVMQKKTQGWEPHSERLFARCGMLIGNNFMALKLEGGGHYLCGFKTTYKAK 179
[SEQIDNO:66]PPsv-2.p  120 SGLNFPPNGPVMQKKTQGWEPHSERLFARCGMLIGNNFMALKLEGGGHYLCGFKTTYKAK 179
[SEQIDNO:68]PPsv-3.p  120 SGLNFPPNGPVMQKKTQGWEPHSERLFARCGMLIGNNFMALKLEGGGHYLCGFKTTYKAK 179
[SEQIDNO:70]PPsv-4.p  120 SGLNFPPNGPVMQKKTRGWEPHSERLFARCGMLIGNNFMALKLEGGGHYLCGFKTTYKAK 179
[SEQIDNO:72]PPsv-5.p  120 SGLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAK 179
[SEQIDNO:74]PPsv-6.p  120 SGLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAK 179
[SEQIDNO:76]Pavsv-A.  120 SGLNFPPNGPVMQKKTQGWVPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAK 179
[SEQIDNO:78]Pavsv-B.  120 SGLNFPPNGPVMQKKTQGWEPHSERLFARCGMLIGNNFMAPKLEGGGHYLCEFKTTYKAK 179
[SEQIDNO:80]Pavsv-C.  120 SGLNFPPNGPVMQKKTQGWEPNTERLSARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAR 179
[SEQIDNO:82]RTsv-1.p  120 SGLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAK 179
[SEQIDNO:84]RTsv-2.p  120 SGLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAK 179
[SEQIDNO:86]RTsv-3.p  120 SGLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAK 179
[SEQIDNO:19]T-aa      121 SGLNFPPNGPVMQKKTQGWEPHSERLFARDGMLIGNNFMALKLEGGGHYLCEFKTTYKAK 180
[SEQIDNO:15]D-aa      121 SGLNFPPNGPVMQKKTQGWEPHSERLFARDGMLIGNTFMALKLEGGGHYLCEFKTTYKAK 180
[SEQIDNO:17]S-aa      121 SGLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAK 180
[SEQIDNO:13]T-aa      121 SGLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAK 180
[SEQIDNO:9]D-aa       121 SGLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAR 180
[SEQIDNO:11]S-aa      121 SGLNFPSNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAK 180
[SEQIDNO:7]A-aa       121 SGLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAK 180
```

Figure 16 continued

```
[SEQIDNO:20]Aasv-1.p   180 KPVMMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA---------- 220
[SEQIDNO:22]Aasv-3.p   180 KPVKMPGYHYVDRKLDVTNHNKDYTSVEQREISIARKPVVA---------- 220
[SEQIDNO:24]Aasv-P.p   165 -----------QRSL------------------------------------ 169
[SEQIDNO:26]Acasv-A.   180 KPVKMPGYHYVDRKLDVTNHNKDYISVEQCEISIARKPVVA---------- 220
[SEQIDNO:28]Acasv-C.   180 KPVKMPGYHCVDRKLDVTNHNKDYTSVEQREISIARKPVVA---------- 220
[SEQIDNO:30]Acasv-D.   180 KPVKMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA---------- 220
[SEQIDNO:32]Ce61-3sv   180 KPVKMPGYHYVDRKLDVTNHNKDYTSVEQREISIARKPVVA---------- 220
[SEQIDNO:34]Ce61-4sv   180 KPVMMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA---------- 220
[SEQIDNO:36]Ce61-5sv   180 KPVKMPGYHYVYST[illegible]VTNHNKDYTSVEQCEISXXRKPVVA---------- 220
[SEQIDNO:38]Ce61-7sv   180 KPVKMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA---------- 220
[SEQIDNO:40]GPd58-2s   180 KPVMMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA---------- 220
[SEQIDNO:42]LGAsv-A.   180 KPVMMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA---------- 220
[SEQIDNO:44]LGAsv-C.   180 KPVKMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA---------- 220
[SEQIDNO:46]LGAsv-D.   180 KPVMMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA---------- 220
[SEQIDNO:48]LGAsv-E.   180 KPVMMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA---------- 220
[SEQIDNO:50]Misv-A.p   180 KPVKMPGYHYVDRKLDVTNHNKDYTSVEQREISIARKPVVA---------- 220
[SEQIDNO:52]Misv-B.p   180 KPVKMPGYHYVDRKLDVTNHNKDYTSVEQREISIARKPVVA---------- 220
[SEQIDNO:54]Misv-F.p   180 KPVKMPGYHYVDRKLDVTNHNKDYTSVEQREISIARKPVVA---------- 220
[SEQIDNO:56]PM1Asv-r   180 KPVMMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA---------- 220
[SEQIDNO:58]PM1Csv-r   180 KPVMMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA---------- 220
[SEQIDNO:60]PMsv-4.p   165 -----------QRSL------------------------------------ 169
[SEQIDNO:62]PMsv-5.p   180 KPVMMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVARFFRVKSRHK 230
[SEQIDNO:64]PPsv-1.p   180 KPVKMPGYHYVDRKLDVTNHNKDYISVEQCEISIARKPVVA---------- 220
[SEQIDNO:66]PPsv-2.p   180 KPVKMPGYHYVDRKLDVTNHNKDYISVEQCEISIARKPVVA---------- 220
[SEQIDNO:68]PPsv-3.p   180 KPVKMPGYHYVDRKLDVTNHNKDYISVEQCETSIARKPVVA---------- 220
[SEQIDNO:70]PPsv-4.p   180 KPVKMPGYHYVDRKLDVTNHNKDYISVEQCEISIARKPVVA---------- 220
[SEQIDNO:72]PPsv-5.p   180 KPVMMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA---------- 220
[SEQIDNO:74]PPsv-6.p   180 KPVMMPGYHYVDRKLDVTNHNKDYTSVEQCGISIARKPVVA---------- 220
[SEQIDNO:76]Pavsv-A.   180 KPVMMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA---------- 220
[SEQIDNO:78]Pavsv-B.   180 KPVKMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA---------- 220
[SEQIDNO:80]Pavsv-C.   180 KPVKMPGYHYVDRKLDVTNHNKDYTSVEQREISIARKPVVA---------- 220
[SEQIDNO:82]RTsv-1.p   180 KPVMMPGYHYVDRKLDVTNHNKDYTSVEQCEI[illegible]IARKPVVA---------- 220
[SEQIDNO:84]RTsv-2.p   180 KPVMMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA---------- 220
[SEQIDNO:86]RTsv-3.p   180 KPVMMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA---------- 220
[SEQIDNO:19]T-aa       181 KPVKMPGYHYVDRKLDVINHNKDYTSVEQCEISIARKPVVALQ-------- 223
[SEQIDNO:15]D-aa       181 KPVKMPGYHYVDRKLDVINHNKDYTSVEQCEISIARKPVVALQ-------- 223
[SEQIDNO:17]S-aa       181 KPVKMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKP[illegible]VALQ-------- 223
[SEQIDNO:13]T-aa       181 KPVKMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVALQ-------- 223
[SEQIDNO:9]D-aa        181 KPVKMPGYHYVDRKLDVTNHNKDYTSVEQREISIARKPVVALQ-------- 223
[SEQIDNO:11]S-aa       181 KPVKMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKP[illegible]VALQ-------- 223
[SEQIDNO:7]A-aa        181 KPVKMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVALQ-------- 223
```

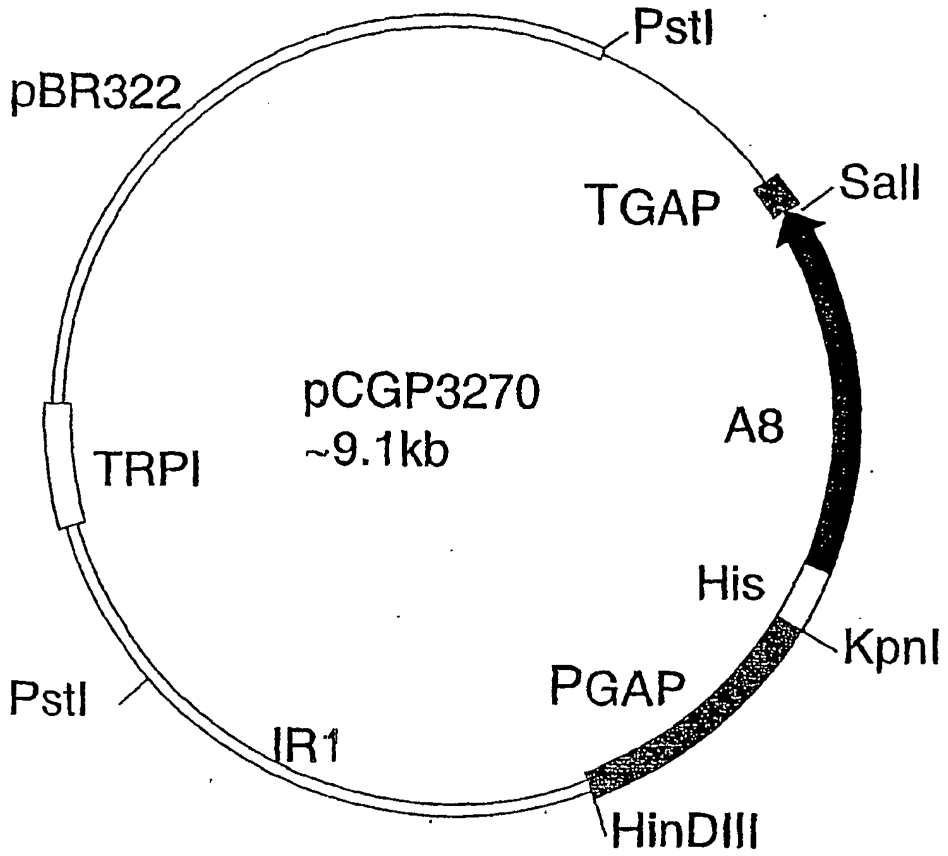
Figure 16 continued



Replicon: pYE22m KpnI/SalI

Insert: ~0.7kb KpnI/SalI PCR products generated using Kpn.6His.F and T1/A8.Sal.R primers and pCGP2921 as template

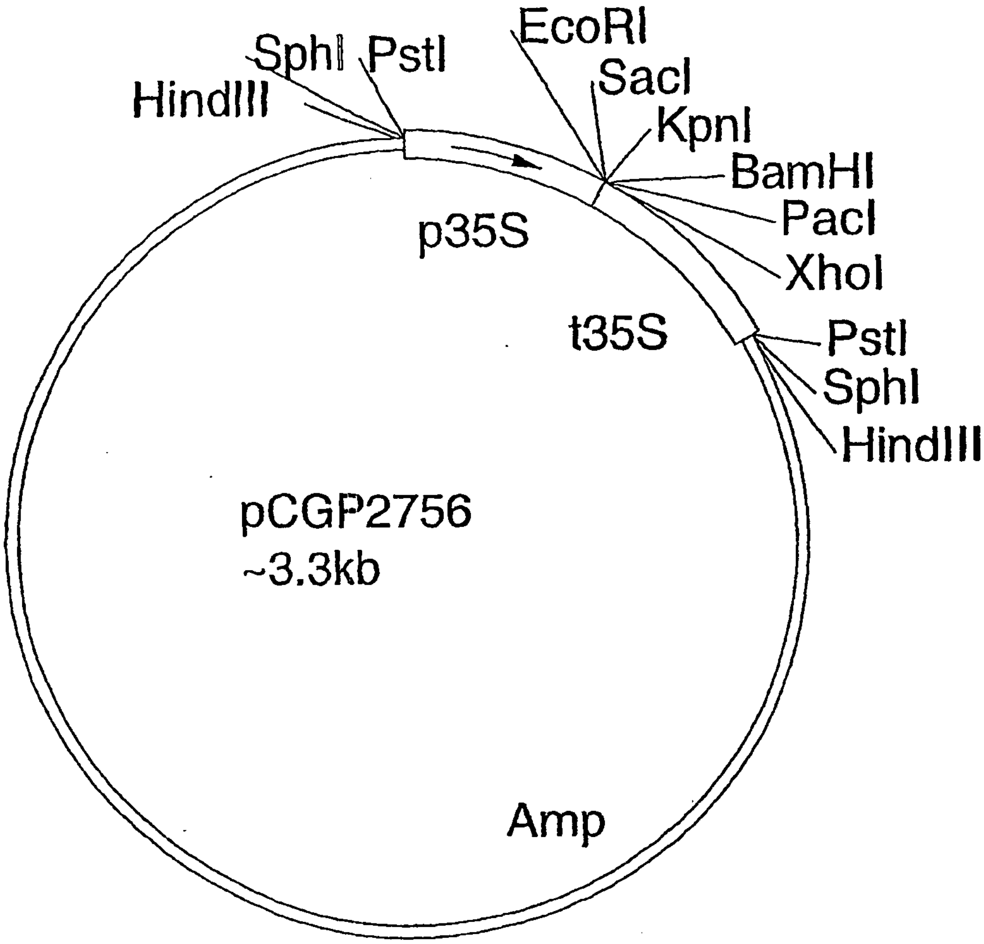
Figure 17



Replicon: pYE22m KpnI/SalI

Insert: ~0.7kb KpnI/SalI PCR products generated using Kpn.6His.F and T1/A8.Sal.R primers and pCGP2918 as template

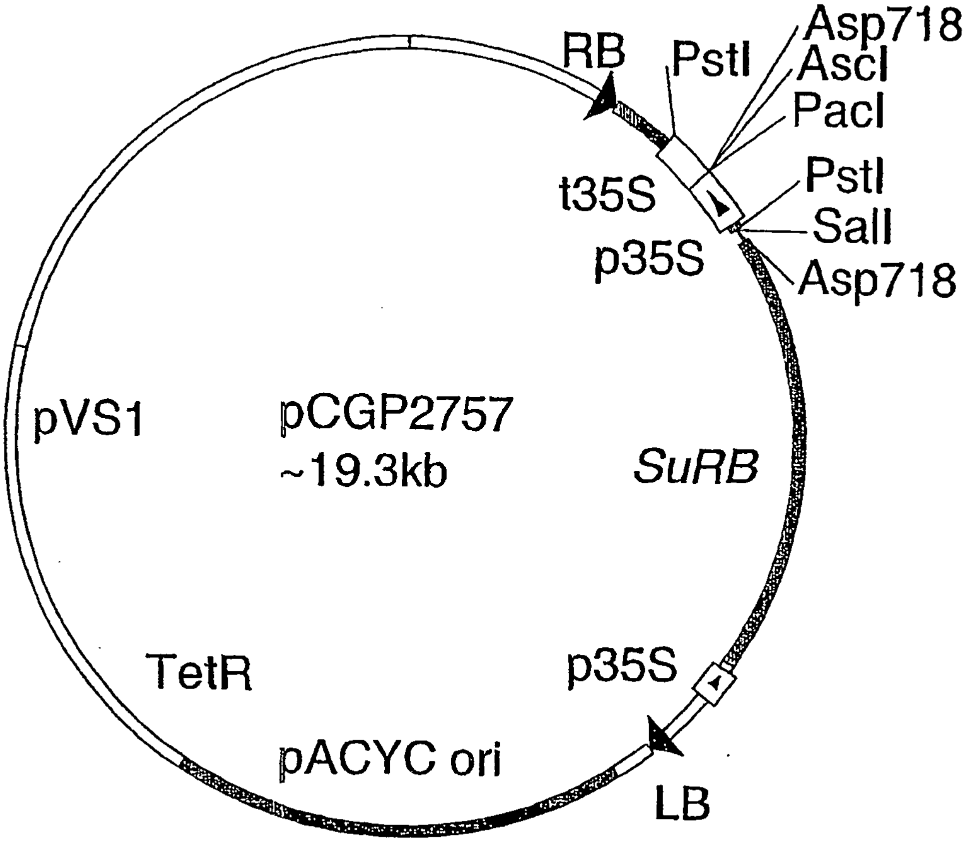
Figure 18



Replicon: pRTppoptc EcoRI/XbaI 3.3kb vector

Insert: ~40bp EcoRI/XbaI fragment containing multiple cloning site from pNEB193

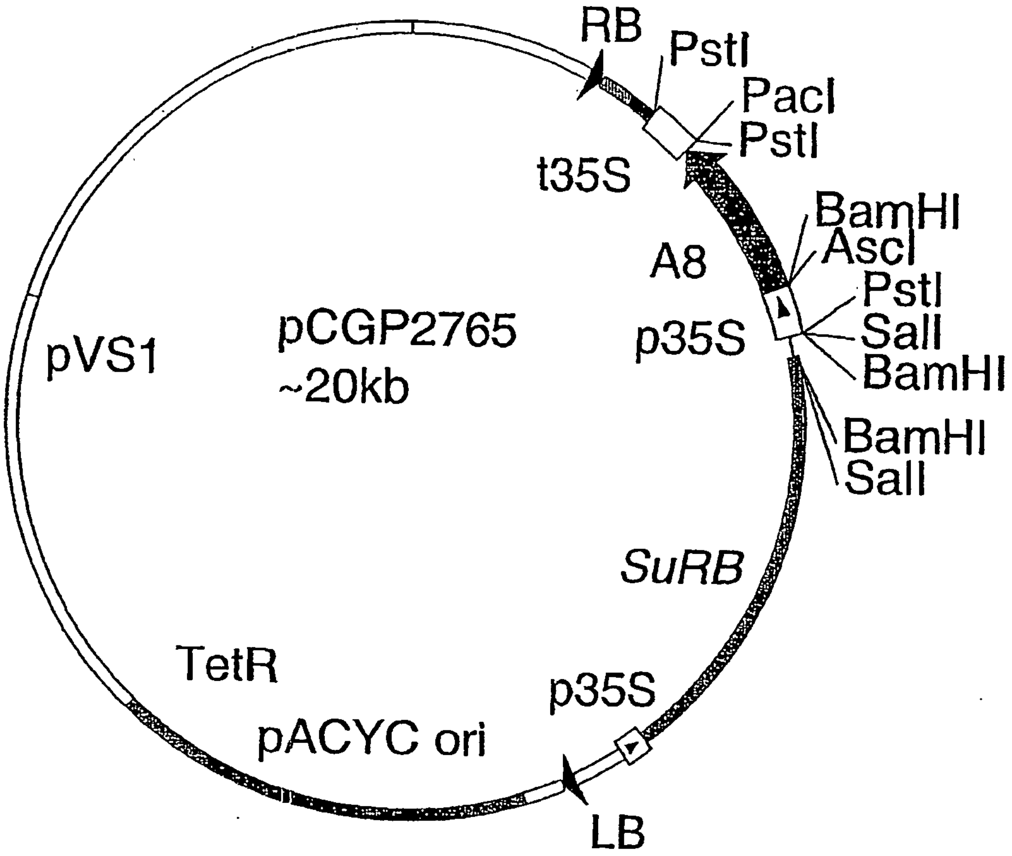
Figure 19



Replicon: pWTT2132 PstI ~18.6kb vector

Insert: ~0.7kb PstI fragment from pCGP2756

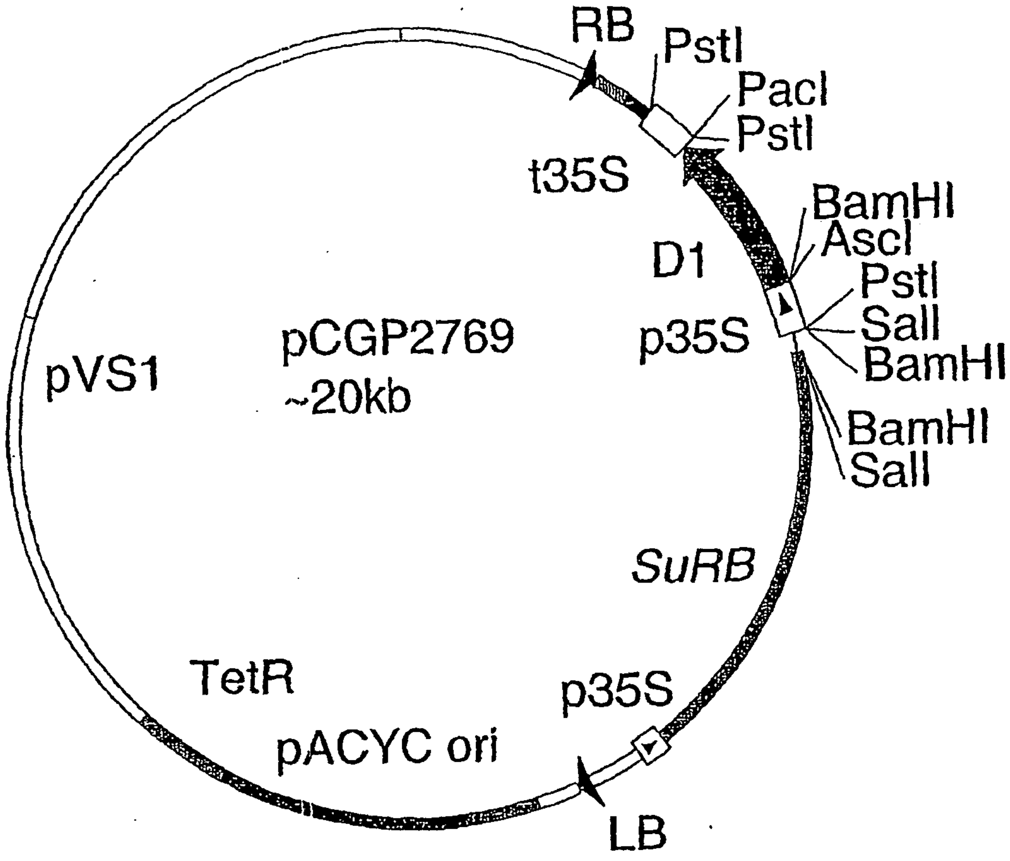
Figure 20



Replicon: pCGP2757 AscI/PacI ~19.3kb vector

Insert: ~0.7kb AscI/PacI A8 PCR product using visproF1 and visproR1 primers and pCGP2918 as template

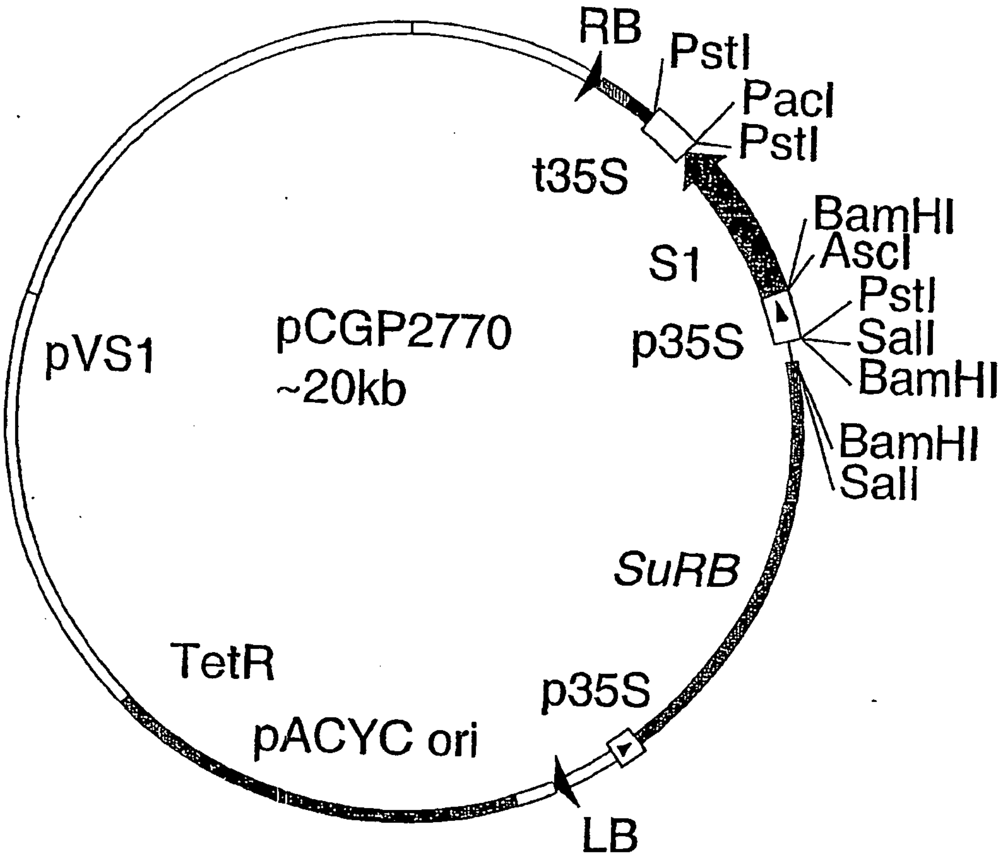
Figure 21



Replicon: pCGP2757 AscI/PacI ~19.3kb vector

Insert: ~0.7kb AscI/PacI D1 PCR product using visproF1 and visproR1 primers and pCGP2919 as template

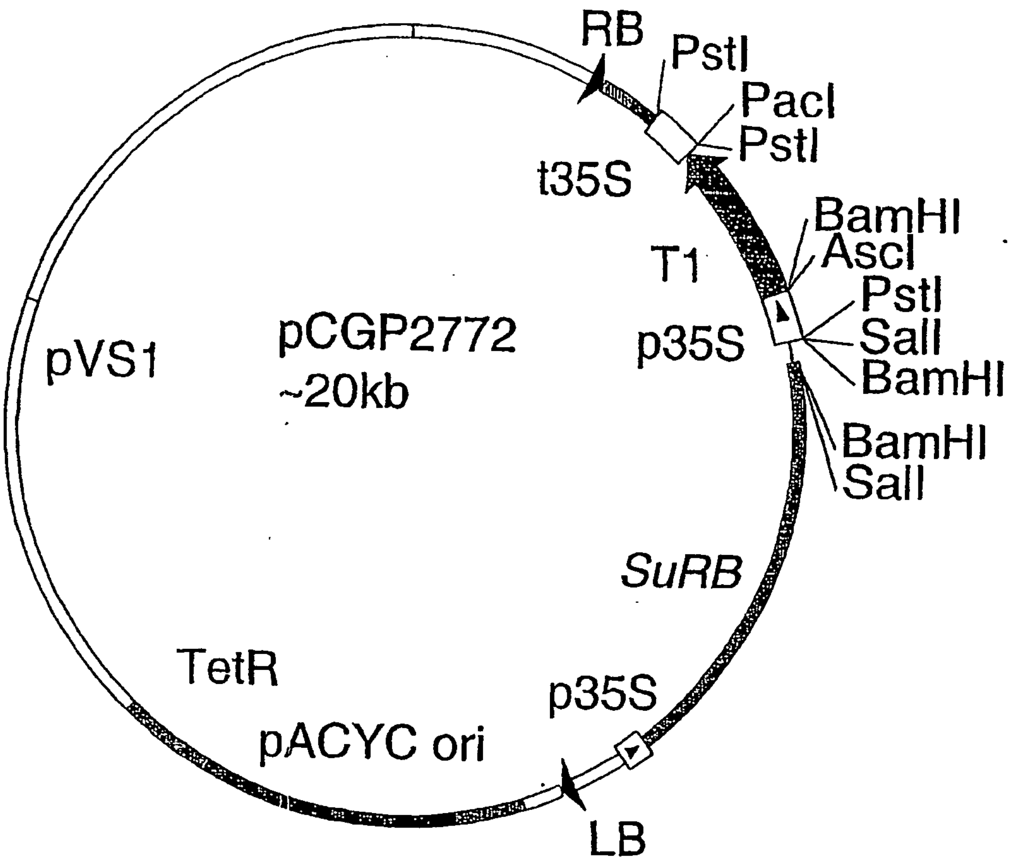
Figure 22



Replicon: pCGP2757 <u>AscI</u>/<u>PacI</u> ~19.3kb vector

Insert: ~0.7kb <u>AscI</u>/<u>PacI</u> S1 PCR product using visproF1 and visproR1 primers and pCGP2923 as template

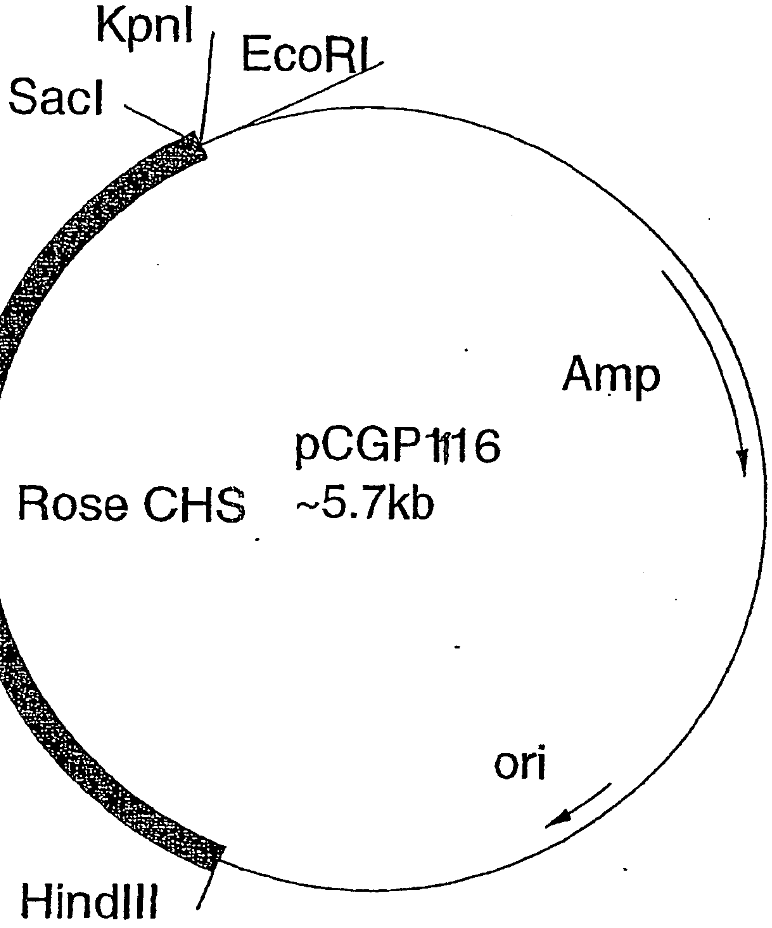
Figure 23



Replicon: pCGP2757 AscI/PacI ~19.3kb vector

Insert: ~0.7kb AscI/PacI T1 PCR product using visproF1 and visproR1 primers and pCGP2921 as template

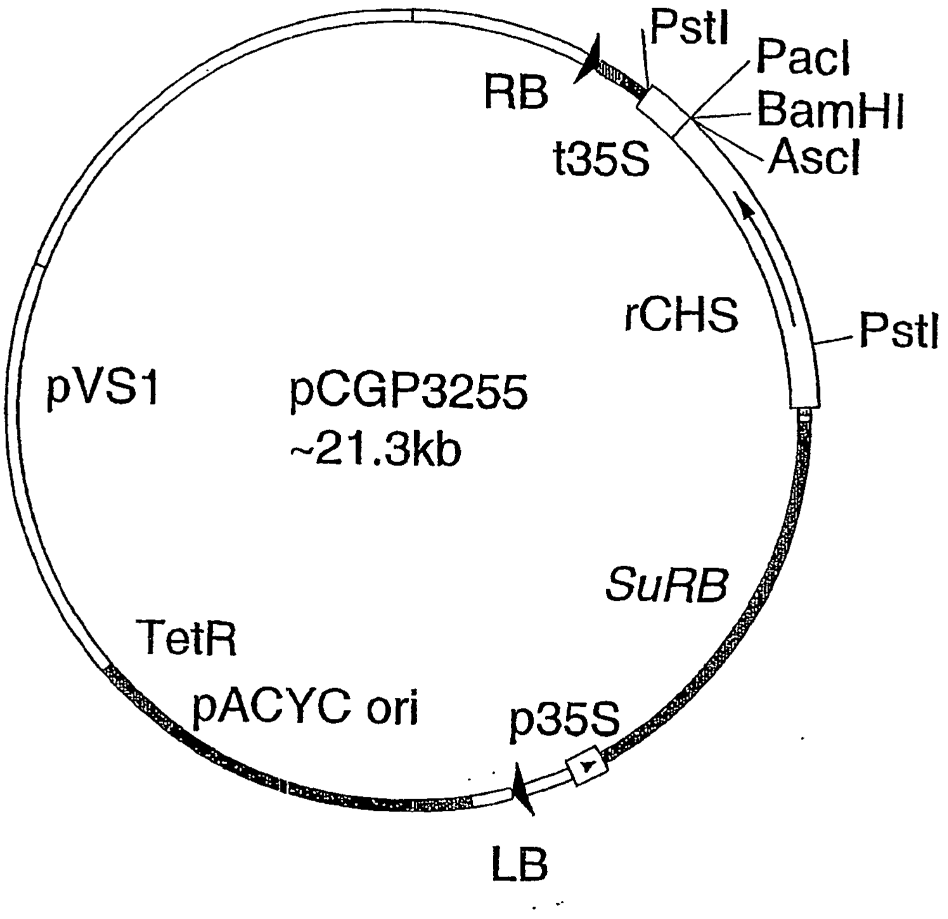
Figure 24



Replicon: pUC19 HindIII/SmaI 2.7kb vector

Insert: HindIII/EcoRV fragment from pCGP1114 containing the Rose CHS promoter fragment

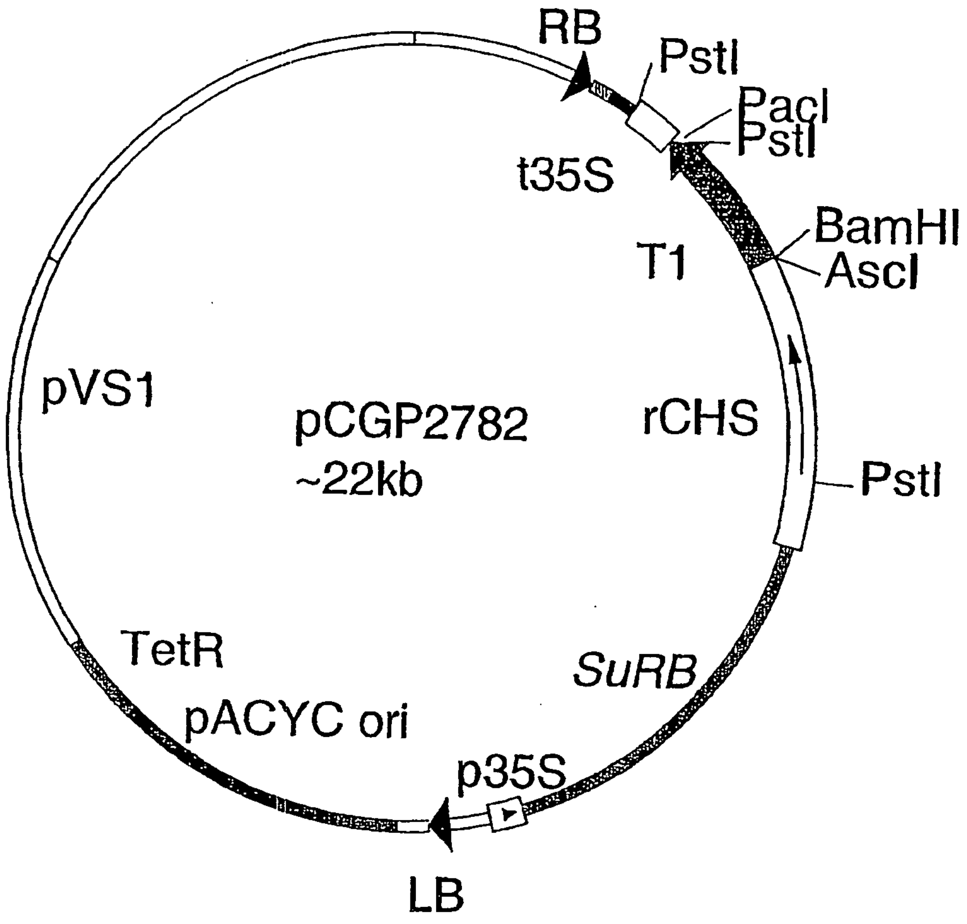
Figure 25



Replicon: pCGP2757 <u>Sal</u>I (blunt)/<u>Asp</u>718 ~18.6kb vector

Insert: ~2.7kb <u>Hin</u>dIII (blunt)/<u>Asp</u>718 fragment from pCGP1116

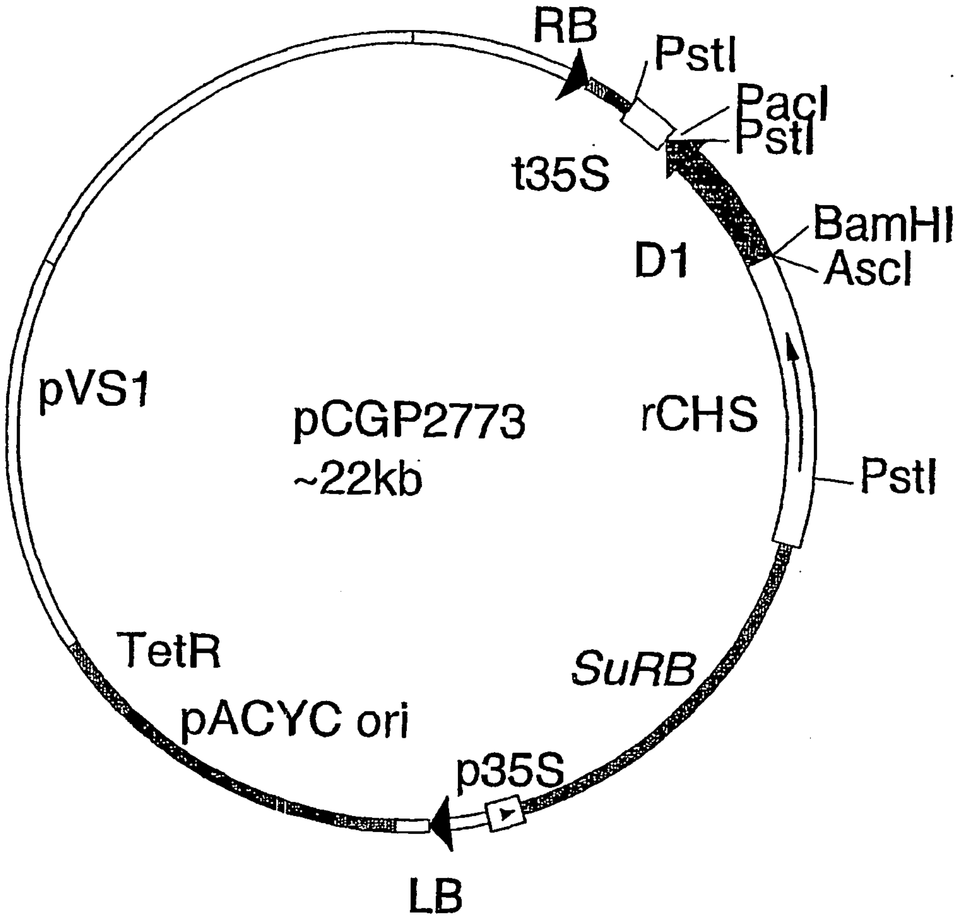
Figure 26



Replicon: pCGP3255 AscI/PacI ~21.3kb vector

Insert: ~0.7kb AscI/PacI T1 PCR product using the primers visproF1 and visproR1 and pCGP2921 as template

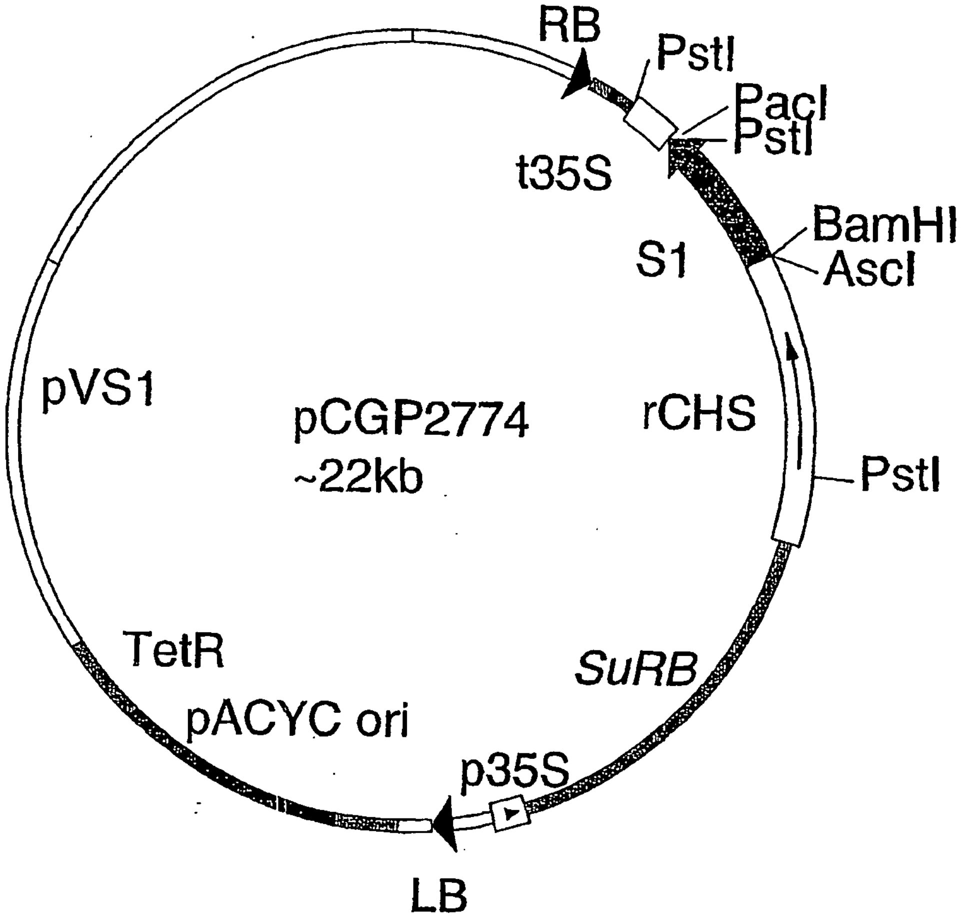
Figure 27



Replicon: pCGP3255 AscI/PacI ~21.3kb vector

Insert: ~0.7kb AscI/PacI D1 PCR product using the primers visproF1 and visproR1 and pCGP2919 as template

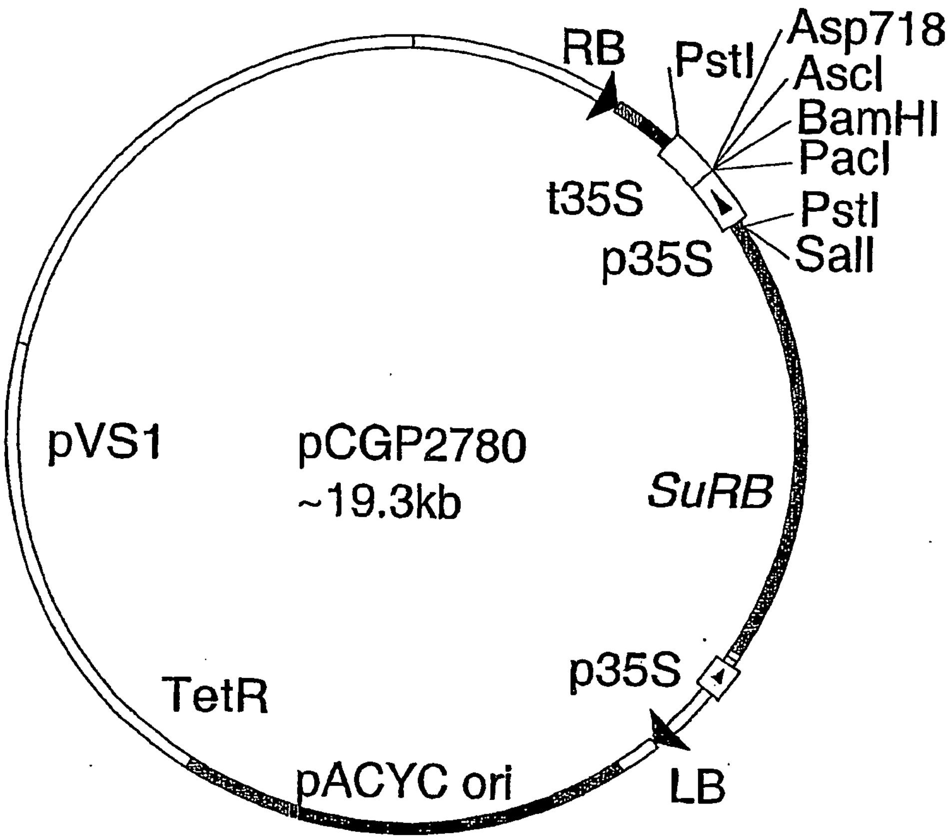
Figure 28



Replicon: pCGP3255 AscI/PacI ~21.3kb vector

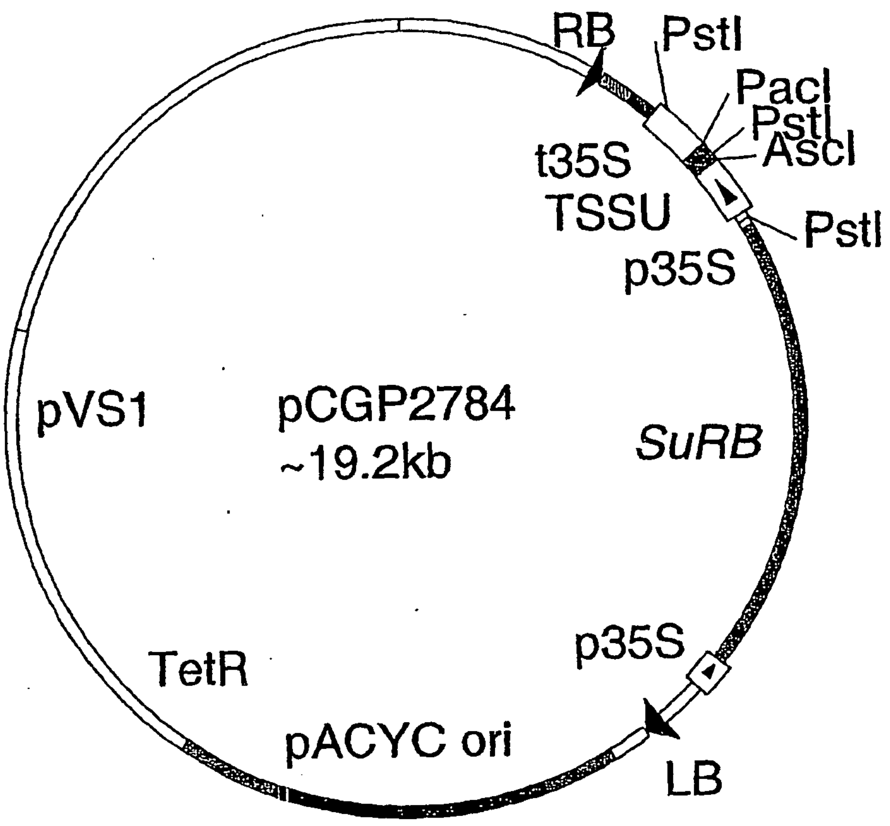
Insert: ~0.7kb AscI/PacI S1 PCR product using the primers visproF1 and visproR1 and pCGP2923 as template

Figure 29



Replicon: Religation of Sall cut pCGP2757 ~19.3kb vector to remove a number of restriction endonuclease recognition sites thereby creating a unique BamHI site

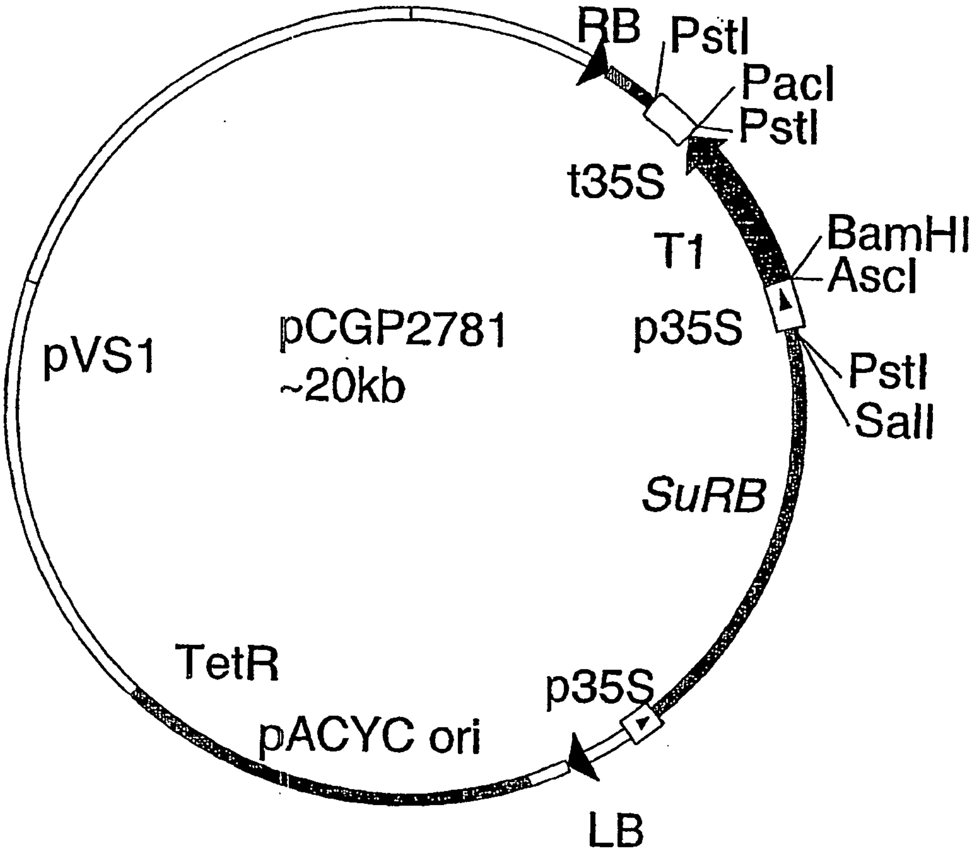
Figure 30



Replicon: pCGP2780 AscI/BamHI ~19kb vector

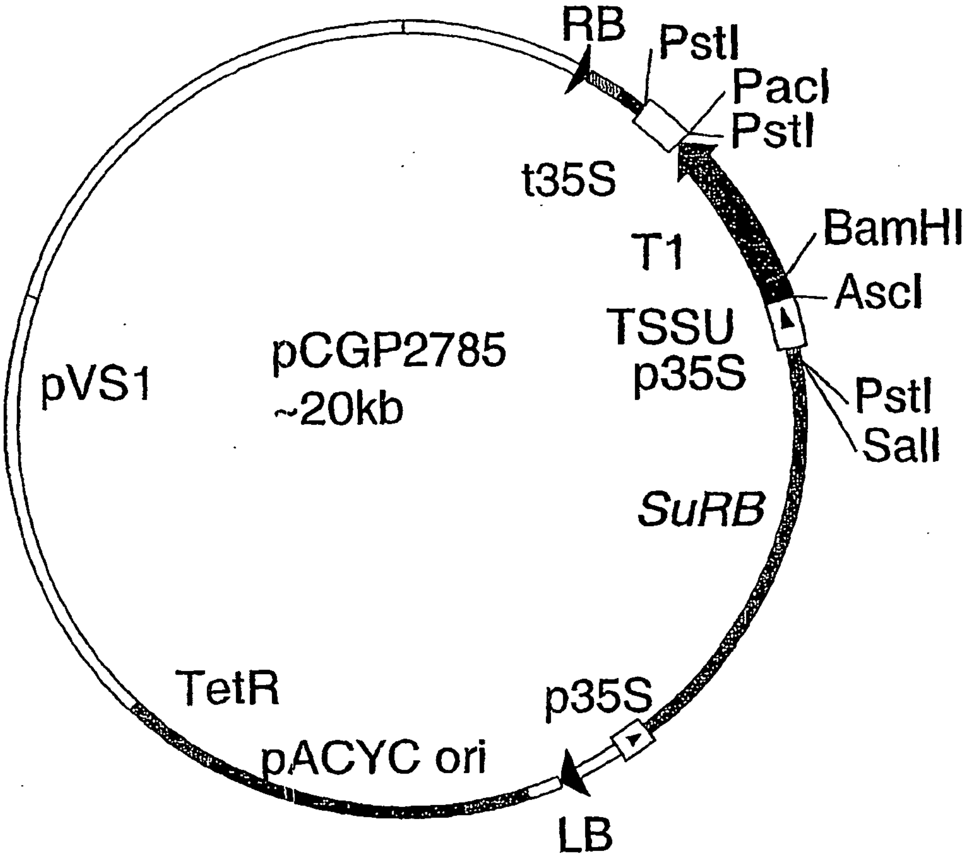
Insert: ~0.2kb AscI/BamHI fragment from pCGP2783 containing a chloroplast transit-peptide sequence from tobacco ribulose bisphosphate carboxylase gene

Figure 31



Replicon: Religation of Sall cut pCGP2772 ~19.3kb vector to remove a number of restriction endonuclease recognition sites thereby creating a unique BamHI site

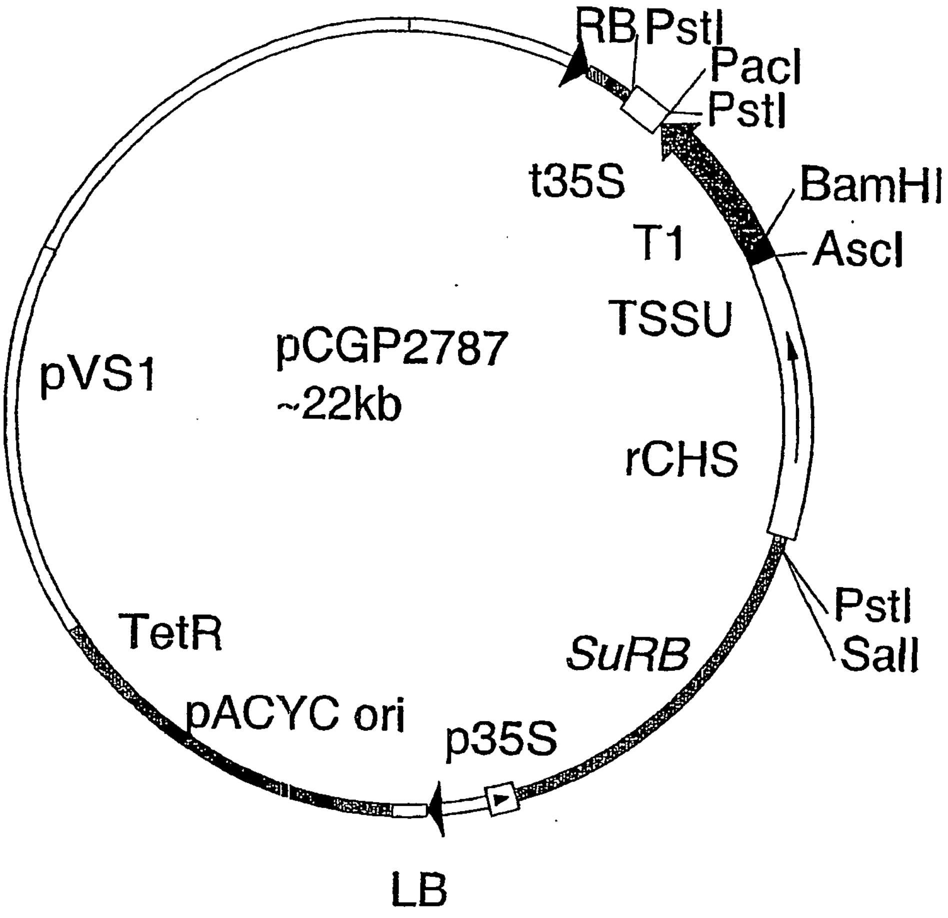
Figure 32



Replicon: pCGP2781 AscI/BamHI ~20kb vector

Insert: ~0.2kb AscI/BamHI fragment from pCGP2783 containing a chloroplast transit-peptide sequence from tobacco ribulose bisphosphate carboxylase ~~gene~~

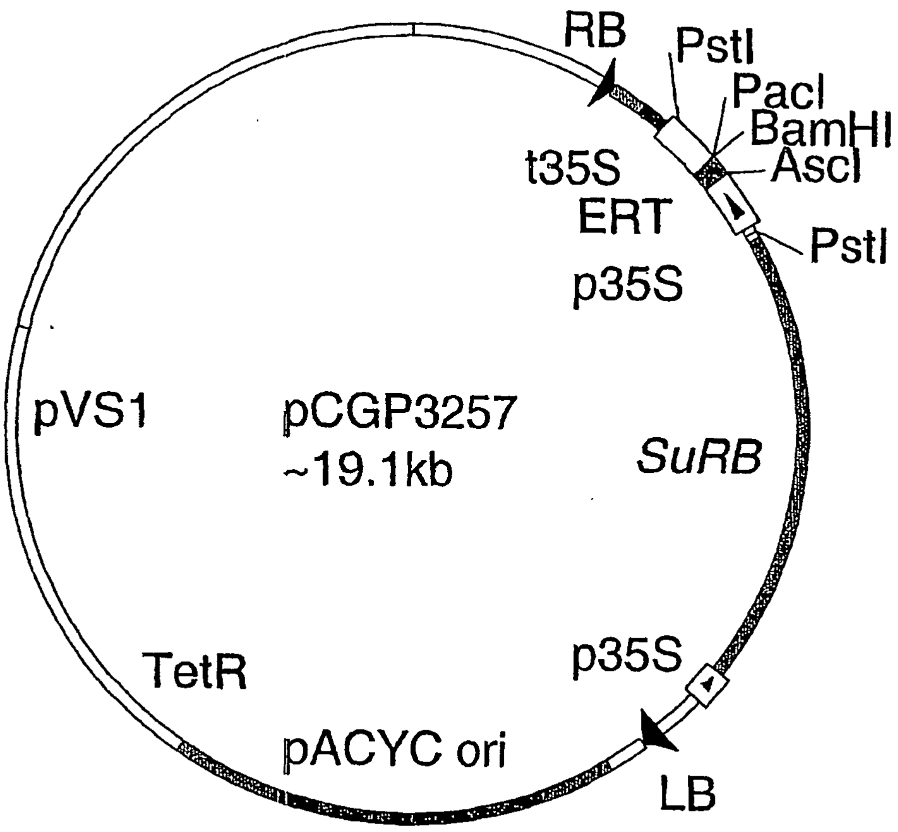
Figure 33



Replicon: pCGP2782 AscI/BamHI ~22kb vector

Insert: ~0.2kb AscI/BamHI fragment from pCGP2783 containing a chloroplast transit-peptide sequence from tobacco ribulose bisphosphate carboxylase gene

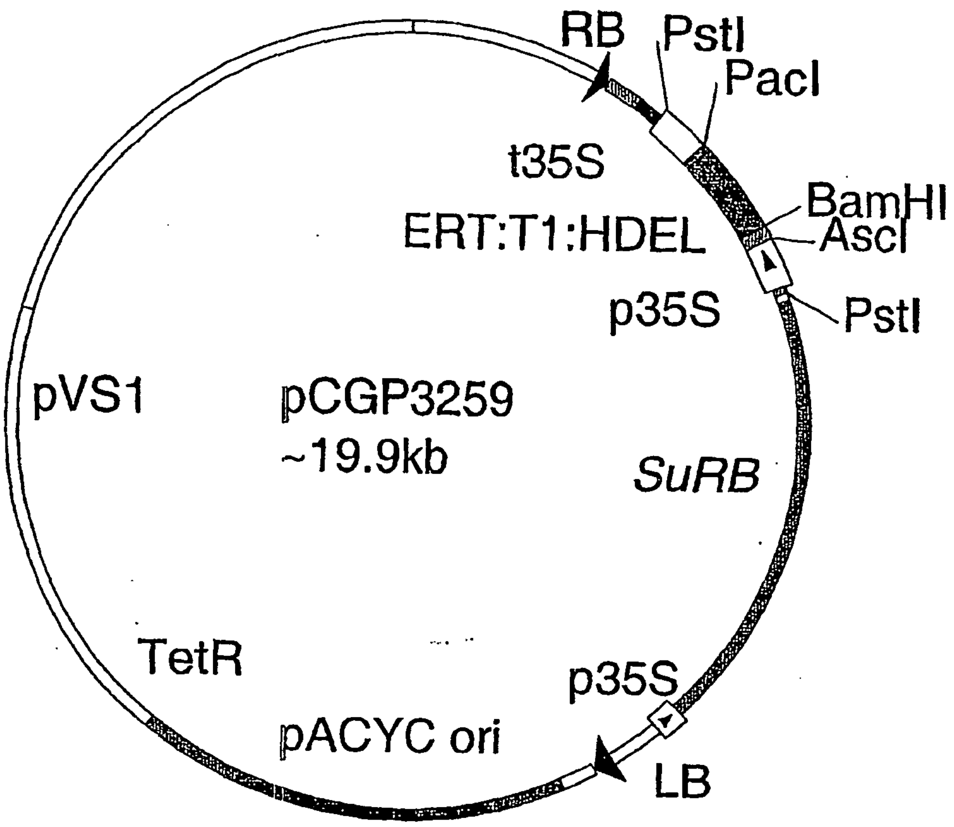
Figure 34



Replicon: pCGP2780 Ascl/BamHI ~19kb vector

Insert: ~0.1kb Ascl/BamHI fragment from pCGP3256 containing an ER-targeting signal sequence from *Arabidopsis* basic chitinase gene

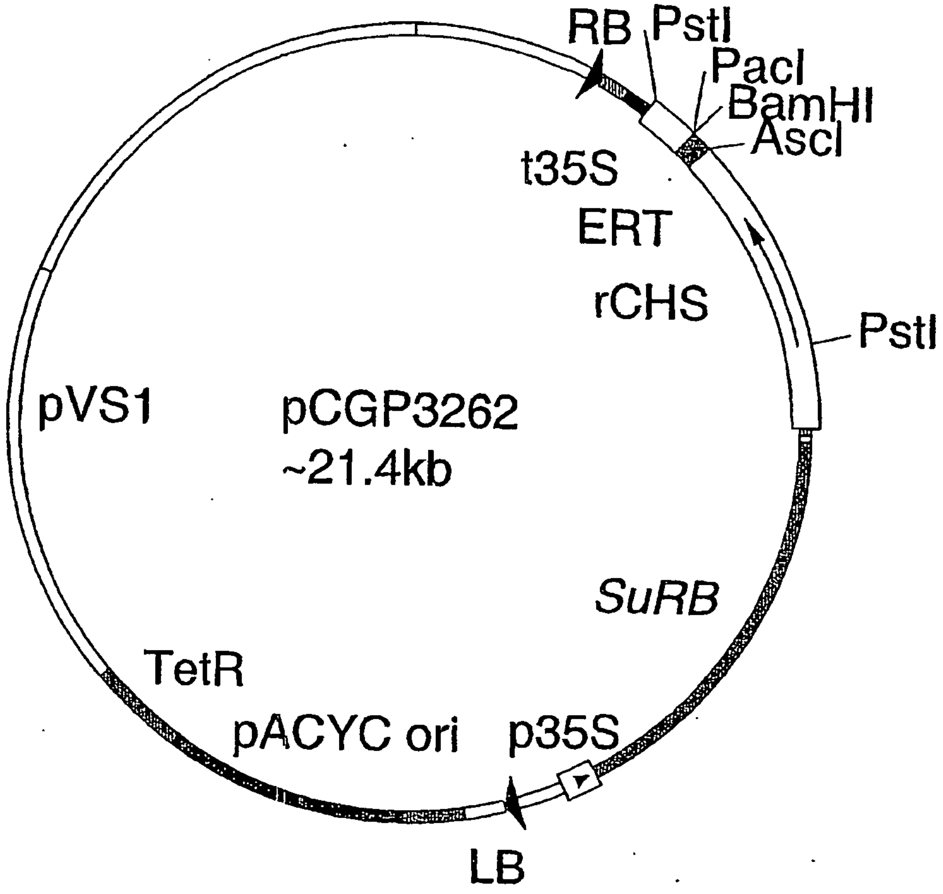
Figure 35



Replicon: pCGP3257 BamHI/PacI ~19.2kb vector

Insert: ~0.7kb BamHI/PacI T1 PCR fragment generated using visproF1 and CPHDELPacR primers and pCGP2779 as template

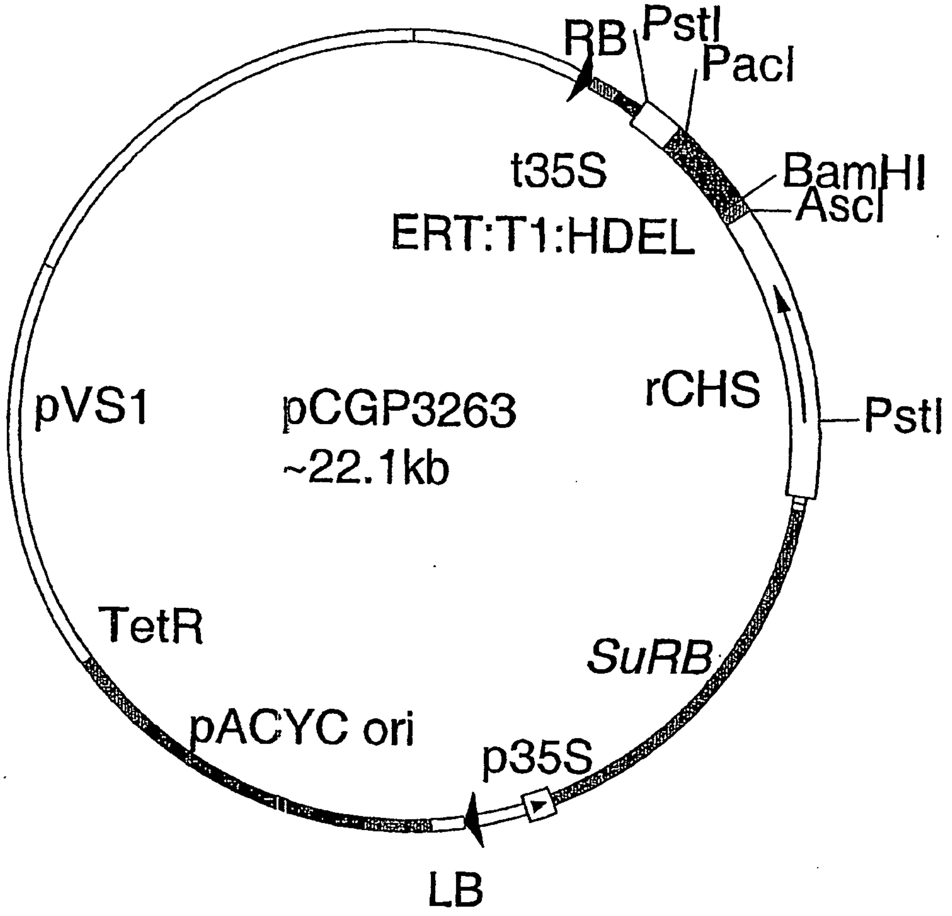
Figure 36



Replicon: pCGP3255 AscI/BamHI ~21.3kb vector

Insert: ~0.1kb AscI/BamHI fragment from pCGP3256 containing an ER-targeting signal sequence from *Arabidopsis* basic chitinase gene

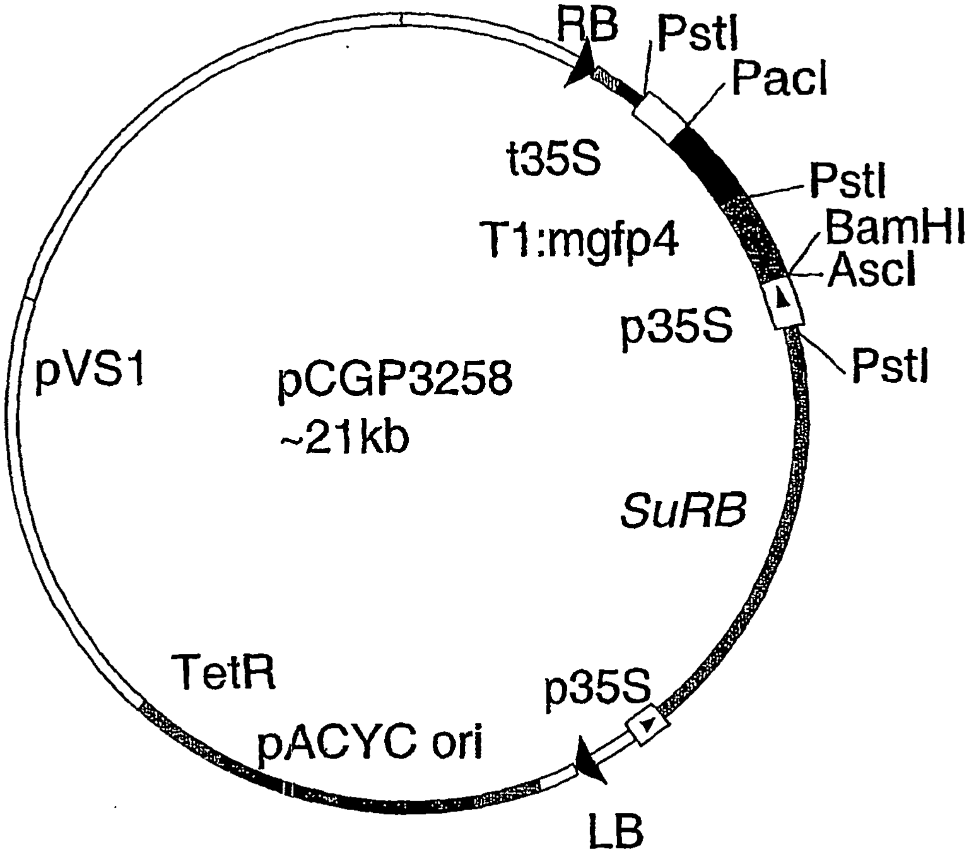
Figure 37



Replicon: pCGP3262 BamHI/PacI ~21.4kb vector

Insert: ~0.7kb BamHI/PacI T1 PCR fragment generated using visproF1 and CPHDELPacR primers and pCGP2779 as template

Figure 38



Replicon: pCGP3257 AscI/PacI ~19.4kb vector

Insert: ~1.4kb AscI/PacI fragment containing fusion of T1 and mgfp4. T1 PCR product generated using visproF1new and visproRI primers and pCGP2779 as template. mgfp4 PCR product generated using mGFP4-PacIR and Pst-mGFP4F as primers and pBIN35Smgfp4ER as template. PCR products digested with PstI and ligated together prior to ligation with vector.

Figure 39

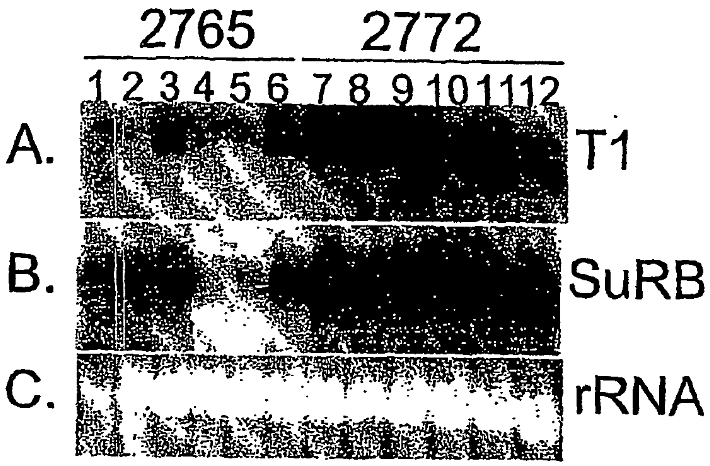


Figure 40

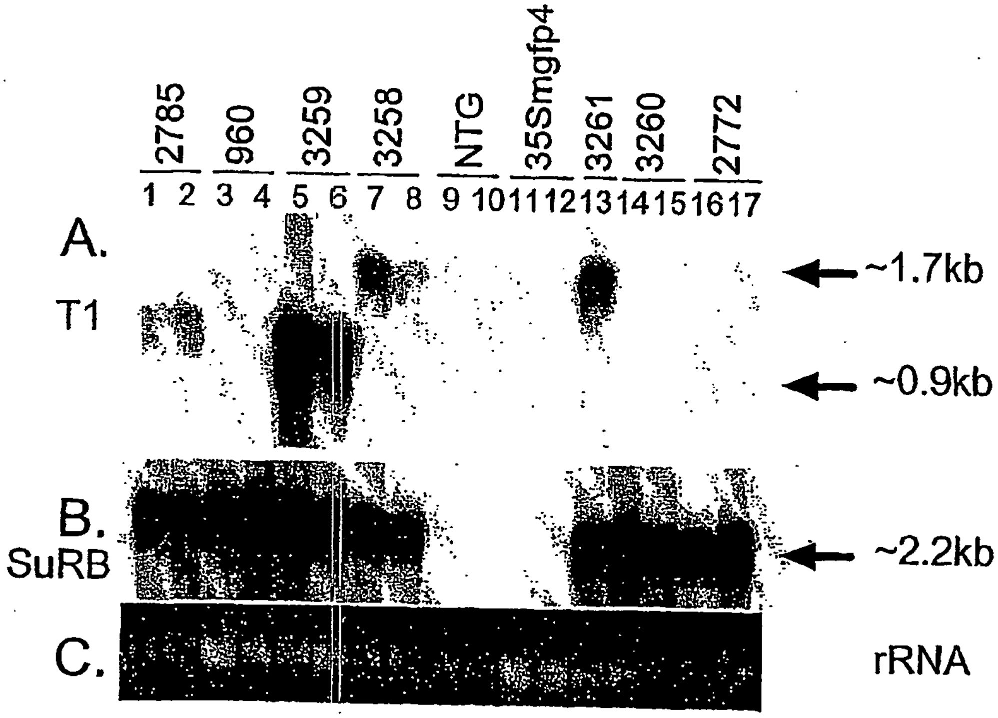

2785
960
3259
3258
NTG
35Smgfp4
3261
3260
2772
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17
A.
T1
~1.7kb
~0.9kb
B.
SuRB
~2.2kb
C.
rRNA

Figure 41

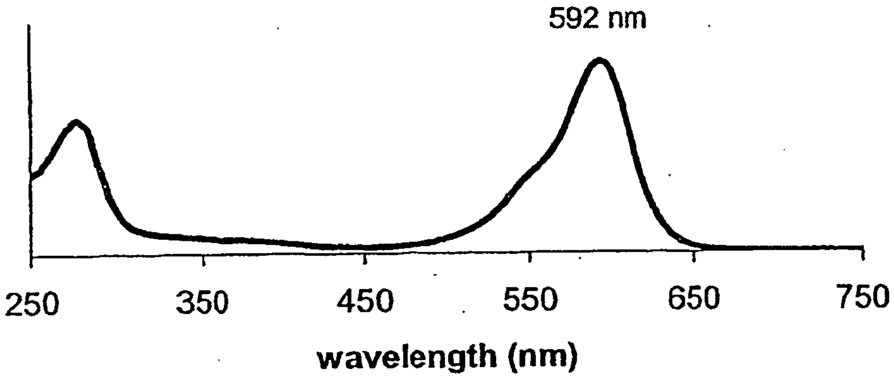


Figure 42(a)

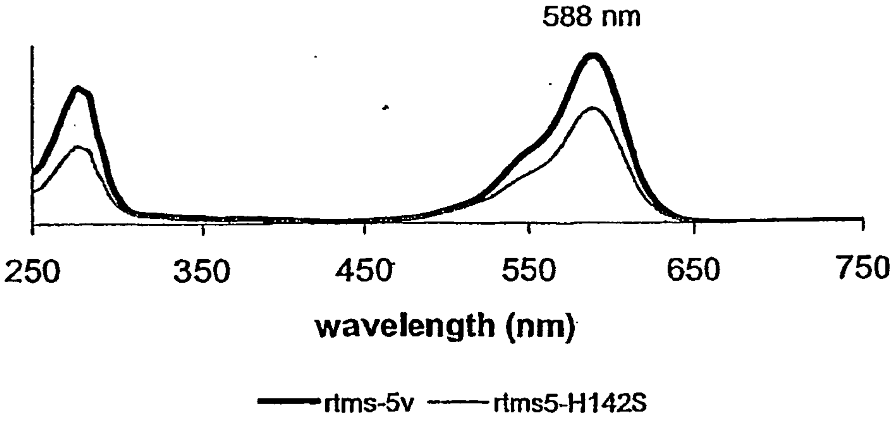


Figure 42(b)

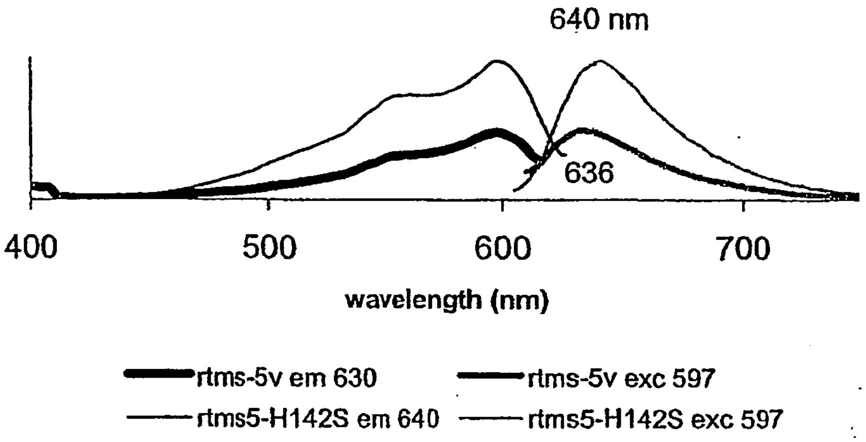

640 nm
636
400
500
600
700
wavelength (nm)
rtms-5v em 630
rtms-5v exc 597
rtms5-H142S em 640
rtms5-H142S exc 597

Figure 42(c)

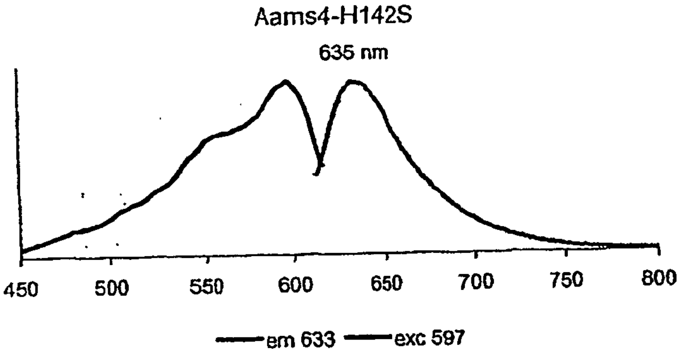


Figure 43(a)

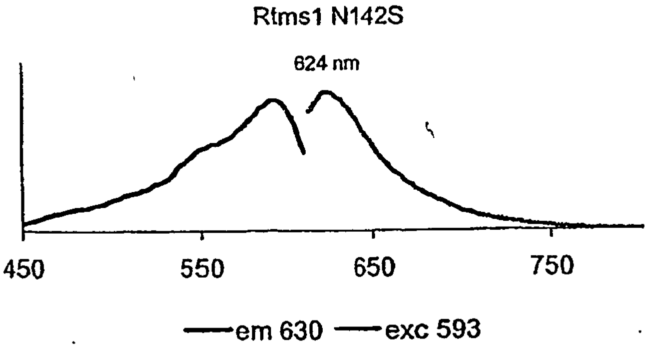
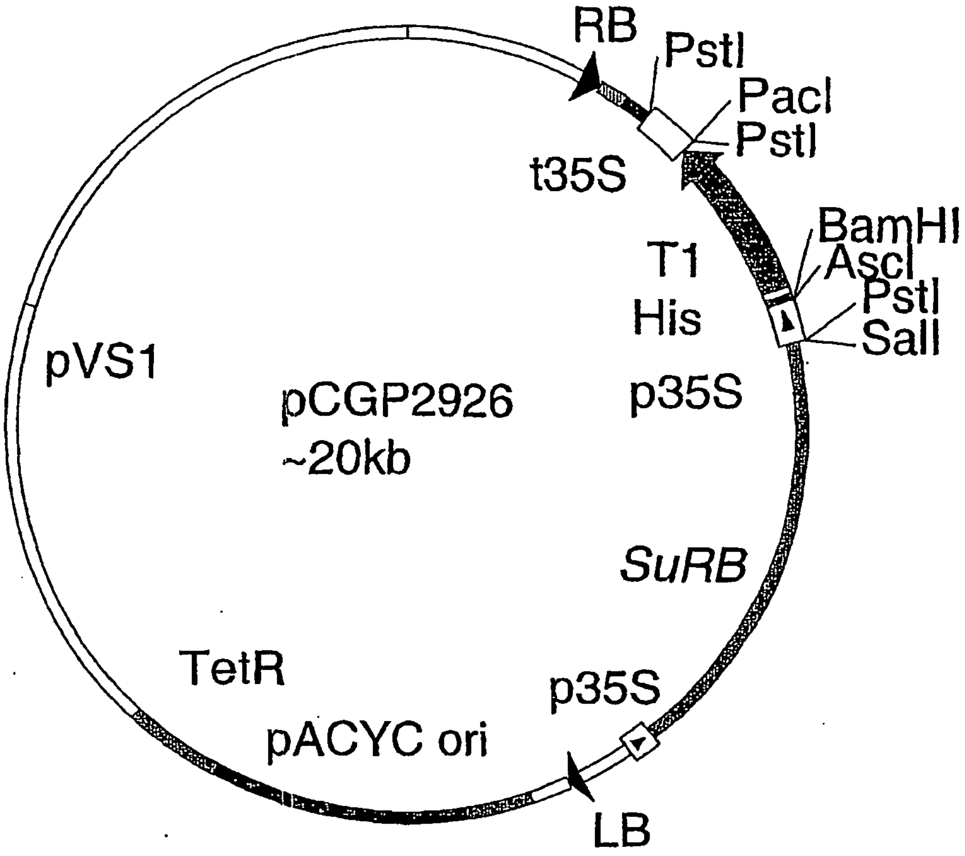


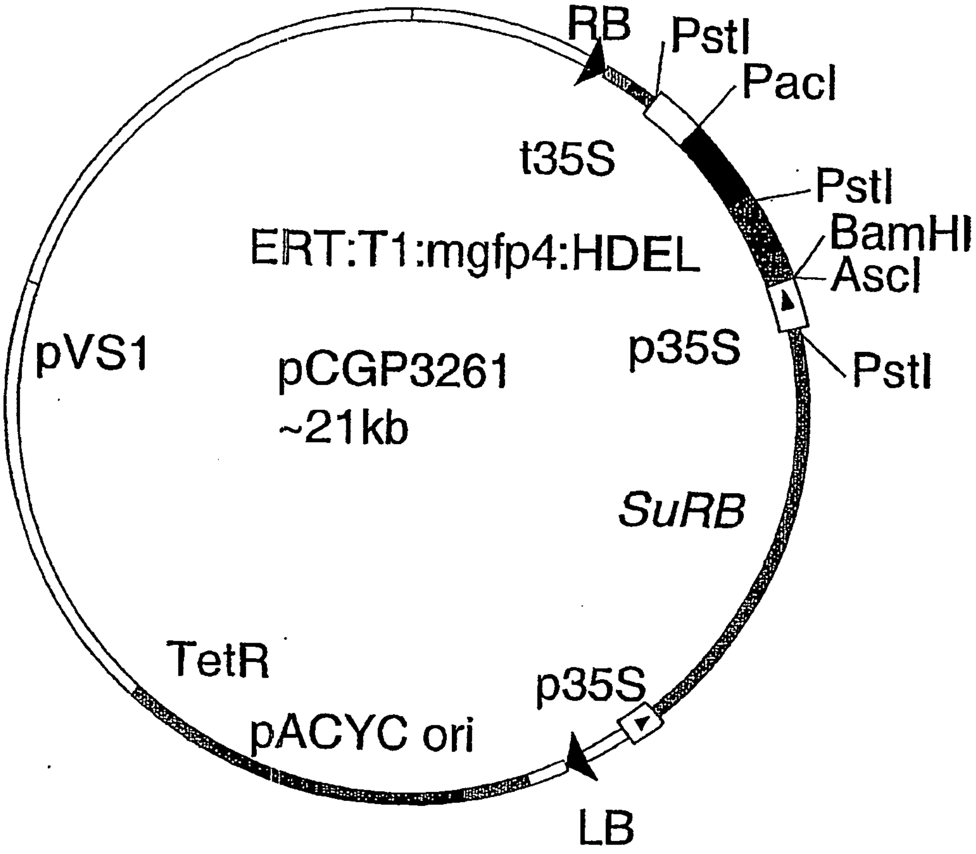
Figure 43(b)



Replicon: pCGP2781 AscI/PacI ~20kb vector

Insert: ~0.1kb AscI/PacI fragment containing
RBS-TICS and RGSHHHHHH epitope

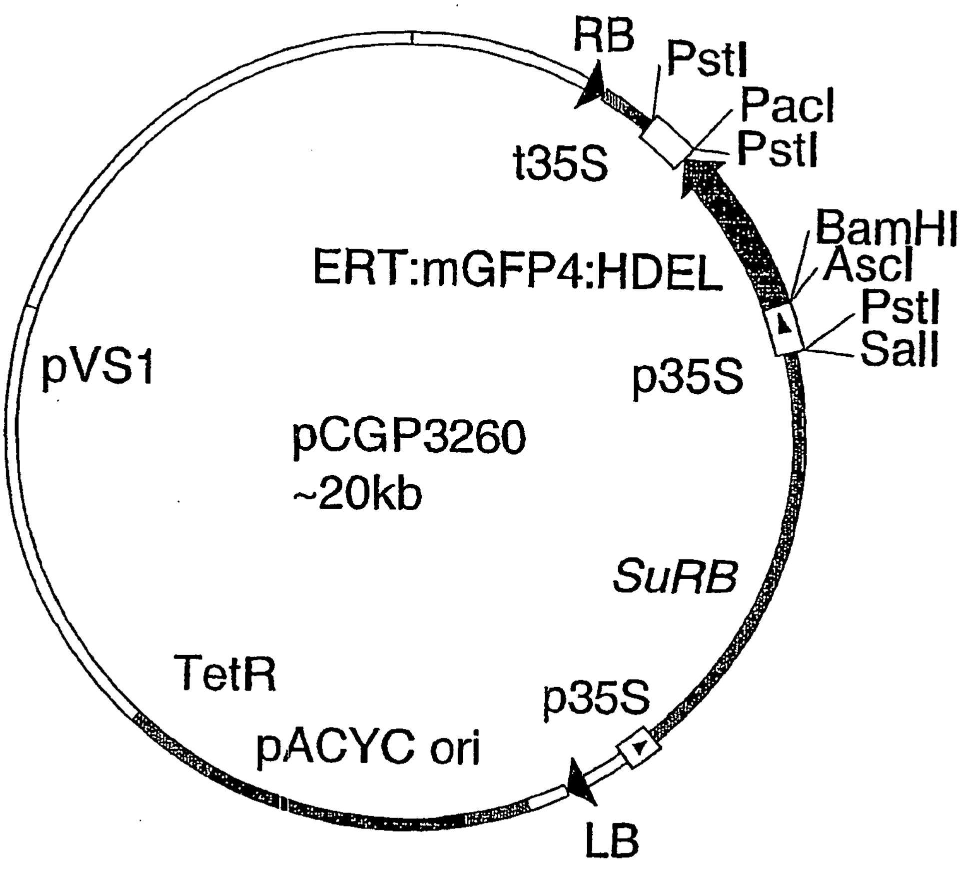
Figure 44



Replicon: pCGP3257 BamHI/PacI ~19.2kb vector

Insert: ~1.4kb BamHI/PacI fragment containing fusion of T1 and mgfp4 amplified from pCGP3258 using primers which incorporated ER targeting (ERT) and retention (HDEL) sequences.

Figure 45



Replicon: pCGP2780 BamHI/PacI (blunt) ~19kb vector

Insert: ~0.7kb SacI(blunt)/BamHI mGFP4 insert from pBIN35Smgfp4ER which includes ERT and HDEL sequences for ER targeting and retention.

Figure 46

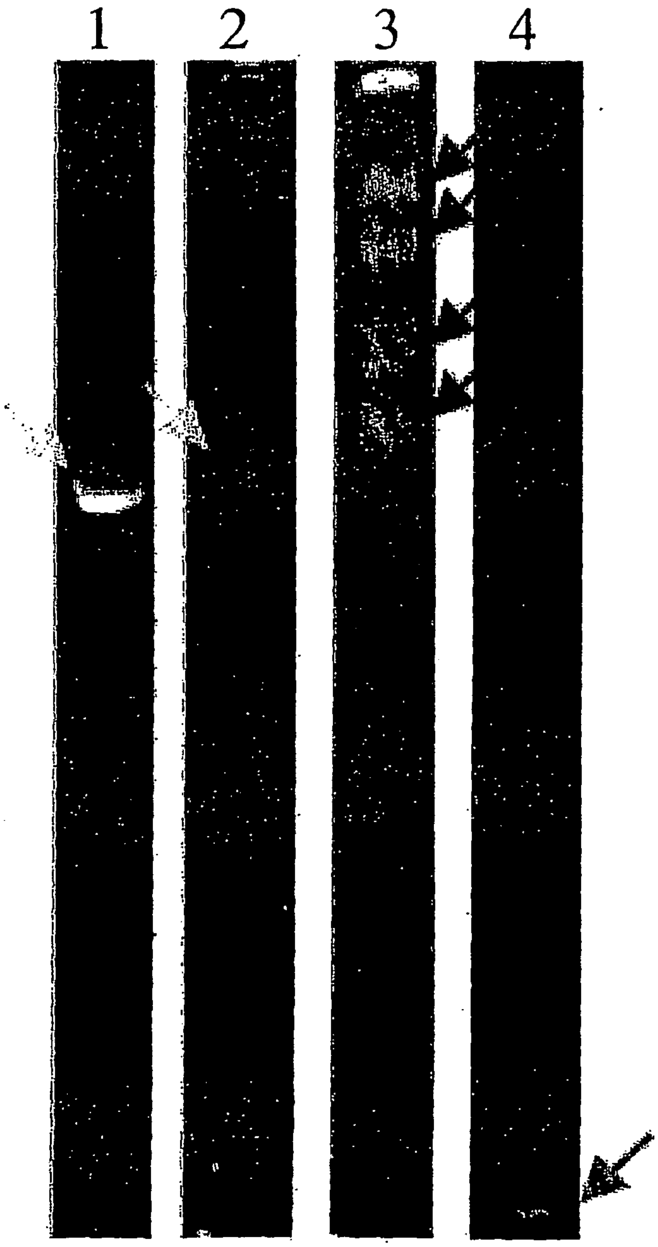


Figure 47

<110> Nufarm Limited

The University of Queensland

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<130> 2505563/EJH

<140> International

<141> 2002-03-01

<150> US 60/273,227

<151> 2001-03-02

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<151> 2001-03-21

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<151> 2001-10-15

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<213>  oligonucleotide


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1               5                   10                  15
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1               5                   10                  15
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1               5                   10                  15
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<223> X = any amino acid except M

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Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggc gga cct         144
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att cta tca cca cag agt cag tac gga agc         192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
    50                  55                  60

ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag cag         240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc cct gag gga tat aca tgg gag agg atc atg aac ttc gaa gat         288
Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggt aac tgt         336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

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        115                 120                 125

cct gtt atg caa aag aag aca cag ggc tgg gaa ccc aac act ggg cgt         432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Gly Arg
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ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt atg gct ctg         480
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145                 150                 155                 160

aag ttg gaa gga ggt ggt cat tat ttg tgt gaa ttc aaa tct act tac         528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

aag gca aag aag cct gtg atg atg cca ggg tat cac tat gtt gac cgc         576
Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aag ttg gat gta acc aat cac aac aag gat tac act tcc gtt gag cag         624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205
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<213>  Acropora aspera


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            20                  25                  30

Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
    50                  55                  60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Gly Arg
    130                 135                 140

Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175
```

```
Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190


Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205


Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
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Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

tac gag ggg gag cag acg gta agg ctg act gtc acc aag ggc gga cct         144
Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att tta tca cca cag tca cag tac gga agc         192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
    50                  55                  60

ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag cag         240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc ccg gag gga tat aca tgg gag agg atc atg aac ttt gaa gat         288
Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac tgt         336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110
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ttc atc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga      384
Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtt atg cag aag aag aca cag ggc tgg gaa ccc aac act gag cgt      432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

ctc tta gca cga gat gga atg ctg ata gga aac aac ttt atg gct ctg      480
Leu Leu Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

aag tta gaa gga ggt ggt cac tat ttg tgt gaa ttc aaa tct act tac      528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

aag gca agg aag cct gtg aag atg cca ggg tat cac tat gtt gac cgc      576
Lys Ala Arg Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aaa ctg gat gta acc aat cac aac aag gat tac act tcc gtt gag cag      624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

cgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                      660
Arg Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220


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<213>  Acropora aspera


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            20                  25                  30


Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45


Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
    50                  55                  60


Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80
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100 105 110

Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
115 120 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
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Leu Leu Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145 150 155 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
165 170 175

Lys Ala Arg Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
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Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

tac gag ggg gag cag acg gta agg ctg act gtc acc aag ggc gga cct       144
Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att tta tca cca cag tca cag tac gga agc       192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
    50                  55                  60

ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag cag       240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc ccg gag gga tat aca tgg gag agg atc atg aac ttt gaa gat       288
Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac tgt       336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

ttc atc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga       384
Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtt atg cag aag aag aca cag ggc tgg gaa ccc aac act gag cgt       432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt atg gct ctg       480
Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

aag tta gaa gga ggt ggt cac tat ttg tgt gaa ttc aaa tct act tac       528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

aag gca aag aag cct gtg agg atg cca ggg tat cac tat gtt gac cgc       576
Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aaa ctg gat gta acc aat cac aac aag gat tac act tcc gtt gag cag       624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc tga                   663
Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
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<210> 24

<211> 220

<212> PRT

<213> Acropora aspera

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<400>  24

Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
    50                  55                  60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
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<210>  25

<211>  660

<212>  DNA

<213>  Acanthastria sp.


<220>

<221>  CDS

<222>  (1)..(660)


<400>  25
tcc gtt atc gct aaa cag atg acc tac aag gtt tat atg tca ggc acg         48
Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga aag cct         96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggc gga cct        144
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att tta tca cca cgg tgt cag tac gga aac        192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Arg Cys Gln Tyr Gly Asn
    50                  55                  60

ata cca ttc acc aag tac cct gaa gac gtc cct gac tat gta aag cag        240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Val Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc ccg gag gga ttt aca tgg gag agg atc atg aac ttt gaa gat        288
Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac tgt        336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

ttc acc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga        384
Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtg atg cag aag aag aca cgg ggc tgg gaa ccc cac tct gag cgt        432
Pro Val Met Gln Lys Lys Thr Arg Gly Trp Glu Pro His Ser Glu Arg
    130                 135                 140

ctc ttt gca cgg ggt gga atg ctg ata gga aac aac ttt atg gct ctg        480
Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160
```

```
aag tta gaa gga ggc ggt cac tat ttg tgt gga ttc aaa act act tac       528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Gly Phe Lys Thr Thr Tyr
                165                 170                 175

aag gca aag aag cct gtg aag atg cca ggg tat cat tat gtt gac cgc       576
Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aaa ctg gat gta acc aat cac aac aag gat tac att tcc gtt gag cag       624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Ile Ser Val Glu Gln
        195                 200                 205

tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                       660
Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
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<210> 26

<211> 220

<212> PRT

<213> Acanthastria sp.

<400> 26

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Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Arg Cys Gln Tyr Gly Asn
    50                  55                  60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Val Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125
```

```
Pro Val Met Gln Lys Lys Thr Arg Gly Trp Glu Pro His Ser Glu Arg
    130                 135                 140


Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160


Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Gly Phe Lys Thr Thr Tyr
                165                 170                 175


Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190


Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Ile Ser Val Glu Gln
        195                 200                 205


Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220


<210>  27

<211>  660

<212>  DNA

<213>  Acanthastria sp.



<220>

<221>  CDS

<222>  (1)..(660)



<400>  27
tcc gtt atc gct aaa cag atg acc tac aaa gtt tat atg tca ggc acg        48
Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga aag cct        96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

tac gag ggg gag cag acg gta agg ctg act gtc acc aag ggc gga cct       144
Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att tta tca cca cag tca cag tac gga agc       192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
    50                  55                  60
```

```
ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag cag       240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc ccg gag gga tat aca tgg gag agg atc atg aac ttt gaa gat       288
Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac tgt       336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

ttc atc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga       384
Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtt atg cag aag aag aca cag ggc tgg gaa ccc aac act gag cgt       432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

ctc tct gca cga gat gga atg ctg ata gga aac aac ttt atg gct ctg       480
Leu Ser Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

aag tta gaa gga ggt ggt cac tat ttg tgt gaa ttc aaa tct act tac       528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

aag gca agg aag cct gtg aag atg cca ggg tat cac tgt gtt gac cgc       576
Lys Ala Arg Lys Pro Val Lys Met Pro Gly Tyr His Cys Val Asp Arg
            180                 185                 190

aaa ctg gat gta acc aat cac aac aag gat tac act tcc gtt gag cag       624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

cgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                       660
Arg Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
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<210> 28

<211> 220

<212> PRT

<213> Acanthastria sp.

<400> 28

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Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30
```

```
Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
    50                  55                  60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

Leu Ser Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

Lys Ala Arg Lys Pro Val Lys Met Pro Gly Tyr His Cys Val Asp Arg
            180                 185                 190

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

Arg Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220

<210>  29

<211>  660

<212>  DNA

<213>  Acanthastria sp.


<220>
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<221>  CDS

<222>  (1)..(660)


<400>  29
tcc gtt atc gct aaa cag atg acc tac aag gtt tat atg tca ggc acg        48
Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga aag cct        96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggc gga cct       144
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att tta tca cca cag tgt cag tac gga agc       192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Ser
    50                  55                  60

ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag cag       240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc ccg gag gga ttt aca tgg gag agg atc atg aac ttt gaa gat       288
Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

ggt gca gtg tgt act gtc agc aat gac tcc agc atc caa ggc aac tgt       336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

ttc acc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat ggg       384
Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtg atg cag aag aag aca cag ggc tgg gaa ccc cac tct gag cgt       432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu Arg
    130                 135                 140

ctc ttt gca cgg ggt gga atg ctg ata gga aac aac ttt atg gct ccg       480
Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala Pro
145                 150                 155                 160

aag tta gaa gga ggc ggt cac tat ttg tgt gaa ttc aaa act act tac       528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr Tyr
                165                 170                 175

aag gca aag aag cct gtg aag atg ccg ggg tat cat tat gtt gac cgc       576
Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aaa ctg gat gta acc aat cac aac aag gat tac act tcc gtt gag cag       624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205
```

tgt gaa atc tcc att gca cgc aaa cct gtg gtc gcc 660
Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
210 215 220

<210> 30

<211> 220

<212> PRT

<213> Acanthastria sp.

<400> 30

Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1 5 10 15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
20 25 30

Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
35 40 45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Ser
50 55 60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65 70 75 80

Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
85 90 95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
100 105 110

Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
115 120 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu Arg
130 135 140

Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala Pro
145 150 155 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr Tyr
165 170 175

```
Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220

<210>  31

<211>  660

<212>  DNA

<213>  Caulastrea ap.


<220>

<221>  CDS

<222>  (1)..(660)


<400>  31
tcc gtt atc gct aaa cag atg acc tac aaa gtt tat atg tca ggc acg         48
Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga aag cct         96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

tac gag ggg gag cag acg gta agg ctg act gtc acc aag ggc gga cct        144
Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att tta tca cca cag tca cag tac gga agc        192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
    50                  55                  60

ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag cag        240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc ccg gag gga tat aca tgg gag agg atc atg aac ttt gaa gat        288
Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac tgt        336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110
```

ttc atc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga 384
Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
115 120 125

cct gtt atg cag aag aag aca cag ggc tgg gaa ccc aac act gag cgt 432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
130 135 140

ctc tct gca cga gat gga atg ctg ata gga aac aac ttt atg gct ctg 480
Leu Ser Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145 150 155 160

aag tta gaa gga ggt ggt cac tat ttg tgt gaa ttc aaa tct act tac 528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
165 170 175

aag gca agg aag cct gtg aag atg cca ggg tat cac tat gtt gac cgc 576
Lys Ala Arg Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
180 185 190

aaa ctg gat gta acc aat cac aac aag gat tac act tcc gtt gag cag 624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
195 200 205

cgt gaa att tcc att gca cgc aaa cct gtg gtc gcc 660
Arg Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
210 215 220

<210> 32

<211> 220

<212> PRT

<213> Caulastrea ap.

<400> 32

Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1 5 10 15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
20 25 30

Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly Pro
35 40 45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
50 55 60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65 70 75 80

```
Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
    115                 120                 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

Leu Ser Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

Lys Ala Arg Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
    195                 200                 205

Arg Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220

<210>  33

<211>  660

<212>  DNA

<213>  Caulastrea ap.


<220>

<221>  CDS

<222>  (1)..(660)


<220>

<221>  misc_feature

<222>  (72)..(72)
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<223> n = any nucleotide

<220>

<221> misc_feature

<222> (133)..(133)

<223> n = any nucleotide

<220>

<221> misc_feature

<222> (166)..(166)

<223> n = any nucleotide

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<221> misc_feature

<222> (193)..(193)

<223> n = any nucleotide

<220>

<221> misc_feature

<222> (486)..(486)

<223> n = any nucleotide

<220>

<221> misc_feature

<222> (495)..(495)

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<223>  n = any nucleotide



<220>

<221>  misc_feature

<222>  (501)..(501)

<223>  n = any nucleotide



<400>  33
tcc gtt atc gct aaa cag atg acc tac aag gtt tat atg tca ggc acg          48
Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

gtc aat gga cac tac ttt gag gtn gaa ggc gat gga aaa gga aag cct          96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

tac gag ggg gag cag acg gta aag ctc act gtc acc nag ggc gga cct         144
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Xaa Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att nta tca cca cag agt cag tac gga agc         192
Leu Pro Phe Ala Trp Asp Ile Xaa Ser Pro Gln Ser Gln Tyr Gly Ser
    50                  55                  60

nta cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag cag         240
Xaa Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc cct gag gga tat aca tgg gag agg atc atg aac ttt gaa gat         288
Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggt aac tgt         336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

ttc atc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat ggg         384
Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtt atg caa aag aag aca cag ggc tgg gaa ccc cac tct gag cgt         432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu Arg
    130                 135                 140

ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt atg gct ctg         480
Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160
```

```
aag ttn gaa gga ggn ggt can tat ttg tgt gaa ttc aaa tct act tac        528
Lys Xaa Glu Gly Gly Gly Thr Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

aag gca aag aag cct gtg atg atg cca ggg tat cac tat gtt gac cgc        576
Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aaa ttg gat gta acc aat cac aac aag gat tac act tcc gtt gag cag        624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

tgt gaa ata tcc att gca cgc aaa cct gtg gtc gcc                        660
Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
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<210> 34

<211> 220

<212> PRT

<213> Caulastrea ap.

<220>

<221> misc_feature

<222> (72)..(72)

<223> n = any nucleotide

<220>

<221> misc_feature

<222> (133)..(133)

<223> n = any nucleotide

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<221> misc_feature

<222> (166)..(166)

<223> n = any nucleotide

<220>

<221> misc_feature

<222> (193)..(193)

<223> n = any nucleotide

<220>

<221> misc_feature

<222> (486)..(486)

<223> n = any nucleotide

<220>

<221> misc_feature

<222> (495)..(495)

<223> n = any nucleotide

<220>

<221> misc_feature

<222> (501)..(501)

<223> n = any nucleotide

<400> 34

Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1 5 10 15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
20 25 30

Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Xaa Gly Gly Pro
35 40 45

Leu Pro Phe Ala Trp Asp Ile Xaa Ser Pro Gln Ser Gln Tyr Gly Ser
50 55 60

Xaa Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65 70 75 80

Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
85 90 95

```
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu Arg
    130                 135                 140

Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

Lys Xaa Glu Gly Gly Gly Thr Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
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<210> 35

<211> 660

<212> DNA

<213> Caulastrea ap.

<220>

<221> CDS

<222> (1)..(660)

<220>

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<222> (637)..(638)

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<222>  (640)..(640)

<223>  n = any nucleotide




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Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga aag cct        96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggc gga cct       144
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att tta tca cca cag tgt cag tac gga agc       192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Ser
    50                  55                  60

ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag cag       240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc ccg gag gga ttt aca tgg gag agg atc atg aac ttt gaa gat       288
Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac tgt       336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

ttc acc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat ggg       384
Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtg atg cag aag aag aca cag ggc tgg gaa ccc cac tct gag cgt       432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu Arg
    130                 135                 140

ctc ttt gca cgg ggt gga atg ctg ata gga aac aac ttt atg gct ctg       480
Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

aag tta gaa ggg ggc ggt cac tat ttg tgt gaa ttc aaa act act tac       528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr Tyr
                165                 170                 175
```

```
aag gca aag aag cct gtg aag atg cca ggg tat cat tat gtt tac agc      576
Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Tyr Ser
            180                 185                 190

acc att cat gta acc aat cac aac aag gat tac act tcc gtt gag cag      624
Thr Ile His Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

tgt gaa att tcc nnt nca cgc aaa cct gtg gtc gcc                      660
Cys Glu Ile Ser Xaa Xaa Arg Lys Pro Val Val Ala
    210                 215                 220
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<210> 36

<211> 220

<212> PRT

<213> Caulastrea ap.

<220>

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<222> (637)..(638)

<223> n = any nucleotide

<220>

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<222> (640)..(640)

<223> n = any nucleotide

<400> 36

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Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Ser
    50                  55                  60
```

```
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu Arg
    130                 135                 140

Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr Tyr
                165                 170                 175

Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Tyr Ser
            180                 185                 190

Thr Ile His Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

Cys Glu Ile Ser Xaa Xaa Arg Lys Pro Val Val Ala
    210                 215                 220
```

<210> 37

<211> 660

<212> DNA

<213> Caulastrea ap.

<220>

<221> CDS

<222> (1)..(660)

<220>

<221> misc_feature

<222> (30)..(30)

<223> n = any nucleotide

<220>

<221> misc_feature

<222> (32)..(32)

<223> n = any nucleotide

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<222> (37)..(37)

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<222> (48)..(48)

<223> n = any nucleotide

<220>

<221> misc_feature

<222> (52)..(52)

<223> n = any nucleotide

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Ser Val Ile Ala Lys Gln Met Thr Tyr Xaa Xaa Tyr Xaa Ser Gly Xaa
1               5                   10                  15

gtc nat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga aag cct       96
Val Xaa Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggc gga cct      144
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att tta tca cca cag tgt cag tac gga agc      192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Ser
    50                  55                  60

ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag cag      240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc ccg gag gga ttt aca tgg gag agg atc atg aac ttt gaa gat      288
Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac tgt      336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

ttc acc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat ggg      384
Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtg atg cag aag aag aca cag ggc tgg gaa ccc cac tct gag cgt      432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu Arg
    130                 135                 140

ctc ttt gca cgg ggt gga atg ctg ata gga aac aac ttt atg gct ctg      480
Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

aag tta gaa gga ggc ggt cac tat ttg tgt gaa ttc aaa act act tac      528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr Tyr
                165                 170                 175

aag gca aag aag cct gtg aag atg cca ggg tat cat tat gtt gac cgc      576
Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aaa ctg gat gta acc aat cac aac aag gat tac act tcc gtt gag cag      624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                      660
Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220


<210>  38
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<211> 220

<212> PRT

<213> Caulastrea ap.

<220>

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<222> (30)..(30)

<223> n = any nucleotide

<220>

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<223> n = any nucleotide

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<223> n = any nucleotide

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<222> (48)..(48)

<223> n = any nucleotide

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<222> (52)..(52)

<223> n = any nucleotide

<400> 38

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Ser Val Ile Ala Lys Gln Met Thr Tyr Xaa Xaa Tyr Xaa Ser Gly Xaa
1               5                   10                  15

Val Xaa Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Ser
    50                  55                  60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu Arg
    130                 135                 140

Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr Tyr
                165                 170                 175

Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
```

<210> 39

<211> 660

<212> DNA

<213> Green Pocillopora

<220>

<221> CDS

<222> (1)..(660)

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tcc gtt atc gct aaa cag atg acc tac aag gtt tat atg tca ggc acg      48
Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

gtc aat gga cac tac ttt gag gtt gaa ggc gat gga aaa gga aag cct      96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggc gga cct      144
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att cta tca cca cag agt cag tac gga agc      192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
    50                  55                  60

ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag cag      240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc cct gag gga tat aca tgg gag agg atc atg aac ttc gaa gat      288
Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggt aac tgt      336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

ttc atc tac aat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga      384
Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtt atg caa aag aag aca cag ggc tgg gaa ccc aac act gag cgt      432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt atg gct ctg      480
Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

aag ttg gaa gga ggt ggt cat tat ttg tgt gaa ttc aaa tct act tac      528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175
```

```
aag gca aag aag cct gtg atg atg cca ggg tat cac tat gtt gac cgc        576
Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aaa ttg gat gta acc aat cac aac aag gat tac act tcc gtt gag cag        624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                        660
Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
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<210> 40

<211> 220

<212> PRT

<213> Green Pocillopora

<400> 40

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Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
    50                  55                  60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140
```

```
Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160


Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175


Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190


Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205


Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220


<210>  41

<211>  660

<212>  DNA

<213>  Acropora nobilis



<220>

<221>  CDS

<222>  (1)..(660)



<400>  41
tcc gtt atc gct aaa cag atg acc tac aag gtt tat atg tca ggc acg         48
Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

gtc aat gga cac tac ttt gag gtt gaa ggc gat gga aaa gga aag cct         96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggc gga cct        144
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att cta tca cca cag agt cag tac gga agc        192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
    50                  55                  60

ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag cag        240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80
```

```
tca ttc cct gag gga tat aca tgg gag agg atc atg aac ttc gaa gat      288
Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggt aac tgt      336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

ttc atc tac aat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga      384
Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtt atg caa aag aag aca cag ggc tgg gaa ccc aac act gag cgt      432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt atg gct ctg      480
Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

aag ttg gaa gga ggt ggt cat tat ttg tgt gaa ttc aaa tct act tac      528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

aag gca aag aag cct gtg atg atg cca ggg tat cac tat gtt gac cgc      576
Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aaa ttg gat gta acc aat cac aac aag gat tac act tcc gtt gag cag      624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                      660
Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220


<210>  42

<211>  220

<212>  PRT

<213>  Acropora nobilis


<400>  42

Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15


Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30


Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45
```

```
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
    50                  55                  60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
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<210> 43

<211> 660

<212> DNA

<213> Acropora nobilis

<220>

<221> CDS

<222> (1)..(660)

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<400>  43
tcc gtt atc gct aaa cag atg acc tac aag gtt tat atg tca ggc acg        48
Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga aag cct        96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggc gga cct       144
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att tta tca cca cag tgt cag tac gga agc       192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Ser
    50                  55                  60

ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag cag       240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc ccg gag gga ttt aca tgg gag agg atc atg aac ttt gaa gat       288
Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac tgt       336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

ttc acc tac cac gtc aag ttc tct ggt ttg gac ttt cct ccc aat ggg       384
Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asp Phe Pro Pro Asn Gly
        115                 120                 125

cct gtg atg cag aag aag aca cag ggc tgg gaa ccc cac tct gag cgt       432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu Arg
    130                 135                 140

ctc ttt gca cgg ggt gga atg ctg ata gga aac aac ttt atg gct ctg       480
Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

aag tta gaa gga ggc ggt cac tat ttg tgt gaa ttc aaa act act tac       528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr Tyr
                165                 170                 175

aag gca aag aag cct gtg aag atg cca gga tat cat tat gtt gac cgc       576
Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aaa ctg gat gta acc aat cac aac aag gat tac act tcc gtt gag cag       624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                       660
Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
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<210> 44

<211> 220

<212> PRT

<213> Acropora nobilis

<400> 44

Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1 5 10 15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
20 25 30

Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
35 40 45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Ser
50 55 60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65 70 75 80

Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
85 90 95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
100 105 110

Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asp Phe Pro Pro Asn Gly
115 120 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu Arg
130 135 140

Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145 150 155 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr Tyr
165 170 175

Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
180 185 190

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Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205


Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
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<210> 45

<211> 660

<212> DNA

<213> Acropora nobilis

<220>

<221> CDS

<222> (1)..(660)

<400> 45

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tcc gtt atc gct aaa cag atg acc tac aag gtt tat atg tca ggc acg       48
Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

gtc aat gga cac tac ttt gag gtt gaa ggc gat gga aaa gga aag cct       96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggc gga cct      144
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att cta tca cca cag agt cag tac gga agc      192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
    50                  55                  60

ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag cag      240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc cct gag gga tat aca tgg gag agg atc atg aac ttc gaa gat      288
Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggt aac tgt      336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

ttc atc tac aat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga      384
Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125
```

```
cct gtt atg caa aag aag aca cag ggc tgg gaa ccc aac act gag cgt       432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt atg gct ctg       480
Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

aag ttg gaa gga ggt ggt cat tat ttg tgt gaa ttc aaa tct act tac       528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

aag gca aag aag cct gtg atg atg cca ggg tat cac tat gtt gac cgc       576
Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aaa ttg gat gta acc aat cac aac aag gat tac act tcc gtt gag cag       624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                       660
Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220


<210>  46

<211>  220

<212>  PRT

<213>  Acropora nobilis


<400>  46

Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15


Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30


Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45


Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
    50                  55                  60


Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80


Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95
```

```
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
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<210> 47

<211> 660

<212> DNA

<213> Acropora nobilis

<220>

<221> CDS

<222> (1)..(660)

<400> 47

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tcc gtt atc gct aaa cag atg acc tac aag gtt tat atg tca ggc acg         48
Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

gtc aat gga cac tac ttt gag gtt gaa ggc gat gga aaa gga aag cct         96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30
```

```
tac gag ggg gag cag acg gta aag ctc act gtc acc gag ggc gga cct     144
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Glu Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att cta tca cca cag agt cag tac gga agc     192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
    50                  55                  60

ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag cag     240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc cct gag gga tat aca tgg gag agg atc atg aac ttc gaa gat     288
Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggt aac tgt     336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

ttc atc tac aat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga     384
Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtt atg caa aag aag aca cag ggc tgg gaa ccc aac act gag cgt     432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt atg gct ctg     480
Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

aag ttg gaa gga ggt ggt cat tat ttg tgt gaa ttc aaa tct act tac     528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

aag gca aag aag cct gtg atg atg cca ggg tat cac tat gtt gac cgc     576
Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aaa ttg gat gta acc aat cac aac aag gat tac act tcc gtt gag cag     624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                     660
Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
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<210> 48

<211> 220

<212> PRT

<213> Acropora nobilis

<400> 48

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Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Glu Gly Gly Pro
        35                  40                  45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
    50                  55                  60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220

<210>  49

<211>  660
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<212>  DNA

<213>  Millepora sp. (Hydrozoan)


<220>

<221>  CDS

<222>  (1)..(660)


<400>  49
tcc gtt atc gct aaa cag atg acc tac aag gtt tat atg tca ggc acg        48
Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

gtc aat gga cac tac ttt gag gtt gaa ggc gat gga aaa gga aag cct        96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggc gga cct       144
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att cta tca cca cag agt cag tac gga agc       192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
    50                  55                  60

ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag cag       240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc cct gag gga tat aca tgg gag agg atc atg aac ttt gaa gat       288
Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac tgt       336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

ttc atc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga       384
Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtt atg cag aag aag aca cag ggc tgg gaa ccc aac act gag cgt       432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt atg gct ctg       480
Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

aag tta gaa gga ggt ggt cac tat tta tgt gaa ttc aaa tct act tac       528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175
```

```
aag gca agg aag cct gtg aag atg cca ggg tat cac tat gtt gac cgc      576
Lys Ala Arg Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aaa ctg gat gta acc aat cac aac aag gat tac act tcc gtt gag cag      624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

cgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                      660
Arg Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
```

<210> 50

<211> 220

<212> PRT

<213> Millepora sp. (Hydrozoan)

<400> 50

```
Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
    50                  55                  60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140
```

```
Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160


Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175


Lys Ala Arg Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190


Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205


Arg Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220


<210>  51

<211>  660

<212>  DNA

<213>  Millepora sp. (Hydrozoan)



<220>

<221>  CDS

<222>  (1)..(660)



<400>  51
tcc gtt atc gct aaa cag atg acc tac aaa gtt tat atg tca ggc acg        48
Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga aag cct        96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

tac gag ggg gag cag acg gta agg ctg act gtc acc aag ggc gga cct       144
Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att tta tca cca cag tca cag tac gga agc       192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
    50                  55                  60

ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag cag       240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80
```

```
tca ttc ccg gag gga tat aca tgg gag agg atc atg aac ttt gaa gat      288
Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac tgt      336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

ttc atc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga      384
Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtt atg cag aag aag aca cag ggc tgg gaa ccc aac act gag cgt      432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt atg gct ctg      480
Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

aag tta gaa gga ggt ggt cac tat ttg tgt gaa ttc aaa tct act tac      528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

aag gca agg aag cct gtg aag atg cca ggg tat cac tat gtt gac cgc      576
Lys Ala Arg Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aaa ctg gat gta acc aat cac aac aag gat tac act tcc gtt gag cag      624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

cgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                      660
Arg Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
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<210> 52

<211> 220

<212> PRT

<213> Millepora sp. (Hydrozoan)

<400> 52

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Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45
```

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
50 55 60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65 70 75 80

Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
85 90 95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
100 105 110

Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
115 120 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
130 135 140

Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145 150 155 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
165 170 175

Lys Ala Arg Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
180 185 190

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
195 200 205

Arg Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
210 215 220

<210> 53

<211> 660

<212> DNA

<213> Millepora sp. (hydrozoan)

<220>

<221> CDS

<222> (1)..(660)

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<400>  53
tcc gtt atc gct aaa cag atg acc tac aaa gtt tat atg tca ggc acg       48
Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga aag cct       96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

tac gag ggg gag cag acg gta agg ctg act gtc acc aag ggc gga cct      144
Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att tta tca cca cag tca cag tac gga agc      192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
    50                  55                  60

ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag cag      240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc ccg gag gga tat aca tgg gag agg atc atg aac ttt gaa gat      288
Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac tgt      336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

ttc atc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga      384
Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtt atg cag aag aag aca cag ggc tgg gaa ccc aac act gag cgt      432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt atg gct ctg      480
Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

aag tta gaa gga ggt ggc cac tat ttg tgt gaa ttc aaa tct act tac      528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

aag gca agg aag cct gtg aag atg cca ggg tat cac tat gtt gac cgc      576
Lys Ala Arg Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aaa ctg gat gta acc aat cac aac aag gat tac act tcc gtt gag cag      624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

cgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                      660
Arg Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
```

<210> 54

<211> 220

<212> PRT

<213> Millepora sp. (hydrozoan)

<400> 54

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Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
    50                  55                  60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

Lys Ala Arg Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190
```

```
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205


Arg Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220


<210>  55

<211>  660

<212>  DNA

<213>  Porites Murrayensis



<220>

<221>  CDS

<222>  (1)..(660)



<400>  55
tcc gtt atc gct aaa cag atg acc tac aag gtt tat atg tca gac acg        48
Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Asp Thr
1               5                   10                  15

gtc aat gga cac tac ttt gag gtt gaa ggc gat gga aaa gga aag cct        96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggc gga cct       144
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att cta tca cca cag agt cag tac gga agc       192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
    50                  55                  60

ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag cag       240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc cct gag gga tat aca tgg gag agg atc atg aac ttc gaa gat       288
Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggt aac tgt       336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

ttc atc tac aat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga       384
Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125
```

cct gtt atg caa aag aag aca cag ggc tgg gaa ccc aac act ggg cgt 432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Gly Arg
130 135 140

ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt atg gct ctg 480
Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145 150 155 160

aag ttg gaa gga ggt ggt cat tat ttg tgt gaa ttc aaa tct act tac 528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
165 170 175

aag gca aag aag cct gtg atg atg cca ggg tat cac tat gtt gac cgc 576
Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp Arg
180 185 190

aag ttg gat gta acc aat cac aac aag gat tac act tcc gtt gag cag 624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
195 200 205

tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc 660
Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
210 215 220

<210> 56

<211> 220

<212> PRT

<213> Porites Murrayensis

<400> 56

Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Asp Thr
1 5 10 15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
20 25 30

Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
35 40 45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
50 55 60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65 70 75 80

Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
85 90 95

```
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110


Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125


Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Gly Arg
    130                 135                 140


Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160


Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175


Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190


Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205


Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220


<210>  57

<211>  660

<212>  DNA

<213>  Porites Murrayensis


<220>

<221>  CDS

<222>  (1)..(660)


<400>  57
tcc gtt atc gct aaa cag atg acc tac aag gtt tat atg tca ggc acg        48
Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

gtc aat gga cac tac ttt gag gtt gaa ggc gat gga aaa gga agg cct        96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Arg Pro
            20                  25                  30
```

```
tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggc gga cct        144
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att cta tca cca cag agt cag tac gga agc        192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
    50                  55                  60

ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag cag        240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc cct gag gga tat aca tgg gag agg atc atg aag ttt gaa gat        288
Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Lys Phe Glu Asp
                85                  90                  95

ggt gca gta tgt act gtc agc aat gat tcc agc atg caa ggc aac tgt        336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Met Gln Gly Asn Cys
            100                 105                 110

ttc atc tac aat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga        384
Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtt atg cag aag aag aca cag ggc tgg gaa ccc aac act gag cga        432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

ctt tat gca cga gat gga atg ctg ata gga aac aac ttt atg gct ctg        480
Leu Tyr Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

aag ttg gaa gga agt ggt cat tat acc tgt gaa ttc aaa tct act tac        528
Lys Leu Glu Gly Ser Gly His Tyr Thr Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

aag gca aag aag cct gtg atg atg cct gga tat cac tat gtt gac cgc        576
Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aaa ttg gat gta acc aat cac aac aag gat tac act tcc gtt gag cag        624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                        660
Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
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<210> 58

<211> 220

<212> PRT

<213> Porites Murrayensis

<400> 58

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Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Arg Pro
            20                  25                  30

Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
    50                  55                  60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Lys Phe Glu Asp
                85                  90                  95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Met Gln Gly Asn Cys
            100                 105                 110

Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

Leu Tyr Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

Lys Leu Glu Gly Ser Gly His Tyr Thr Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
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<210> 59

<211> 656

<212> DNA

<213> Porites Murrayensis

<220>

<221> CDS

<222> (1)..(507)

<400> 59

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tcc gtt atc gct aaa cag atg acc tac aag gtt tat atg tca ggc acg        48
Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

gtc aat gga cac tac ttt gag gtt gaa ggc gat gga aaa gga aag cct        96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggc gga cct       144
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att cta tca cca cag agt cag tac gga agc       192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
    50                  55                  60

ata cca ttc acc aag tac cct gag gac atc cct gac tat gta aag cag       240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc cct gag gga tat aca tgg gag agg atc gtg aac ttc gaa gat       288
Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Val Asn Phe Glu Asp
                85                  90                  95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac tgt       336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

ttc atc tac aat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga       384
Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtt atg cag aag aag aca cag ggc tgg gaa ccc aac act gag cgt       432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

ctt tat gca cgg gat gga atg ctg ata gga aac aac ttt atg gct ctg       480
Leu Tyr Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

aag ttg gaa gga ggg caa aga agc ctg tgatgatgcc agggtatcac             527
Lys Leu Glu Gly Gly Gln Arg Ser Leu
                165
```

tatgttgacc gcgaattgga tgtaaccaat cacaacaagg attacacttc cgttgagcag 587

tgtgagattt ccatcgcacg caaacctgtg gtcgcctgac gttttttcag agtcaaatca 647

aggcacaaa 656

<210> 60

<211> 169

<212> PRT

<213> Porites Murrayensis

<400> 60

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Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
    50                  55                  60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Val Asn Phe Glu Asp
                85                  90                  95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

Leu Tyr Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

Lys Leu Glu Gly Gly Gln Arg Ser Leu
                165
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<210> 61

<211> 693

<212> DNA

<213> Porites Murrayensis

<220>

<221> CDS

<222> (1)..(660)

<400> 61

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tcc gtt atc gct aaa cag atg acc tac aag gtt tat atg tca ggc acg       48
Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

gtc aat gga cac tac ttt gag gtc caa ggc gat gga aaa gga aag cct       96
Val Asn Gly His Tyr Phe Glu Val Gln Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggc gga cct      144
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att cta tca cca cag agt cag tac gga agc      192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
    50                  55                  60

ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag cag      240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc cct gag gga tat aca tgg gag agg atc atg aac ttc aaa gat      288
Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Lys Asp
                85                  90                  95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac tgt      336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

ttc atc tac aat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga      384
Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtt atg caa aag aag aca cag ggc tgg gaa ccc aac act gag cgt      432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

ctc ttt gca cga gat gga gtg ctg ata gga aac aac ttt atg gct ctg      480
Leu Phe Ala Arg Asp Gly Val Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160
```

```
aag ttg gaa gga ggt ggt cat tat ttg tgt gaa ttc aaa tct act tac        528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

aag gca aag aag cct gtg atg atg cca ggg tat cac tat gtt gac cgc        576
Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185             190

aaa ttg gat gta acc aat cac aac aag gat tac act tcc gtt gag cag        624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

tgt gag att tcc atc gca cgc aaa cct gtg gtc gcc tgacgtttt              670
Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220

tcagagtcaa atcaaggcac aaa                                              693
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<210> 62

<211> 220

<212> PRT

<213> Porites Murrayensis

<400> 62

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Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

Val Asn Gly His Tyr Phe Glu Val Gln Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
    50                  55                  60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Lys Asp
                85                  90                  95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125
```

```
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

Leu Phe Ala Arg Asp Gly Val Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220

<210>  63

<211>  660

<212>  DNA

<213>  Platygyra sp.


<220>

<221>  CDS

<222>  (1)..(660)


<400>  63
tcc gtt atc gct aaa cag atg acc tac aag gtt tat atg tca ggc acg       48
Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

gtc aat gga cac tac ttt gag gtc gaa ggc gat aga aaa gga aag cct       96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Arg Lys Gly Lys Pro
            20                  25                  30

tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggc gga cct      144
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att tta tca cca cag tgt cag tac gga aac      192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Asn
    50                  55                  60
```

ata cca ttc acc aag tac cct gaa gac gtc cct gac tat gta aag cag 240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Val Pro Asp Tyr Val Lys Gln
65 70 75 80

tca ttc ccg gag gga ttt aca tgg gag agg atc atg aac ttt gaa gat 288
Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
85 90 95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac tgt 336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
100 105 110

ttc acc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga 384
Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
115 120 125

cct gtg atg cag aag aag aca cag ggc tgg gaa ccc cac tct gag cgt 432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu Arg
130 135 140

ctc ttt gca cgg ggt gga atg ctg ata gga aac aac ttt atg gct ctg 480
Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145 150 155 160

aag tta gaa gga ggc ggt cac tat ttg tgt gga ttc aaa act act tac 528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Gly Phe Lys Thr Thr Tyr
165 170 175

aag gca aag aag cct gtg aag atg cca ggg tat cat tat gtt gac cgc 576
Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
180 185 190

aaa ctg gat gta acc aat cac aac aag gat tac att tcc gtt gag cag 624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Ile Ser Val Glu Gln
195 200 205

tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc 660
Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
210 215 220

<210> 64

<211> 220

<212> PRT

<213> Platygyra sp.

<400> 64

Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1 5 10 15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Arg Lys Gly Lys Pro
20 25 30

```
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Asn
    50                  55                  60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Val Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu Arg
    130                 135                 140

Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Gly Phe Lys Thr Thr Tyr
                165                 170                 175

Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Ile Ser Val Glu Gln
        195                 200                 205

Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
```

<210> 65

<211> 660

<212> DNA

<213> Platygyra sp.

<220>

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<221>  CDS

<222>  (1)..(660)


<400>  65
tcc gtt atc gct aaa cag atg acc tac aag gtt tat atg tca ggc acg        48
Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

gtc aat gga cac tac ttt gag gtc gaa ggc gat ggg aaa gga aag cct        96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggc gga cct       144
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att tta tca cca cag tgt cag tac gga aac       192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Asn
    50                  55                  60

ata cca ttc acc aag tac cct gaa gac gtc cct gac tat gta aag cag       240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Val Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc ccg gag gga ttt aca tgg gag agg atc atg aac ttt gaa gat       288
Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac tgt       336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

ttc acc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga       384
Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtg atg cag aag aag aca cag ggc tgg gaa ccc cac tct gag cgt       432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu Arg
    130                 135                 140

ctc ttt gca cgg ggt gga atg ctg ata gga aac aac ttt atg gct ctg       480
Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

aag tta gaa gga ggc ggt cac tat ttg tgt gga ttc aaa act act tac       528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Gly Phe Lys Thr Thr Tyr
                165                 170                 175

aag gca aag aag cct gtg aag atg cca ggg tat cat tat gtt gac cgc       576
Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aaa ctg gat gta acc aat cac aac aag gat tac att tcc gtt gag cag       624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Ile Ser Val Glu Gln
        195                 200                 205
```

```
tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                     660
Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220


<210>  66

<211>  220

<212>  PRT

<213>  Platygyra sp.



<400>  66

Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15


Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30


Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45


Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Asn
    50                  55                  60


Ile Pro Phe Thr Lys Tyr Pro Glu Asp Val Pro Asp Tyr Val Lys Gln
65                  70                  75                  80


Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95


Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110


Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125


Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu Arg
    130                 135                 140


Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160


Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Gly Phe Lys Thr Thr Tyr
                165                 170                 175
```

```
Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190


Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Ile Ser Val Glu Gln
        195                 200                 205


Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
```

<210> 67

<211> 660

<212> DNA

<213> Platygyra sp.

<220>

<221> CDS

<222> (1)..(660)

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<400> 67
tcc gtt atc gct aaa cag atg acc tac aag gtt tat atg tca ggc acg          48
Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga aag cct          96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggc gga cct         144
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att tta tca cca cag tgt cag tac gga aac         192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Asn
    50                  55                  60

ata cca ttc acc aag tac cct gaa gac gtc cct gac tat gta aag cag         240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Val Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc ccg gag gga ttt aca tgg gag agg atc atg aac ttt gaa gat         288
Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac tgt         336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110
```

```
ttc acc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga       384
Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtg atg cag aag aag aca cag ggc tgg gaa ccc cac tct gag cgt       432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu Arg
    130                 135                 140

ctc ttt gca cgg ggt gga atg ctg ata gga aac aac ttt atg gct ctg       480
Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

aag tta gaa gga ggc ggt cac tat ttg tgt gga ttc aaa act act tac       528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Gly Phe Lys Thr Thr Tyr
                165                 170                 175

aag gca aag aag cct gtg aag atg cca ggg tat cat tat gtt gac cgc       576
Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aaa ctg gat gta acc aat cac aac aag gat tac att tcc gtt gag cag       624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Ile Ser Val Glu Gln
        195                 200                 205

tgt gaa act tcc att gca cgc aaa cct gtg gtc gcc                       660
Cys Glu Thr Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
```

<210> 68

<211> 220

<212> PRT

<213> Platygyra sp.

<400> 68

```
Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Asn
    50                  55                  60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Val Pro Asp Tyr Val Lys Gln
65                  70                  75                  80
```

```
Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu Arg
    130                 135                 140

Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Gly Phe Lys Thr Thr Tyr
                165                 170                 175

Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Ile Ser Val Glu Gln
        195                 200                 205

Cys Glu Thr Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220

<210>  69

<211>  623

<212>  DNA

<213>  Platygyra sp.


<220>

<221>  CDS

<222>  (1)..(621)


<400>  69
tcc gtt atc gct aaa cag atg acc tac aag gtt tat atg tca ggc acg        48
Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15
```

```
gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga aag cct        96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggc gga cct       144
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att tta tca cca cgg tgt cag tac gga aac       192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Arg Cys Gln Tyr Gly Asn
    50                  55                  60

ata cca ttc acc aag tac cct gaa gac gtc cct gac tat gta aag cag       240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Val Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc ccg gag gga ttt aca tgg gag agg atc atg aac ttt gaa gat       288
Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac tgt       336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

ttc acc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga       384
Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtg atg cag aag aag aca cgg ggc tgg gaa ccc cac tct gag cgt       432
Pro Val Met Gln Lys Lys Thr Arg Gly Trp Glu Pro His Ser Glu Arg
    130                 135                 140

ctc ttt gca cgg ggt gga atg ctg ata gga aac aac ttt atg gct ctg       480
Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

aag ttg gaa gga ggg caa aga agc ctg tga aga tgc cag ggt atc att       528
Lys Leu Glu Gly Gly Gln Arg Ser Leu     Arg Cys Gln Gly Ile Ile
                165                     170                 175

atg ttg acc gca aac tgg atg taa cca atc aca aca agg att aca ttt       576
Met Leu Thr Ala Asn Trp Met     Pro Ile Thr Thr Arg Ile Thr Phe
                180                     185                 190

ccg ttg agc agt gtg aaa ttt cca ttg cac gca aac ctg tgg tcg cc        623
Pro Leu Ser Ser Val Lys Phe Pro Leu His Ala Asn Leu Trp Ser
                195                 200                 205
```

<210> 70

<211> 169

<212> PRT

<213> Platygyra sp.

<400> 70

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Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Arg Cys Gln Tyr Gly Asn
    50                  55                  60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Val Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

Pro Val Met Gln Lys Lys Thr Arg Gly Trp Glu Pro His Ser Glu Arg
    130                 135                 140

Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

Lys Leu Glu Gly Gly Gln Arg Ser Leu
                165
```

<210> 71

<211> 13

<212> PRT

<213> Platygyra sp.

<400> 71

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Arg Cys Gln Gly Ile Ile Met Leu Thr Ala Asn Trp Met
1               5                   10
```

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<210>  72

<211>  23

<212>  PRT

<213>  Platygyra sp.


<400>  72

Pro Ile Thr Thr Arg Ile Thr Phe Pro Leu Ser Ser Val Lys Phe Pro
1               5                   10                  15


Leu His Ala Asn Leu Trp Ser
            20


<210>  73

<211>  660

<212>  DNA

<213>  Platygyra sp.


<220>

<221>  CDS

<222>  (1)..(660)


<400>  73
tcc gtt atc gct aaa cag atg acc tac aag gtt tat atg tca ggc acg       48
Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

gtc aat gga cac tac ttt gag gtt gaa ggc gat gga aaa gga aag cct       96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggc gga cct      144
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att cta tca cca cag agt cag tac gga agc      192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
    50                  55                  60

ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag cag      240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80
```

tca ttc cct gag gga tat aca tgg gag agg atc atg aac ttc gaa gat 288
Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
85 90 95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggt aac tgt 336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
100 105 110

ttc atc tac aat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga 384
Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
115 120 125

cct gtt atg caa aag aag aca cag ggc tgg gaa ccc aac act gag cgt 432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
130 135 140

ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt atg gct ctg 480
Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145 150 155 160

aag ttg gaa gga ggt ggt cat tat ttg tgt gaa ttc aaa tct act tac 528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
165 170 175

aag gca aag aag cct gtg atg atg cca ggg tat cac tat gtt gac cgc 576
Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp Arg
180 185 190

aaa ttg gat gta acc aat cac aac aag gat tac act tcc gtt gag cag 624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
195 200 205

tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc 660
Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
210 215 220

<210> 74

<211> 220

<212> PRT

<213> Platygyra sp.

<400> 74

Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1 5 10 15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
20 25 30

Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
35 40 45

```
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
    50                  55                  60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
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<210> 75

<211> 660

<212> DNA

<213> Platygyra sp.

<220>

<221> CDS

<222> (1)..(660)

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<400>  75
tcc gtt atc gct aaa cag atg acc tac aag gtt tat atg tca ggc acg          48
Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

gtc aat gga cac tac ttt gag gtt gaa ggc gat gga aaa gga aag cct          96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggc gga cct         144
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att cta tca cca cag agt cag tac gga agc         192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
    50                  55                  60

ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag cag         240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc cct gag gga tat aca tgg gag agg atc atg aac ttc gaa gat         288
Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggt agc tgt         336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Ser Cys
            100                 105                 110

ttc atc tac aat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga         384
Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtt atg caa aag aag aca cag ggc tgg gaa ccc aac act gag cgt         432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt atg gct ctg         480
Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

aag ttg gaa gga ggt ggt cat tat ttg tgt gaa ttc aaa tct act tac         528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

aag gca aag aag cct gtg atg atg cca ggg tat cac tat gtt gac cgc         576
Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aaa ttg gat gta acc aat cac aac aag gat tac act tcc gtt gag cag         624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

tgt gga att tcc att gca cgc aaa cct gtg gtc gcc                         660
Cys Gly Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
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<210> 76

<211> 220

<212> PRT

<213> Platygyra sp.

<400> 76

Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1 5 10 15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
20 25 30

Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
35 40 45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
50 55 60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65 70 75 80

Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
85 90 95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Ser Cys
100 105 110

Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
115 120 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
130 135 140

Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145 150 155 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
165 170 175

Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp Arg
180 185 190

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
195 200 205

Cys Gly Ile Ser Ile Ala Arg Lys Pro Val Val Ala
210 215 220

<210> 77

<211> 660

<212> DNA

<213> Pavona decussaca

<220>

<221> CDS

<222> (1)..(660)

<400> 77
tcc gtt atc gct aaa cag atg acc tac aag gtt aat atg tca ggc acg 48
Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Asn Met Ser Gly Thr
1 5 10 15

gtc aat gga cac tac ttt gag gtt gaa ggc gat gga aaa gga aag cct 96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
20 25 30

tac gag ggg gag cag acg gta aag ctc act gtc acc gag ggc gga cct 144
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Glu Gly Gly Pro
35 40 45

ctg cca ttt gct tgg gat att cta tca cca cag agt cag tac gga agc 192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
50 55 60

gta cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag cag 240
Val Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65 70 75 80

tca ttc cct gag gga tat aca tgg gag agg atc atg aac ttc gaa gat 288
Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
85 90 95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggt aac tgt 336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
100 105 110

ttc atc tac aat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga 384
Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
115 120 125

```
cct gtt atg caa aag aag aca cag ggc tgg gta ccc aac act gag cgt        432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Val Pro Asn Thr Glu Arg
    130                 135                 140

ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt atg gct ctg        480
Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

aag ttg gaa gga ggt ggt cat tat ttg tgt gaa ttc aaa tct act tac        528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

aag gca aag aag cct gtg atg atg cca ggg tat cac tat gtt gac cgc        576
Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aaa ttg gat gta acc aat cac aac aag gat tac act tcc gtt gag cag        624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                        660
Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
```

```
<210>  78

<211>  220

<212>  PRT

<213>  Pavona decussaca


<400>  78

Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Asn Met Ser Gly Thr
1               5                   10                  15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Glu Gly Gly Pro
        35                  40                  45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
    50                  55                  60

Val Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95
```

```
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110


Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125


Pro Val Met Gln Lys Lys Thr Gln Gly Trp Val Pro Asn Thr Glu Arg
    130                 135                 140


Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160


Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175


Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190


Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205


Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220


<210>  79

<211>  660

<212>  DNA

<213>  Pavona decussaca



<220>

<221>  CDS

<222>  (1)..(660)



<400>  79
tcc gtt atc gct aaa cag atg acc tac aag gtt tat atg tca ggc acg        48
Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga aag cct        96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30
```

```
tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggc gga cct         144
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att tta tca cca cag tgt cag tac gga agc         192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Ser
    50                  55                  60

ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag cag         240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc ccg gag gga ttt aca tgg gag agg atc atg aac ttt gaa gat         288
Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac tgt         336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

ttc acc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat ggg         384
Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtg atg cag aag aag aca cag ggc tgg gaa ccc cac tct gag cgt         432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu Arg
    130                 135                 140

ctc ttt gca cgg ggt gga atg ctg ata gga aac aac ttt atg gct ccg         480
Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala Pro
145                 150                 155                 160

aag tta gaa gga ggc ggt cac tat ttg tgt gaa ttc aaa act act tac         528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr Tyr
                165                 170                 175

aag gca aag aag cct gtg aag atg ccg ggg tat cat tat gtt gac cgc         576
Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aaa ctg gat gta acc aat cac aac aag gat tac act tcc gtt gag cag         624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

tgt gaa atc tcc att gca cgc aaa cct gtg gtc gcc                         660
Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
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<210> 80

<211> 220

<212> PRT

<213> Pavona decussaca

<400> 80

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Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Ser
    50                  55                  60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu Arg
    130                 135                 140

Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala Pro
145                 150                 155                 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr Tyr
                165                 170                 175

Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
```

<210> 81

<211> 660

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<212>  DNA

<213>  Pavona decussaca


<220>

<221>  CDS

<222>  (1)..(660)


<400>  81
tcc gtt atc gct aaa cag atg acc tac aag gtt tat atg tca ggc acg       48
Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

gtc aat gga cac tac ttt gag gtt gaa ggc gat gga aaa gga aag cct       96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

tac gag ggg gag cag acg gta aag ctc act gtc acc gag ggc gga cct      144
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Glu Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att cta tca cca cag agt cag tac gga agc      192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
    50                  55                  60

gta cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag cag      240
Val Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc ccg gag gga tat aca tgg gag agg atc atg aac ttt gaa gat      288
Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac tgt      336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

ttc atc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga      384
Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtt atg cag aag aag aca cag ggc tgg gaa ccc aac act gag cgt      432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

ctc tct gca cga gat gga atg cta ata gga aac aac ttt atg gct ctg      480
Leu Ser Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

aag tta gaa gga ggt ggt cac tat ttg tgt gaa ttc aaa tct act tac      528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175
```

```
aag gca agg aag cct gtg aag atg cca ggg tat cac tat gtt gac cgc          576
Lys Ala Arg Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aaa ctg gat gta acc aat cac aac aag gat tac act tcc gtt gag cag          624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

cgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                          660
Arg Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220


<210>  82

<211>  220

<212>  PRT

<213>  Pavona decussaca



<400>  82

Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15


Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30


Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Glu Gly Gly Pro
        35                  40                  45


Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
    50                  55                  60


Val Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80


Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95


Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110


Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125


Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140
```

```
Leu Ser Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

Lys Ala Arg Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

Arg Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220

<210>  83

<211>  600

<212>  DNA

<213>  Montipora sp.


<220>

<221>  CDS

<222>  (1)..(600)


<400>  83
tcc gtt atc gct aaa cag atg acc tac aag gtt tat atg tca ggc acg        48
Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

gtc aat gga cac ctc act gtc acc aag ggc gga cct ctg cca ttt gct        96
Val Asn Gly His Leu Thr Val Thr Lys Gly Gly Pro Leu Pro Phe Ala
            20                  25                  30

tgg gat att cta tca cca cag agt cag tac gga agc ata cca ttc acc       144
Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser Ile Pro Phe Thr
        35                  40                  45

aag tac cct gaa gac atc cct gac tat gta aag cag tca ttc cct gag       192
Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln Ser Phe Pro Glu
    50                  55                  60

gga tat aca tgg gag agg atc atg aac ttc gaa gat ggt gca gtg tgt       240
Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp Gly Ala Val Cys
65                  70                  75                  80
```

```
act gtc agc aat gat tcc agc atc caa ggt aac tgt ttc atc tac aat         288
Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys Phe Ile Tyr Asn
                85                  90                  95

gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga cct gtt atg caa         336
Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly Pro Val Met Gln
            100                 105                 110

aag aag aca cag ggc tgg gaa ccc aac act gag cgt ctc ttt gca cga         384
Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg Leu Phe Ala Arg
        115                 120                 125

gat gga atg ctg ata gga aac aac ttt atg gct ctg aag ttg gaa gga         432
Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu Lys Leu Glu Gly
    130                 135                 140

ggt ggt cat tat ttg tgt gaa ttc aaa tct act tac aag gca aag aag         480
Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr Lys Ala Lys Lys
145                 150                 155                 160

cct gtg atg atg cca ggg tat cac tat gtt gac cgc aaa ttg gat gta         528
Pro Val Met Met Pro Gly Tyr His Tyr Val Asp Arg Lys Leu Asp Val
                165                 170                 175

acc aat cac aac aag gat tac act tcc gtt gag cag tgt gaa att ccc         576
Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln Cys Glu Ile Pro
            180                 185                 190

att gca cgc aaa cct gtg gtc gcc                                         600
Ile Ala Arg Lys Pro Val Val Ala
        195                 200


<210>  84

<211>  200

<212>  PRT

<213>  Montipora sp.


<400>  84

Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15


Val Asn Gly His Leu Thr Val Thr Lys Gly Gly Pro Leu Pro Phe Ala
            20                  25                  30


Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser Ile Pro Phe Thr
        35                  40                  45


Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln Ser Phe Pro Glu
    50                  55                  60
```

```
Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp Gly Ala Val Cys
65                  70                  75                  80

Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys Phe Ile Tyr Asn
                85                  90                  95

Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly Pro Val Met Gln
            100                 105                 110

Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg Leu Phe Ala Arg
        115                 120                 125

Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu Lys Leu Glu Gly
    130                 135                 140

Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr Lys Ala Lys Lys
145                 150                 155                 160

Pro Val Met Met Pro Gly Tyr His Tyr Val Asp Arg Lys Leu Asp Val
                165                 170                 175

Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln Cys Glu Ile Pro
            180                 185                 190

Ile Ala Arg Lys Pro Val Val Ala
        195                 200

<210>  85

<211>  660

<212>  DNA

<213>  Montipora sp.


<220>

<221>  CDS

<222>  (1)..(660)


<400>  85
tcc gtt atc gct aaa cag atg acc tac aag gtt tat atg tca ggc acg         48
Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15
```

```
gtc aat gga cac tac ttt gag gtt gaa ggc gat gga aaa gga aag cct           96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggc gga cct          144
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att cta tca cca cag agt cag tac gga agc          192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
    50                  55                  60

ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag cag          240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc cct gag gga tat aca tgg gag agg atc atg aac ttc gaa gat          288
Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggt aac tgt          336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

ttc atc tac aat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga          384
Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtt atg caa aag aag aca cag ggc tgg gaa ccc aac act gag cgt          432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt atg gct ctg          480
Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

aag ttg gaa gga ggt ggt cat tat ttg tgt gaa ttc aaa tct act tac          528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

aag gca aag aag cct gtg atg atg cca ggg tat cac tat gtt gac cgc          576
Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aaa ttg gat gta acc aat cac aac aag gat tac act tcc gtt gag cag          624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                          660
Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
```

<210> 86

<211> 220

<212> PRT

<213> Montipora sp.

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<400>  86

Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
    50                  55                  60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
```

<210> 87

<211> 660

<212> DNA

<213> Montipora sp.

<220>

<221> CDS

<222> (1)..(660)

<400> 87

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tcc gtt atc gct aaa cag atg acc tac aag gtt tat atg tca ggc acg         48
Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

gtc aat gga cac tac ttt gag gtt gaa ggc gat gga aaa gga aag cct         96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggc gga cct        144
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att cta tca cca cag agt cag tac gga agc        192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
    50                  55                  60

ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag cag        240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc cct gag gga tat aca tgg gag agg atc atg aac ttc gaa gat        288
Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggt aac tgt        336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

ttc atc tac aat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga        384
Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtt atg caa aag aag aca cag ggc tgg gaa ccc aac act gag cgt        432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt atg gct ctg        480
Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160
```

```
aag ttg gaa gga ggt ggt cat tat ttg tgt gaa ttc aaa tct act tac     528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

aag gca aag aag cct gtg atg atg cca ggg tat cac tat gtt gac cgc     576
Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aaa ttg gat gta acc aat cac aac aag gat tac act tcc gtt gag cag     624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                     660
Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
```

```
<210>  88

<211>  220

<212>  PRT

<213>  Montipora sp.


<400>  88

Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15


Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30


Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45


Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
    50                  55                  60


Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80


Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95


Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110


Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125
```

```
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140


Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160


Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175


Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190


Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205


Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220


<210>  89

<211>  765

<212>  DNA

<213>  Acropora aspera



<220>

<221>  CDS

<222>  (1)..(765)



<400>  89
gcg acc aca ggt ttg cgt gta atg gac atc agc atc tct ttc acg gaa        48
Ala Thr Thr Gly Leu Arg Val Met Asp Ile Ser Ile Ser Phe Thr Glu
1               5                   10                  15

gga gct act taa gaa acg ttt gcg aat cgt tgt tct gcg cta ctt att        96
Gly Ala Thr     Glu Thr Phe Ala Asn Arg Cys Ser Ala Leu Leu Ile
                20                  25                  30

ctc aat atg agt gtg atc gct aca caa atg acc tac aag gtt tat atg       144
Leu Asn Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met
            35                  40                  45

tca ggc acg gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa       192
Ser Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys
        50                  55                  60
```

```
gga aag cct tac gag ggg gag cag acg gta agg ctg gct gtc acc aag       240
Gly Lys Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Ala Val Thr Lys
    65                  70                  75

ggc gga cct ctg cca ttt gct tgg gat att tta tca cca cag tgt cag       288
Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln
80                  85                  90                  95

tac gga agc ata cca ttc acc aag tac cct gaa gac atc cct gac tat       336
Tyr Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr
            100                 105                 110

gta aag cag tca ttc ccg gag gga ttt aca tgg gag agg atc atg aac       384
Val Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn
        115                 120                 125

ttt gaa gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa       432
Phe Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln
    130                 135                 140

ggc aac tgt ttc atc tac cat gtc aag ttc tct ggt ttg aac ttt cct       480
Gly Asn Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro
    145                 150                 155

ccc aat gga cct gtt atg cag aag aag aca cag ggc tgg gaa ccc cac       528
Pro Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His
160                 165                 170                 175

tct gag cgt ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt       576
Ser Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe
                180                 185                 190

atg gct ctg aag tta gaa gga ggc ggt cac tat ttg tgt gaa ttc aaa       624
Met Ala Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys
            195                 200                 205

act act tac aag gca aag aag cct gtg aag atg cca ggg tat cat tat       672
Thr Thr Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr
        210                 215                 220

gtt gac cgc aaa ctg gat gta acc aat cac aac aag gat tac act tcc       720
Val Asp Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser
    225                 230                 235

gtt gag cag tgt gaa att tcc att aca cgc aaa cct gtg gtc gcc           765
Val Glu Gln Cys Glu Ile Ser Ile Thr Arg Lys Pro Val Val Ala
240                 245                 250
```

<210> 90

<211> 19

<212> PRT

<213> Acropora aspera

<400> 90

Ala Thr Thr Gly Leu Arg Val Met Asp Ile Ser Ile Ser Phe Thr Glu
1   5   10   15

Gly Ala Thr

<210> 91

<211> 235

<212> PRT

<213> Acropora aspera

<400> 91

Glu Thr Phe Ala Asn Arg Cys Ser Ala Leu Leu Ile Leu Asn Met Ser
1   5   10   15

Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr Val
            20   25   30

Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro Tyr
        35   40   45

Glu Gly Glu Gln Thr Val Arg Leu Ala Val Thr Lys Gly Gly Pro Leu
    50   55   60

Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Ser Ile
65   70   75   80

Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln Ser
                85   90   95

Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu Asp Gly
            100   105   110

Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys Phe
        115   120   125

Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly Pro
    130   135   140

Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu Arg Leu
145   150   155   160

```
Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu Lys
                165                 170                 175

Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr Tyr Lys
            180                 185                 190

Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg Lys
        195                 200                 205

Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln Cys
    210                 215                 220

Glu Ile Ser Ile Thr Arg Lys Pro Val Val Ala
225                 230                 235

<210>  92

<211>  765

<212>  DNA

<213>  Acropora aspera


<220>

<221>  CDS

<222>  (1)..(765)


<400>  92
gcg acc aca ggt ttg cgt gta atg gac atc agc atc tct ttc acg gaa       48
Ala Thr Thr Gly Leu Arg Val Met Asp Ile Ser Ile Ser Phe Thr Glu
1               5                   10                  15

gga gct act taa gaa acg ttt gcg aat cgt tgt tct gcg cta ctt att       96
Gly Ala Thr     Glu Thr Phe Ala Asn Arg Cys Ser Ala Leu Leu Ile
                20                  25                  30

ctc aat atg agt gtg atc gct aca caa atg acc tac aag gtt tat atg      144
Leu Asn Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met
            35                  40                  45

tca ggc acg gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa      192
Ser Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys
        50                  55                  60

gga aag cct tac gag ggg gag cag acg gta agg ctg gct gtc acc aag      240
Gly Lys Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Ala Val Thr Lys
    65                  70                  75
```

```
ggc gga cct ctg cca ttt gct tgg gat att tta tca cca cag tgt cag       288
Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln
80                  85                  90                  95

tac gga agc ata cca ttc acc aag tac cct gaa gac atc cct gac tat       336
Tyr Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr
                100                 105                 110

gta aag cag tca ttc ccg gag gga ttt aca tgg gag agg atc atg aac       384
Val Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn
            115                 120                 125

ttt gaa gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa       432
Phe Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln
        130                 135                 140

ggc aac tgt ttc atc tac cat gtc aag ttc tct ggt ttg aac ttt cct       480
Gly Asn Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro
    145                 150                 155

ccc aat gga cct gtt atg cag aag aag aca cag ggc tgg gaa ccc cac       528
Pro Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His
160                 165                 170                 175

tct gag cgt ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt       576
Ser Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe
                180                 185                 190

atg gct ctg aag tta gaa gga ggc ggt cac tat ttg tgt gaa ttc aaa       624
Met Ala Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys
            195                 200                 205

act act tac aag gca aag aag cct gtg aag atg cca ggg tat cat tat       672
Thr Thr Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr
        210                 215                 220

gtt gac cgc aaa ctg gat gta acc aat cac aac aag gat tac act tcc       720
Val Asp Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser
    225                 230                 235

gtt gag cag tgt gaa att tcc att aca cgc aaa cct gtg gtc gcc           765
Val Glu Gln Cys Glu Ile Ser Ile Thr Arg Lys Pro Val Val Ala
240                 245                 250


<210>  93

<211>  19

<212>  PRT

<213>  Acropora aspera


<400>  93

Ala Thr Thr Gly Leu Arg Val Met Asp Ile Ser Ile Ser Phe Thr Glu
1               5                   10                  15
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```
Gly Ala Thr


<210>  94

<211>  235

<212>  PRT

<213>  Acropora aspera


<400>  94

Glu Thr Phe Ala Asn Arg Cys Ser Ala Leu Leu Ile Leu Asn Met Ser
1               5                   10                  15

Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr Val
                20                  25                  30

Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro Tyr
            35                  40                  45

Glu Gly Glu Gln Thr Val Arg Leu Ala Val Thr Lys Gly Gly Pro Leu
        50                  55                  60

Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Ser Ile
65                  70                  75                  80

Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln Ser
                85                  90                  95

Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu Asp Gly
            100                 105                 110

Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys Phe
        115                 120                 125

Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly Pro
    130                 135                 140

Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu Arg Leu
145                 150                 155                 160

Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu Lys
                165                 170                 175
```

```
Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr Tyr Lys
            180                 185                 190


Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg Lys
        195                 200                 205


Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln Cys
    210                 215                 220


Glu Ile Ser Ile Thr Arg Lys Pro Val Val Ala
225                 230                 235


<210>  95

<211>  660

<212>  DNA

<213>  Acropora aspera



<220>

<221>  CDS

<222>  (1)..(660)



<400>  95
agt ggg atc gct aca caa atg acc tac aag gtt tat atg tca ggc acg       48
Ser Gly Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga aag cct       96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

tac gag ggg gag cag acg gta agg ctg gct gtc acc aag ggc gga cct      144
Tyr Glu Gly Glu Gln Thr Val Arg Leu Ala Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att tta tca cca cag tgt cag tac gga agc      192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Ser
    50                  55                  60

ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag cag      240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc ccg gag gga ttt aca tgg gag agg atc atg aac ttt gaa gat      288
Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95
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ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac tgt 336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
100 105 110

ttc atc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga 384
Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
115 120 125

cct gtt atg cag aag aag aca cag ggc tgg gaa ccc cac tct gag cgt 432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu Arg
130 135 140

ctc ttt gca cga gac gga atg ctg ata gga aac aac ttt atg gct ctg 480
Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145 150 155 160

aag tta gaa gga ggc ggt cac tat ttg tgt gaa ttc aaa act act tac 528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr Tyr
165 170 175

aag gca aag aag cct gtg aag atg cca ggg tat cat tat gtt gac cgc 576
Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
180 185 190

aaa ctg gat gta atc aat cac aac aag gat tac act tcc gtt gag cag 624
Lys Leu Asp Val Ile Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
195 200 205

tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc 660
Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
210 215 220

<210> 96

<211> 220

<212> PRT

<213> Acropora aspera

<400> 96

Ser Gly Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1 5 10 15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
20 25 30

Tyr Glu Gly Glu Gln Thr Val Arg Leu Ala Val Thr Lys Gly Gly Pro
35 40 45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Ser
50 55 60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65 70 75 80

Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
85 90 95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
100 105 110

Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
115 120 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu Arg
130 135 140

Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145 150 155 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr Tyr
165 170 175

Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
180 185 190

Lys Leu Asp Val Ile Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
195 200 205

Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
210 215 220

<210> 97

<211> 660

<212> DNA

<213> Acropora aspera

<220>

<221> CDS

<222> (1)..(660)

<400> 97

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agt gtg atc gct aca caa atg acc tac aag gtt tat atg tca ggc acg       48
Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga aag cct       96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

tac gag ggg gag cag acg gta agg ctg gct gtc acc aag ggc gga cct      144
Tyr Glu Gly Glu Gln Thr Val Arg Leu Ala Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg cca ttt gcc tgg gat att tta tca cca cag tgt cag tac gga agc      192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Ser
    50                  55                  60

ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag cag      240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc ccg gag gga ttt aca tgg gag agg atc atg aac ttt gaa gat      288
Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac tgt      336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

ttc atc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga      384
Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtt atg cag aag aag aca cag ggc tgg gaa ccc cac tct gag cgt      432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu Arg
    130                 135                 140

ctc ttt gca cga gac gga atg ctg ata gga aac aac ttt atg gct ctg      480
Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

aag tta gaa gga ggc ggt cac tat ttg tgt gaa ttc aaa act act tac      528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr Tyr
                165                 170                 175

aag gca aag aag cct gtg aag atg cca ggg tat cat tat gtt gac cgc      576
Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aaa ctg gat gta atc aat cac aac aag gat tac act tcc gtt gag cag      624
Lys Leu Asp Val Ile Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

tgt gaa att tcc att gca cgc aac cct gtg gtc gcc                      660
Cys Glu Ile Ser Ile Ala Arg Asn Pro Val Val Ala
    210                 215                 220
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<210> 98

<211> 220

<212> PRT

<213> Acropora aspera

<400> 98

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Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

Tyr Glu Gly Glu Gln Thr Val Arg Leu Ala Val Thr Lys Gly Gly Pro
        35                  40                  45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Ser
    50                  55                  60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu Arg
    130                 135                 140

Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr Tyr
                165                 170                 175

Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

Lys Leu Asp Val Ile Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205
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Cys Glu Ile Ser Ile Ala Arg Asn Pro Val Val Ala
210 215 220

<210> 99

<211> 663

<212> DNA

<213> Acropora aspera

<220>

<221> CDS

<222> (1)..(663)

<400> 99
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Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1 5 10 15

acg gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga aag 96
Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
20 25 30

cct tac gag ggg gag cag acg gta agg ctg gct gtc acc aag ggc gga 144
Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Ala Val Thr Lys Gly Gly
35 40 45

cct ctg cca ttt gct tgg gat att tta tca cca cag tgt cag tac gga 192
Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly
50 55 60

agc ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag 240
Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65 70 75 80

cag tca ttc ccg gag gga ttt aca tgg gag agg atc atg aac ttt gaa 288
Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu
85 90 95

gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac 336
Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
100 105 110

tgt ttc atc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat 384
Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
115 120 125

gga cct gtt atg cag aag aag aca cag ggc tgg gaa ccc cac tct gag 432
Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu
130 135 140

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cgt ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt atg gct         480
Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160

ctg aag tta gaa gga ggc ggt cac tat ttg tgt gaa ttc aaa act act         528
Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr
                165                 170                 175

tac aag gca aag aag cct gtg aag atg cca ggg tat cat tat gtt gac         576
Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190

cgc aaa ctg gat gta acc aat cac aac aag gat tac act tcc gtt gag         624
Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
        195                 200                 205

cag tgt gaa att tcc att aca cgc aaa cct gtg gtc gcc                     663
Gln Cys Glu Ile Ser Ile Thr Arg Lys Pro Val Val Ala
    210                 215                 220
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<210> 100

<211> 221

<212> PRT

<213> Acropora aspera

<400> 100

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Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15

Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30

Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Ala Val Thr Lys Gly Gly
        35                  40                  45

Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly
    50                  55                  60

Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80

Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110
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Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
115 120 125

Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu
130 135 140

Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145 150 155 160

Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr
165 170 175

Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
180 185 190

Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
195 200 205

Gln Cys Glu Ile Ser Ile Thr Arg Lys Pro Val Val Ala
210 215 220

<210> 101

<211> 663

<212> DNA

<213> Acropora aspera

<220>

<221> CDS

<222> (1)..(663)

<400> 101
atg agt gtg atc gct aca caa atg acc tac aag gtt tat atg tca ggc 48
Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1 5 10 15

acg gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga aag 96
Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
20 25 30

cct tac gag ggg gag cag acg gta agg ctg gct gtc acc aag ggc gga 144
Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Ala Val Thr Lys Gly Gly
35 40 45

cct ctg cca ttt gct tgg gat att tta tca cca cag tgt cag tac gga 192
Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly
50 55 60

agc ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag 240
Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65 70 75 80

cag tca ttc ccg gag gga ttt aca tgg gag agg atc atg aac ttt gaa 288
Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu
85 90 95

gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac 336
Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
100 105 110

tgt ttc atc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat 384
Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
115 120 125

gga cct gtt atg cag aag aag aca cag ggc tgg gaa ccc cac tct gag 432
Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu
130 135 140

cgt ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt atg gct 480
Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145 150 155 160

ctg aag tta gaa gga ggc ggt cac tat ttg tgt gaa ttc aaa act act 528
Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr
165 170 175

tac aag gca aag aag cct gtg aag atg cca ggg tat cat tat gtt gac 576
Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
180 185 190

cgc aaa ctg gat gta acc aat cac aac aag gat tac act tcc gtt gag 624
Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
195 200 205

cag tgt gaa att tcc att aca cgc aaa cct gtg gtc gcc 663
Gln Cys Glu Ile Ser Ile Thr Arg Lys Pro Val Val Ala
210 215 220

<210> 102

<211> 221

<212> PRT

<213> Acropora aspera

<400> 102

Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1 5 10 15

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Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30

Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Ala Val Thr Lys Gly Gly
        35                  40                  45

Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly
    50                  55                  60

Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80

Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110

Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125

Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu
    130                 135                 140

Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160

Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr
                165                 170                 175

Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190

Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
        195                 200                 205

Gln Cys Glu Ile Ser Ile Thr Arg Lys Pro Val Val Ala
    210                 215                 220
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<210> 103

<211> 663

<212> DNA

<213> Acanthastrea sp.

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<220>

<221>  CDS

<222>  (1)..(663)


<400>  103
atg agt gtg atc gct aca caa atg acc tac aag gtt tat atg tca ggc         48
Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15

acg gcc aat gga cac tac ttt gag gtt gaa ggc gat gga aaa gga aag         96
Thr Ala Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30

cct tac gaa ggg gag cag acg gta agg ctc att gtc aca aag ggc gga        144
Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Ile Val Thr Lys Gly Gly
        35                  40                  45

cct ctg cca ttt gct tga gat att tta tca cca cag tat cag tac gga        192
Pro Leu Pro Phe Ala     Asp Ile Leu Ser Pro Gln Tyr Gln Tyr Gly
    50                  55                  60

agc ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag        240
Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
    65                  70                  75

cag tca ttc ccg gaa gga tat aca tgg gag agg atc atg aac ttt gaa        288
Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu
80                  85                  90                  95

gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac        336
Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
                100                 105                 110

tgt ttc atc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat        384
Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
            115                 120                 125

gga cct gtg atg cag aag aag aca cag ggc tgg gaa ccc aac act gag        432
Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
        130                 135                 140

cgt ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt atg gct        480
Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
    145                 150                 155

ctg aag tta gaa gga ggc ggt cac tat ttg tgt gaa ttc aaa tct act        528
Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr
160                 165                 170                 175

tac aag gca aag aag cct gtg aag atg cca ggg tat cac tat gtt gac        576
Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
                180                 185                 190
```

```
cgc aaa ctg gat gta acc aat cac aac aag gat tac act tcc gtt gag        624
Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
            195                 200                 205

cag tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                    663
Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
        210                 215                 220
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<210> 104

<211> 53

<212> PRT

<213> Acanthastrea sp.

<400> 104

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Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15

Thr Ala Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30

Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Ile Val Thr Lys Gly Gly
        35                  40                  45

Pro Leu Pro Phe Ala
    50
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<210> 105

<211> 167

<212> PRT

<213> Acanthastrea sp.

<400> 105

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Asp Ile Leu Ser Pro Gln Tyr Gln Tyr Gly Ser Ile Pro Phe Thr Lys
1               5                   10                  15

Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln Ser Phe Pro Glu Gly
            20                  25                  30

Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp Gly Ala Val Cys Thr
        35                  40                  45
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```
Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys Phe Ile Tyr His Val
    50                  55                  60


Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly Pro Val Met Gln Lys
65                  70                  75                  80


Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg Leu Phe Ala Arg Asp
                85                  90                  95


Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu Lys Leu Glu Gly Gly
            100                 105                 110


Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr Lys Ala Lys Lys Pro
        115                 120                 125


Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg Lys Leu Asp Val Thr
    130                 135                 140


Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln Cys Glu Ile Ser Ile
145                 150                 155                 160


Ala Arg Lys Pro Val Val Ala
                165


<210>  106

<211>  663

<212>  DNA

<213>  Acanthastrea sp.


<220>

<221>  CDS

<222>  (1)..(663)


<400>  106
atg agt gtg atc gct aca caa atg acc tac aag gtt tat atg tca ggc       48
Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15

acg gcc aat gga cac tac ttt gag gtt gaa ggc gat gga aaa gga aag       96
Thr Ala Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30
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```
cct tac gaa ggg gag cag acg gta agg ctc att gtc aca aag ggc gga         144
Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Ile Val Thr Lys Gly Gly
        35                  40                  45

cct ctg cca ttt gct tga gat att tta tca cca cag tat cag tac gga         192
Pro Leu Pro Phe Ala     Asp Ile Leu Ser Pro Gln Tyr Gln Tyr Gly
    50                      55                  60

agc ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag         240
Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
    65                  70                  75

cag tca ttc ccg gaa gga tat aca tgg gag agg atc atg aac ttt gaa         288
Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu
80                  85                  90                  95

gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac         336
Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
                100                 105                 110

tgt ttc atc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat         384
Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
            115                 120                 125

gga cct gtg atg cag aag aag aca cag ggc tgg gaa ccc aac act gag         432
Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
        130                 135                 140

cgt ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt atg gct         480
Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
    145                 150                 155

ctg aag tta gaa gga ggc ggt cac tat ttg tgt gaa ttc aaa tct act         528
Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr
160                 165                 170                 175

tac aag gca aag aag cct gtg aag atg cca ggg tat cac tat gtt gac         576
Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
                180                 185                 190

cgc aaa ctg gat gta acc aat cac aac aag gat tac act tcc gtt gag         624
Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
            195                 200                 205

cag tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                     663
Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
        210                 215                 220


<210>  107

<211>  53

<212>  PRT

<213>  Acanthastrea sp.


<400>  107
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Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15

Thr Ala Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30

Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Ile Val Thr Lys Gly Gly
        35                  40                  45

Pro Leu Pro Phe Ala
    50
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<210> 108

<211> 167

<212> PRT

<213> Acanthastrea sp.

<400> 108

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Asp Ile Leu Ser Pro Gln Tyr Gln Tyr Gly Ser Ile Pro Phe Thr Lys
1               5                   10                  15

Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln Ser Phe Pro Glu Gly
            20                  25                  30

Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp Gly Ala Val Cys Thr
        35                  40                  45

Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys Phe Ile Tyr His Val
    50                  55                  60

Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly Pro Val Met Gln Lys
65                  70                  75                  80

Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg Leu Phe Ala Arg Asp
                85                  90                  95

Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu Lys Leu Glu Gly Gly
            100                 105                 110

Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr Lys Ala Lys Lys Pro
        115                 120                 125
```

```
Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg Lys Leu Asp Val Thr
    130                 135                 140


Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln Cys Glu Ile Ser Ile
145                 150                 155                 160


Ala Arg Lys Pro Val Val Ala
                165


<210>  109

<211>  663

<212>  DNA

<213>  Acanthastrea sp.



<220>

<221>  CDS

<222>  (1)..(663)



<400>  109
atg agt gtg atc gct aca caa atg acc tac aag gtt tat atg tca ggc       48
Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15

acg gcc aat gga cac tac ttt gag gtt gaa ggc gat gga aaa gga aag       96
Thr Ala Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30

cct tac gaa ggg gag cag acg gta agg ctc act gtc aca aag ggc gga      144
Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly
        35                  40                  45

cct ctg cca ttt gct tgg gat att tta tca cca cag tat cag tac gga      192
Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Tyr Gln Tyr Gly
    50                  55                  60

agc ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag      240
Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80

cag tca ttc ccg gaa gga tat aca tgg gag agg atc atg aac ttt gaa      288
Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac      336
Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110
```

```
tgt ttc atc cac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat        384
Cys Phe Ile His His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125

gga cct gtg atg cag aag aag aca cag ggc tgg gaa ccc aac act gag        432
Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
    130                 135                 140

cgt ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt atg gct        480
Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160

ctg aag tta gaa gga ggc ggt cac tat ttg tgt gaa ttc aaa tct act        528
Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr
                165                 170                 175

tac aag gca aag aag cct gtg aag atg cca ggg tat cac tat gtt gac        576
Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190

cgc aaa ctg gat gta acc aat cac aac aag gat tac act tcc gtt gag        624
Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
        195                 200                 205

cag tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                    663
Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220


<210>  110

<211>  221

<212>  PRT

<213>  Acanthastrea sp.


<400>  110

Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15


Thr Ala Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30


Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly
        35                  40                  45


Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Tyr Gln Tyr Gly
    50                  55                  60


Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80
```

```
Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110

Cys Phe Ile His His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125

Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
    130                 135                 140

Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160

Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr
                165                 170                 175

Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190

Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
        195                 200                 205

Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
```

<210> 111

<211> 659

<212> DNA

<213> Acanthastrea sp.

<400> 111

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agtgtgatcg ctacacaaat gacctacaag gtttatatgt caggcacggt caatggacac     60

tactttgagg tcgaaggcga tggaaaagga aagcctacga gggggagcag acggtaaagc    120

tcactgtcac caagggcgga cctctgccat ttgcttggga tattttatca ccacagtgtc    180

agtacggaaa cataccattc accaagtacc ctgaagacgt ccctgactat gtaaagcagt    240

cattcccgga gggatttaca tgggagagga tcatgaactt tgaagatggt gcagtgtgta    300

ctgtcagcaa tgattccagc atccaaggca actgtttcac ctaccatgtc aagttctctg    360

gtttgaactt tcctcccaat ggacctgtga tgcagaagga gacacagggc tgggaacccc    420
```

```
actctgagcg tctctttgca cggggtggaa tgctgatagg aaacaacttt gtggctctga     480

agttagaagg aggcggtcac tatttgtgtg gattcaaaac tacttacaag gcaaagaaac     540

ctgtgaagat gccagggtat cattatgttg accgcaaact ggatgtaacc aatcacaaca     600

aggattacat ttccgttgag cagtgtgaaa tttccattgc acgcaaacct gtggtcgcc      659


<210>  112

<211>  663

<212>  DNA

<213>  Caulastrea sp.



<220>

<221>  CDS

<222>  (1)..(663)



<400>  112
atg agt gtg atc gct aca caa atg acc tac aag gtt tat atg tca ggc        48
Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15

acg gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga aag        96
Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30

cct tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggc gga       144
Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly
        35                  40                  45

cct ctg cca ttt gct tgg gat att tta tca cca cag tgt cag tac gga       192
Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly
    50                  55                  60

aat ata cca ttc acc aag tac cct gaa gac gtc cct gac tat gta aag       240
Asn Ile Pro Phe Thr Lys Tyr Pro Glu Asp Val Pro Asp Tyr Val Lys
65                  70                  75                  80

cgg tca ttc ccg gag gga ttt aca tgg gag agg atc atg aac ttt gaa       288
Arg Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac       336
Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110

tgt ttc acc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat       384
Cys Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125
```

```
gga cct gtg atg cag aag aag aca cag ggc tgg gaa ccc cac tct gag        432
Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu
    130                 135                 140

cgt ctc ttt gca cgg ggt gga atg ctg ata gga aac aac ttt atg gct        480
Arg Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160

ctg aag tta gaa gga ggc ggt cac tat ttg tgt gga ttc aaa act act        528
Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Gly Phe Lys Thr Thr
                165                 170                 175

tac aag gca aag aag cct gtg aag atg cca ggg tat cat tat gtt gac        576
Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190

cgc aaa ctg gat gta acc aat cac aac aag gat tac att tcc gtt gag        624
Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Ile Ser Val Glu
        195                 200                 205

cag tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                    663
Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220


<210>  113

<211>  221

<212>  PRT

<213>  Caulastrea sp.


<400>  113

Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15


Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30


Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly
        35                  40                  45


Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly
    50                  55                  60


Asn Ile Pro Phe Thr Lys Tyr Pro Glu Asp Val Pro Asp Tyr Val Lys
65                  70                  75                  80


Arg Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95
```

```
Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110

Cys Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125

Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu
    130                 135                 140

Arg Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160

Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Gly Phe Lys Thr Thr
                165                 170                 175

Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190

Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Ile Ser Val Glu
        195                 200                 205

Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220

<210>  114

<211>  663

<212>  DNA

<213>  Caulastrea sp.


<220>

<221>  CDS

<222>  (1)..(663)


<400>  114
atg agt gtg atc gct aca caa atg acc tac aag gtt tat atg tcg ggc        48
Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15

acg gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga aag        96
Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30
```

```
cct tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggc gga       144
Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly
        35                  40                  45

cct ctg cca ttt gct tgg gat att tta tca cca cag tgt cag tac gga       192
Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly
    50                  55                  60

aac ata cca ttc acc aag tac cct gaa gac gtc cct gac tat gta aag       240
Asn Ile Pro Phe Thr Lys Tyr Pro Glu Asp Val Pro Asp Tyr Val Lys
65                  70                  75                  80

cag tca ttc ccg gag gga ttt aca tgg gag agg atc atg aac ttt gaa       288
Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac       336
Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110

tgt ttc acc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat       384
Cys Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125

gga cct gtg atg cag aag aag aca cag ggc tgg gaa ccc cac tct gag       432
Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu
    130                 135                 140

cgt ctc ctt gca cgg ggt gga atg ctg ata gga aac aac ttt atg gct       480
Arg Leu Leu Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160

ctg aag tta gaa gga ggc ggt cac tat ttg tgt gga ttc aaa act act       528
Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Gly Phe Lys Thr Thr
                165                 170                 175

tac aag gca aag aag cct gtg aag atg cca ggg tat cat tat gtt gac       576
Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190

cgc aaa ctg gat gta acc aat cac aac aag gat tac att tcc gtt gag       624
Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Ile Ser Val Glu
        195                 200                 205

cag tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                   663
Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220


<210>  115

<211>  221

<212>  PRT

<213>  Caulastrea sp.


<400>  115
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Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1 5 10 15

Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
20 25 30

Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly
35 40 45

Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly
50 55 60

Asn Ile Pro Phe Thr Lys Tyr Pro Glu Asp Val Pro Asp Tyr Val Lys
65 70 75 80

Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu
85 90 95

Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
100 105 110

Cys Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
115 120 125

Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu
130 135 140

Arg Leu Leu Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145 150 155 160

Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Gly Phe Lys Thr Thr
165 170 175

Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
180 185 190

Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Ile Ser Val Glu
195 200 205

Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
210 215 220

<210> 116

<211> 660

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<212>  DNA

<213>  Caulastrea sp.


<220>

<221>  CDS

<222>  (1)..(660)


<400>  116
agt gtg atc gct aca caa atg acc tac aag gtt tat atg tca ggc acg        48
Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga aag cct        96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggc gga cct       144
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att tta tca cca cag tgt cag tac gga aac       192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Asn
    50                  55                  60

ata cca ttc acc aag tac cct gaa gac gtc cct gac tat gta aag cag       240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Val Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc ccg gag gga ttt aca tgg gag agg atc atg aac ttt gaa gat       288
Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac tgt       336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

ttc acc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga       384
Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtg atg cag aag aag aca cag ggc tgg gaa ccc cac tct gag cgt       432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu Arg
    130                 135                 140

ctc ttt gca cgg ggt gga atg ctg ata gga aac aac ttt atg gct ctg       480
Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

aag tta gaa gga ggc ggt cac tat ttg tgt gga ttc aaa act act tac       528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Gly Phe Lys Thr Thr Tyr
                165                 170                 175
```

```
aag gca aag aag ctt gtg aag atg cca ggg tat cat tat gtt gac cgc        576
Lys Ala Lys Lys Leu Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aaa ctg gat gta acc aat cac aac aag gat tac att tcc gtt gag cag        624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Ile Ser Val Glu Gln
        195                 200                 205

tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                        660
Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
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<210> 117

<211> 220

<212> PRT

<213> Caulastrea sp.

<400> 117

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Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Asn
    50                  55                  60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Val Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu Arg
    130                 135                 140
```

```
Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Gly Phe Lys Thr Thr Tyr
                165                 170                 175

Lys Ala Lys Lys Leu Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Ile Ser Val Glu Gln
        195                 200                 205

Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
```

<210> 118

<211> 660

<212> DNA

<213> Caulastrea sp.

<220>

<221> CDS

<222> (1)..(660)

<400> 118

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agt gtg atc gct aca caa atg acc tac aag gtt tat atg tca ggc acg          48
Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga aag cct          96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggc gga cct         144
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att tta tca cca cag tgt cag tac gga aac         192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Asn
    50                  55                  60

ata cca ttc acc aag tac cct gaa gac gtc cct gac tat gta aag cag         240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Val Pro Asp Tyr Val Lys Gln
65                  70                  75                  80
```

```
tca ttc ccg gag gga ttt aca tgg gag agg atc atg aac ttt gaa gat      288
Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac tgt      336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

ttc acc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga      384
Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtg atg tag aag aag aca cag ggc tgg gaa ccc cac tct gag cgt      432
Pro Val Met     Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu Arg
    130                     135                 140

ctc ttt gca cgg ggt gga atg ctg ata gga aac aac ttt atg gct ctg      480
Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
    145                 150                 155

aag tta gaa gga ggt ggt cac tat ttg tgt gaa ttc aaa act act tac      528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr Tyr
160                 165                 170                 175

aag gca aag aag cct gtg aag atg cca ggg tat cat tat gtt gac cgc      576
Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
                180                 185                 190

aaa ctg gat gta acc aat cac aac aag gat tac att tcc gtt gag cag      624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Ile Ser Val Glu Gln
            195                 200                 205

tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                      660
Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
        210                 215


<210>  119

<211>  131

<212>  PRT

<213>  Caulastrea sp.


<400>  119

Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15


Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30


Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45
```

```
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Asn
    50                  55                  60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Val Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

Pro Val Met
    130

<210>  120

<211>  88

<212>  PRT

<213>  Caulastrea sp.


<400>  120

Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu Arg Leu Phe Ala Arg
1               5                   10                  15

Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu Lys Leu Glu Gly
            20                  25                  30

Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr Tyr Lys Ala Lys Lys
        35                  40                  45

Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg Lys Leu Asp Val
    50                  55                  60

Thr Asn His Asn Lys Asp Tyr Ile Ser Val Glu Gln Cys Glu Ile Ser
65                  70                  75                  80

Ile Ala Arg Lys Pro Val Val Ala
                85
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<210> 121

<211> 663

<212> DNA

<213> Acropora nobilis

<220>

<221> CDS

<222> (1)..(663)

<400> 121

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atg agt gtg atc gct aca caa atg acc tac aag gtt tat atg tca ggc      48
Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15

acg gtc aat gga cac tac ttt gag gtt gaa ggc gat gga aaa gga aag      96
Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30

cct tac gaa ggg gag cag acg gta agg ctc act gtc aca aag ggc gga     144
Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly
        35                  40                  45

cct ctg cca ttt gct tgg gat att tta tca cca cag tat cag tac gga     192
Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Tyr Gln Tyr Gly
    50                  55                  60

agc ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag     240
Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80

cag tca ttc ccg gaa gga tat aca tgg gag agg atc atg aac ttt gaa     288
Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac     336
Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110

tgt ttc atc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aac     384
Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125

gga cct gtg atg cag aag aag aca cag ggc tgg gaa ccc aac act gag     432
Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
    130                 135                 140

cgt ctc tta gca cga gat gga atg ctg ata gga aac aac ttt atg gct     480
Arg Leu Leu Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160
```

```
ctg aag tta gaa gga ggc ggt cac tat ttg tgt gaa ttc aaa tct act        528
Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr
                165                 170                 175

tac aag gca aag aag cct gtg aag atg cca ggg tat cac tat gtt gac        576
Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190

cgc aaa ctg gat gta acc aat cac aac aag gat tac act tcc gtt gag        624
Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
        195                 200                 205

cag tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                    663
Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
```

```
<210>  122

<211>  221

<212>  PRT

<213>  Acropora nobilis


<400>  122

Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15


Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30


Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly
        35                  40                  45


Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Tyr Gln Tyr Gly
    50                  55                  60


Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80


Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95


Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110


Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125
```

```
Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
    130                 135                 140

Arg Leu Leu Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160

Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr
                165                 170                 175

Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190

Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
        195                 200                 205

Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220

<210>  123

<211>  663

<212>  DNA

<213>  Acropora nobilis


<220>

<221>  CDS

<222>  (1)..(663)


<400>  123
atg agt gtg atc gct aca caa atg acc tac aag gtt tat atg tca ggc        48
Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15

aca gtc aat gga cac tac ctt gag gtc gaa ggc gat gga aaa gga aag        96
Thr Val Asn Gly His Tyr Leu Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30

cct tac gag ggg gag cag acg gta agg ctc act gtc acc aag ggc gga       144
Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly
        35                  40                  45

cct ctg cca ttt gct tgg gat att ttg tca cca cag tat cag tac gga       192
Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Tyr Gln Tyr Gly
    50                  55                  60
```

```
agc ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag       240
Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80

tag tca ttc ccg gag gga ttt aca tgg gac agg atc atg gac ttt gaa       288
    Ser Phe Pro Glu Gly Phe Thr Trp Asp Arg Ile Met Asp Phe Glu
                    85                  90                  95

gat ggt gca gtg tgt acc gtc agc aat gat tcc agc atc caa ggc aac       336
Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
                100                 105                 110

tgt ttc atc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat       384
Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
            115                 120                 125

gga cct gtt atg cag aag aag aca cag ggc tgg gaa ccc aac act gag       432
Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
        130                 135                 140

cgt ctc ttt gca cga gat gga atg ctg cta gga aac aac ttt atg gct       480
Arg Leu Phe Ala Arg Asp Gly Met Leu Leu Gly Asn Asn Phe Met Ala
    145                 150                 155

ctg aag tta gaa gga ggt ggt cac tat ttg tgt gaa ttc aaa act act       528
Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr
160                 165                 170                 175

tac aag gca aag aag cct gtg aag atg cca ggg tat cac tat gtt gac       576
Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
                180                 185                 190

cgc aaa ctg gat gta acc aat cac aac aag gat tac act tcc gtt gag       624
Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
            195                 200                 205

cag tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                   663
Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
        210                 215                 220


<210>  124

<211>  80

<212>  PRT

<213>  Acropora nobilis


<400>  124

Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15


Thr Val Asn Gly His Tyr Leu Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30
```

```
Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly
        35                  40                  45

Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Tyr Gln Tyr Gly
    50                  55                  60

Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80

<210>  125

<211>  140

<212>  PRT

<213>  Acropora nobilis


<400>  125

Ser Phe Pro Glu Gly Phe Thr Trp Asp Arg Ile Met Asp Phe Glu Asp
1               5                   10                  15

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            20                  25                  30

Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        35                  40                  45

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    50                  55                  60

Leu Phe Ala Arg Asp Gly Met Leu Leu Gly Asn Asn Phe Met Ala Leu
65                  70                  75                  80

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr Tyr
                85                  90                  95

Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            100                 105                 110

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        115                 120                 125

Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    130                 135                 140
```

<210> 126

<211> 660

<212> DNA

<213> Millepora sp.

<220>

<221> CDS

<222> (1)..(660)

<400> 126

```
agt gtg atc gct aca caa atg acc tac aag gtt tat atg tca ggc acg       48
Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

gtc gat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga aag cct       96
Val Asp Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

tac gag ggc gag cag act gta aag ctc act gtc acc aag ggc gga cct      144
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att tta tca cca cag tgt cag tac gga agc      192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Ser
    50                  55                  60

ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag cag      240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc ccg gag gga ttt aca tgg gag agg atc atg aac ttt gaa aat      288
Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu Asn
                85                  90                  95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac tgt      336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

ttc acc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga      384
Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtg atg cag aag aag aca cag ggc tgg gaa ccc cac tct gag cgt      432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu Arg
    130                 135                 140

ctc ttt gca cgg ggt gga atg ctg ata gga aac aac ttt atg gct ctg      480
Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160
```

```
aag tta gaa gga ggc ggt cac tat ttg tgt gaa ttc aaa act act tac        528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr Tyr
                165                 170                 175

aag gca aag aag cct gtg aag atg cca ggg tat cat tat gtt gac cgc        576
Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aaa ctg gat gta acc aat cac aac aag gat tac act tcc gtt gag cag        624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                        660
Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
```

<210> 127

<211> 220

<212> PRT

<213> Millepora sp.

<400> 127

```
Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

Val Asp Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Ser
    50                  55                  60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu Asn
                85                  90                  95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125
```

```
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu Arg
    130                 135                 140

Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr Tyr
                165                 170                 175

Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
```

<210> 128

<211> 663

<212> DNA

<213> Millepora sp.

<220>

<221> CDS

<222> (1)..(663)

<400> 128

```
atg agt gtg atc gct aca caa atg acc tac aag gtt tat atg tca ggc        48
Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15

acg gtc gat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga aag        96
Thr Val Asp Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30

cct tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggc gga       144
Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly
        35                  40                  45

cct ctg cca ttt gct tgg gat att tta tca cca cag tgt cag tac gga       192
Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly
    50                  55                  60
```

```
agc ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag         240
Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80

cag tca ttc ccg gag gga ttt aca tgg gag agg atc atg aac ttt gaa         288
Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac         336
Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110

tgt ttc acc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat         384
Cys Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125

gga cct gtg atg cag aag aag aca cag ggc tgg gaa ccc cac tct gag         432
Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu
    130                 135                 140

cgt ctc ttt gca cgg ggt gga atg ctg ata gga aac aac ttt atg gct         480
Arg Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160

ctg aag tta gaa gga ggc ggt cac tat ttg tgt gaa ttc aaa act act         528
Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr
                165                 170                 175

tac aag gca aag aag cct gtg aag atg cca ggg tat cat tat gtt gac         576
Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190

cgc aaa ctg gat gta acc aat cac aac aag gat tac act tcc gtt gag         624
Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
        195                 200                 205

cag tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                     663
Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220


<210>  129

<211>  221

<212>  PRT

<213>  Millepora sp.


<400>  129

Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15


Thr Val Asp Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30
```

```
Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly
        35                  40                  45


Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly
    50                  55                  60


Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80


Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95


Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110


Cys Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125


Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu
    130                 135                 140


Arg Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160


Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr
                165                 170                 175


Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190


Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
        195                 200                 205


Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220


<210>  130

<211>  663

<212>  DNA

<213>  Millepora sp.


<220>
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```
<221>  CDS

<222>  (1)..(663)


<400>  130
atg agt gtg atc gct aca caa atg acc tac aag gtt tat atg tca ggc       48
Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15

acg gtc gat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga aag       96
Thr Val Asp Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30

cct tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggc gga      144
Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly
        35                  40                  45

cct ctg cca ttt gct tgg gat att tta tca cca cag tgt cag tac gga      192
Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly
    50                  55                  60

agc ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag      240
Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80

cag tca ttc ccg gag gga ttt aca tgg gag agg atc atg aac ttt gaa      288
Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

gat ggt gca gtg tgt act gtc agc aat ggt tcc agc atc caa ggc aac      336
Asp Gly Ala Val Cys Thr Val Ser Asn Gly Ser Ser Ile Gln Gly Asn
            100                 105                 110

tgt ttc acc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat      384
Cys Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125

gga cct gtg atg cag aag aag aca cag ggc tgg gaa ccc cac tct gag      432
Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu
    130                 135                 140

cgt ctc ttt gca cgg ggt gga atg ctg ata gga aac aac ttt atg gct      480
Arg Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160

ctg aag tta gga gga ggc ggt cac tat ttg tgt gaa ttc aaa act act      528
Leu Lys Leu Gly Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr
                165                 170                 175

tac agg gca aag aag cct gtg aag atg cca ggg tat cat tat gtt gac      576
Tyr Arg Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190

cgc aaa ctg gat gta acc aat cac aac aag gat tac act tcc gtt gag      624
Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
        195                 200                 205
```

```
cag tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc              663
Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220


<210>  131

<211>  221

<212>  PRT

<213>  Millepora sp.


<400>  131

Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15


Thr Val Asp Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30


Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly
        35                  40                  45


Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly
    50                  55                  60


Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80


Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95


Asp Gly Ala Val Cys Thr Val Ser Asn Gly Ser Ser Ile Gln Gly Asn
            100                 105                 110


Cys Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125


Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu
    130                 135                 140


Arg Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160


Leu Lys Leu Gly Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr
                165                 170                 175
```

```
Tyr Arg Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190

Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
        195                 200                 205

Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
```

<210> 132

<211> 660

<212> DNA

<213> Millepora sp.

<220>

<221> CDS

<222> (1)..(660)

<400> 132

```
agt gtg atc gct aca caa atg acc tac aag gtt tat atg tca ggc acg        48
Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

gtc gat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga aag cct        96
Val Asp Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggc gga cct       144
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att tta tca cca cag tgt cag tac gga agc       192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Ser
    50                  55                  60

ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag cag       240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc ccg gag gga ttt aca tgg gag agg atc atg aac ttt gaa gat       288
Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac tgt       336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110
```

```
ttc acc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga       384
Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtg atg cag aag aag aca cag ggc tgg gaa ccc cac tct gag cgt       432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu Arg
    130                 135                 140

ctc ttt gca cgg ggt gga atg ctg ata gga aac aac ttt atg gct ctg       480
Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

aag tta gaa gga ggc ggt cac tat ttg tgt gaa ttc aaa act act tac       528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr Tyr
                165                 170                 175

aag gca aag aag cct gtg aag atg cca ggg tat cat tat gtt gac cgc       576
Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aaa ctg gat gta acc aat cac aac aag gat tac act tcc gtt gag cag       624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                       660
Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
```

<210> 133

<211> 220

<212> PRT

<213> Millepora sp.

<400> 133

```
Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

Val Asp Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Ser
    50                  55                  60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80
```

```
Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu Arg
    130                 135                 140

Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr Tyr
                165                 170                 175

Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220

<210>  134

<211>  663

<212>  DNA

<213>  Porites murrayensis


<220>

<221>  CDS

<222>  (1)..(663)


<400>  134
atg agt gtg atc gct aca caa atg acc tac aag gtt tat atg cca ggc        48
Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Pro Gly
1               5                   10                  15
```

```
acg gtc aat gga cac tac ttt gag gtt gaa ggc gat gga aaa gga aag       96
Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30

cct tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggc gga      144
Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly
        35                  40                  45

cct ctg cca ttt gct tgg gat att cta tca cca cag agt cag tac gga      192
Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly
    50                  55                  60

agc ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag      240
Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80

cag tca ttc cct gag gga tat aca tgg gag agg atc atg aac ttc gaa      288
Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggt aac      336
Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110

tgt ttc atc tac aat gtc aag ttc tct ggt ttg aac ttt cct ccc aat      384
Cys Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125

gga cct gtt atg caa aag aag aca cag ggc tgg gaa ccc aac act gag      432
Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
    130                 135                 140

cgt ctt tat gca cga gat gga atg ctg ata gga aac aac ttt atg gct      480
Arg Leu Tyr Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160

ctg aag ttg gaa gga ggt ggt cat tat ttg tgt gaa ttc aaa tct act      528
Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr
                165                 170                 175

tac aag gca aag aag cct gtg atg atg cct gga tat cac tat gtt gac      576
Tyr Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190

cgc aaa ttg gat gta acc aat cac aac aag gat tac act tcc gtt gag      624
Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
        195                 200                 205

cag tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                  663
Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
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<210> 135

<211> 221

<212> PRT

<213> Porites murrayensis

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<400>  135

Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Pro Gly
1               5                   10                  15

Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30

Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly
        35                  40                  45

Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly
    50                  55                  60

Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80

Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110

Cys Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125

Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
    130                 135                 140

Arg Leu Tyr Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160

Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr
                165                 170                 175

Tyr Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190

Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
        195                 200                 205

Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
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<210>  136

<211>  663

<212>  DNA

<213>  Porites murrayensis


<220>

<221>  CDS

<222>  (1)..(663)


<400>  136
atg agt gtg atc gct aca caa atg acc tac aag gtt tat atg tca ggc        48
Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15

acg gtc aat gga cac tac ttt gag gtt gaa ggc gat gga aaa gga aag        96
Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30

cct tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggc gga       144
Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly
        35                  40                  45

cct ctg cca ttt gct tgg gat att cta tca cca cag agt cag tac gga       192
Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly
    50                  55                  60

agc ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag       240
Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80

cag tca ttc cct gag gga tat aca tgg gag agg atc atg aac ttc gaa       288
Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggt aac       336
Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110

tgt ttc atc tac aat gtc aag ttc tct ggt ttg aac ttt cct ccc aat       384
Cys Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125

gga cct gtt atg caa aag aag aca cag ggt tgg gaa ccc aac act gag       432
Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
    130                 135                 140

cgt ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt atg gct       480
Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160
```

```
ctg aag ttg gaa gga ggt ggt cat tat ttg tgt gaa ttc aaa tct act        528
Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr
                165                 170                 175

tac aag gca aag aag cct gtg atg atg cca ggg tat cac tat gtt gac        576
Tyr Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190

cgc aaa ttg gat gta acc aat cac aac aag gat tac act tcc gtt gag        624
Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
        195                 200                 205

cag tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                    663
Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220


<210>  137

<211>  221

<212>  PRT

<213>  Porites murrayensis


<400>  137

Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15

Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30

Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly
        35                  40                  45

Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly
    50                  55                  60

Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80

Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110

Cys Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125
```

```
Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
    130                 135                 140


Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160


Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr
                165                 170                 175


Tyr Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190


Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
        195                 200                 205


Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
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<210> 138

<211> 660

<212> DNA

<213> Porites murrayensis

<220>

<221> CDS

<222> (1)..(660)

<400> 138

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agt gtg atc gct aca caa atg acc tac aag gtt tat atg tca ggc acg        48
Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

gtc aat gga cac tac ttt gag gtc caa ggc gat gga aaa gga aag cct        96
Val Asn Gly His Tyr Phe Glu Val Gln Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

tac gag ggc gag cag act gta aag ctc act gtc acc aag ggc gga cct       144
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg ccc ttt gct tgg gat att tta tca cct cag act cag tac gga agc       192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Thr Gln Tyr Gly Ser
    50                  55                  60
```

```
ata cca ttc acc aag tac cct gac gac atc cct gac tat gta aaa cag       240
Ile Pro Phe Thr Lys Tyr Pro Asp Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc cct gag gga tat aca tgg gag agg atc atg aag ttt gaa gat       288
Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Lys Phe Glu Asp
                85                  90                  95

ggt gca gtg tgt act gtc acc aat gac tcc agc atg caa ggc aac tgt       336
Gly Ala Val Cys Thr Val Thr Asn Asp Ser Ser Met Gln Gly Asn Cys
            100                 105                 110

ttc atc tac aat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga       384
Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtt atg cag aag aag aca cag ggc tgg gaa ccc aac act ggg cgt       432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Gly Arg
    130                 135                 140

ctt tat gca cga gat gga atg ctg ata gga aac aac ttt atg gct ctg       480
Leu Tyr Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

aag ttg gaa gga ggt ggt cat tat acc tgt gaa ttc aaa tct act tac       528
Lys Leu Glu Gly Gly Gly His Tyr Thr Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

aag gca aag aag cct gtg atg atg cct gga tat cac tat gtt gac cgc       576
Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aaa ttg gat gta acc aat cac aac aag gat tac act tcc gtt gag cag       624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                       660
Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
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<210> 139

<211> 220

<212> PRT

<213> Porites murrayensis

<400> 139

```
Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

Val Asn Gly His Tyr Phe Glu Val Gln Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30
```

```
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Thr Gln Tyr Gly Ser
    50                  55                  60

Ile Pro Phe Thr Lys Tyr Pro Asp Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Lys Phe Glu Asp
                85                  90                  95

Gly Ala Val Cys Thr Val Thr Asn Asp Ser Ser Met Gln Gly Asn Cys
            100                 105                 110

Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Gly Arg
    130                 135                 140

Leu Tyr Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

Lys Leu Glu Gly Gly Gly His Tyr Thr Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220

<210>  140

<211>  660

<212>  DNA

<213>  Porites murrayensis


<220>
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<221>  CDS

<222>  (1)..(660)


<400>  140
agt gtg atc gct aca caa atg acc tac aag gtt tat atg tca ggc acg         48
Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

gtc aat gga cac tac ttt gag gtt gaa ggc gat gga caa gga aag cct         96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Gln Gly Lys Pro
            20                  25                  30

tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggc gga cct        144
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att cta tca cca cag agt cag tac gga agc        192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
    50                  55                  60

ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag cag        240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc cct gag gga tat aca tgg gag agg atc atg aac ttc gaa gat        288
Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac tgt        336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

ttc atc tac aat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga        384
Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtt atg caa aag aag aca cag ggc tgg gaa ccc aac act gag cgt        432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt atg gct ctg        480
Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

aag tcg gaa gga ggt ggt cat tat ttg tgt gaa ttc aaa tct act tac        528
Lys Ser Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

aag gca aag aag cct gtg atg atg cca ggg tat cac tat gtt gac cgc        576
Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aaa ttg gat gta acc aat cac aac aag gat tac act tcc gtt gag cag        624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205
```

```
tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                      660
Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
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<210> 141

<211> 220

<212> PRT

<213> Porites murrayensis

<400> 141

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Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Gln Gly Lys Pro
            20                  25                  30

Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
    50                  55                  60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

Lys Ser Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175
```

```
Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190


Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205


Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220


<210>  142

<211>  660

<212>  DNA

<213>  Porites murrayensis



<220>

<221>  CDS

<222>  (1)..(660)



<400>  142
agt gtg atc gct aca caa atg acc tac aag gtt tat atg tca ggc acg        48
Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

gtc aat gga cac tac ttt gag gtt gaa ggc gat gga aaa gga aag cct        96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggc gga cct       144
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att cta tca cca cag agt cag tac gga agc       192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
    50                  55                  60

ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag cag       240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc cct gag gga tat aca tgg gag agg atc atg aac ttc gaa gat       288
Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac tgt       336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110
```

```
ttc atc tac aat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga        384
Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtt atg caa aag aag aca cag ggc tgg gaa ccc aac aca gag cgt        432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt atg gct ctg        480
Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

aag ttg gaa gga ggt ggt cat tat ttg tgt gaa ttc aaa tct act tac        528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

aag gca aag aag cct gtg atg atg cca ggg tat cac tat gtt gac cgc        576
Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aaa ttg gat gta acc aat cac aac aag gat tac act tcc gtt gag cag        624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                        660
Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220


<210>  143

<211>  220

<212>  PRT

<213>  Porites murrayensis


<400>  143

Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
    50                  55                  60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80
```

```
Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
```

<210> 144

<211> 660

<212> DNA

<213> Pink Pocillopora

<220>

<221> CDS

<222> (1)..(660)

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<400> 144
agt gtg atc gct aca caa atg acc tac aag gtt tat atg tca ggc acg        48
Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15
```

```
gtc aat gga cac tac ttt gag gtt gaa ggc gat gga aaa gga aag cct          96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

tac gag ggc gag cag act gta aag ctc act gtc acc aag ggc gga cct         144
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg ccg ttt gct tgg gat att tta tca cca cag act cag tac gga agc         192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Thr Gln Tyr Gly Ser
    50                  55                  60

ata cca ttc acc aag tac cct gaa gac att cct gac tat gta aaa cag         240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc cct gag gga tat aca tgg gag agg atc atg aag ttt gaa gat         288
Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Lys Phe Glu Asp
                85                  90                  95

ggt gca gta tgt act gtc agc aat gat tcc agc atg caa ggc aac tgt         336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Met Gln Gly Asn Cys
            100                 105                 110

ttc atc tac aat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga         384
Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtt atg cag aag aag aca cag ggc tgg gaa ccc aac act gag cgt         432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

ctt tat gca cga gat gga atg ctg ata gga aac aac ttt atg gct ctg         480
Leu Tyr Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

aag ttg gaa gga ggt ggt cat tat acc tgt gaa ttc aaa tct act tac         528
Lys Leu Glu Gly Gly Gly His Tyr Thr Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

aag gca aag aag cct gtg atg atg cct gga tat cac tat gtt gac cgc         576
Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aaa ttg gat gta acc aat cac aac aag gat tac act tcc gtt gag cag         624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                         660
Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
```

<210> 145

<211> 220

<212> PRT

<213> Pink Pocillopora

```
<400>  145

Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Thr Gln Tyr Gly Ser
    50                  55                  60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Lys Phe Glu Asp
                85                  90                  95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Met Gln Gly Asn Cys
            100                 105                 110

Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

Leu Tyr Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

Lys Leu Glu Gly Gly Gly His Tyr Thr Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
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<210>  146

<211>  663

<212>  DNA

<213>  Pink Pocillopora


<220>

<221>  CDS

<222>  (1)..(663)


<400>  146
atg agt gtg atc gct aca caa atg acc tac aag gtt tat atg tca ggc       48
Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15

acg gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga aag       96
Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30

cct tac gag ggg gag cag acg gta agg ctg gct gtc acc aag ggc gga      144
Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Ala Val Thr Lys Gly Gly
        35                  40                  45

cct ctg cca ttt gct tgg gat att tta tca cca cag tgt cag tac gga      192
Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly
    50                  55                  60

agc ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag      240
Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80

cag tca ttc ccg gag gga ttt aca tgg gag agg atc atg aac ttt gaa      288
Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac      336
Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110

tgt ttc atc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat      384
Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125

gga cct gtt atg cag aag aag aca cag ggc tgg gaa ccc cac tct gag      432
Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu
    130                 135                 140

cgt ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt atg gct      480
Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160
```

```
ctg aag tta gaa gga ggc ggt cac tat ttg tgt gaa ttc aaa act act      528
Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr
                165                 170                 175

tac aag gca aag aag cct gtg aag atg cca ggg tat cat tat gtt gac      576
Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190

cgc aaa ctg gat gta acc aat cac aac aag gat tac act tcc gtt gag      624
Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
        195                 200                 205

cag tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                  663
Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220


<210>  147

<211>  221

<212>  PRT

<213>  Pink Pocillopora


<400>  147

Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15


Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30


Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Ala Val Thr Lys Gly Gly
        35                  40                  45


Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly
    50                  55                  60


Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80


Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95


Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110


Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125
```

```
Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu
    130                 135                 140

Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160

Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr
                165                 170                 175

Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190

Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
        195                 200                 205

Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
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<210> 148

<211> 663

<212> DNA

<213> Pink Pocillopora

<220>

<221> CDS

<222> (1)..(663)

<400> 148

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atg agt gtg atc gct aca caa atg acc tac aag gtt tat atg tca ggc         48
Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15

acg gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga aag         96
Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30

cct tac gag ggg gag cag acg gta agg ctg gct gtc acc aag ggc gga        144
Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Ala Val Thr Lys Gly Gly
        35                  40                  45

cct ctg cca ttt gct tgg gat att tta tca cca cag tgt cag tac gga        192
Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly
    50                  55                  60
```

```
agc ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag       240
Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80

cag tca ttc ccg gag gga ttt aca tgg gag agg atc atg aac ttt gaa       288
Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac       336
Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110

tgt ttc atc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat       384
Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125

gga cct gtt atg cag aag aag aca cag ggc tgg gaa ccc cac tct gag       432
Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu
    130                 135                 140

cgt ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt atg gct       480
Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160

ctg aag tta gaa gga ggc ggt cac tat ttg tgt gaa ttc aaa act act       528
Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr
                165                 170                 175

tac aag gca aag aag cct gtg aag atg cca ggg tat cat tat gtt gac       576
Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190

cgc aaa ctg gat gta acc aat cac aac aag gat tac act tcc gtt gag       624
Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
        195                 200                 205

cag tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                   663
Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220


<210>  149

<211>  221

<212>  PRT

<213>  Pink Pocillopora


<400>  149

Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15


Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30
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Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Ala Val Thr Lys Gly Gly
35 40 45

Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly
50 55 60

Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65 70 75 80

Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu
85 90 95

Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
100 105 110

Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
115 120 125

Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu
130 135 140

Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145 150 155 160

Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr
165 170 175

Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
180 185 190

Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
195 200 205

Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
210 215 220

<210> 150

<211> 660

<212> DNA

<213> Pink Pocillopora

<220>

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<221>  CDS

<222>  (1)..(660)


<400>  150
agt gtg atc gct aca caa atg acc tac aag gtt tat atg tca ggc acg           48
Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

gtc aat gga cac tac ttt gag gtt gaa ggc gat gga aaa gga aag cct           96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggc gga cct          144
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att cta tca cca cag agt cag tac gga agc          192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
    50                  55                  60

ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag cag          240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc cct gag gga tat aca tgg gag agg atc atg aac ttc gaa gat          288
Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac tgt          336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

ttc atc tac aat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga          384
Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtt atg caa aag aag aca cag ggc tgg gaa ccc aac act gag cgt          432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt atg gct ctg          480
Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

aag ttg gaa gga ggt ggt cat tat ttg tgt gaa ttc aaa tct act tac          528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

aag gca aag aag cct gtg atg atg cca ggg tat cac tat gtt gac cgc          576
Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aaa ttg gat gta acc aat cac aac aag gat tac act tcc gtt gag cag          624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205
```

tgt gag att tcc att gca cgc aaa cct gtg gtc gcc 660
Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
210 215 220

<210> 151

<211> 220

<212> PRT

<213> Pink Pocillopora

<400> 151

Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1 5 10 15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
20 25 30

Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
35 40 45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
50 55 60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65 70 75 80

Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
85 90 95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
100 105 110

Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
115 120 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
130 135 140

Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145 150 155 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
165 170 175

```
Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190


Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205


Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220


<210>  152

<211>  663

<212>  DNA

<213>  Platygyra sp.



<220>

<221>  CDS

<222>  (1)..(663)



<400>  152
atg agt gtg atc gct aca caa atg acc tac aag gtt tat atg tca ggc        48
Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15

acg gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga aag        96
Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30

cct tac gag ggg gag cgg acg gta aag ctc act gtc acc aag ggc gga       144
Pro Tyr Glu Gly Glu Arg Thr Val Lys Leu Thr Val Thr Lys Gly Gly
        35                  40                  45

cct ctg ccg ttt gct tgg gat att tta tca cca cag tgt cag tac gga       192
Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly
    50                  55                  60

aac ata cca ttc acc aag tac cct gaa gac gtc cct gac tat gta aag       240
Asn Ile Pro Phe Thr Lys Tyr Pro Glu Asp Val Pro Asp Tyr Val Lys
65                  70                  75                  80

cag tca ttc ccg gag gga ttt aca tgg gag agg atc atg aac ttt gaa       288
Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac       336
Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110
```

```
tgt ttc acc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat        384
Cys Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125

gga cct gtg atg cag aag aag aca cag ggc tgg gaa ccc cac tct gag        432
Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu
    130                 135                 140

cgt ctc ttt gca cgg ggt gga atg ctg ata gga aac aac ttt atg gct        480
Arg Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160

ctg aag tta gaa gga ggc ggt cac tat ttg tgt gga ttc aaa act act        528
Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Gly Phe Lys Thr Thr
                165                 170                 175

tac aag gca aag aag cct gtg aag atg cca ggg tat cat tat gtt gac        576
Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190

cgc aaa ctg gat gta acc aat cac aac aag gat tac att tcc gtt gag        624
Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Ile Ser Val Glu
        195                 200                 205

cag tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                    663
Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220


<210>  153

<211>  221

<212>  PRT

<213>  Platygyra sp.


<400>  153

Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15


Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30


Pro Tyr Glu Gly Glu Arg Thr Val Lys Leu Thr Val Thr Lys Gly Gly
        35                  40                  45


Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly
    50                  55                  60


Asn Ile Pro Phe Thr Lys Tyr Pro Glu Asp Val Pro Asp Tyr Val Lys
65                  70                  75                  80
```

```
Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110

Cys Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125

Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu
    130                 135                 140

Arg Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160

Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Gly Phe Lys Thr Thr
                165                 170                 175

Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190

Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Ile Ser Val Glu
        195                 200                 205

Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220

<210>  154

<211>  663

<212>  DNA

<213>  Platygyra sp.


<220>

<221>  CDS

<222>  (1)..(663)


<400>  154
atg agt gtg atc gct aca caa atg acc tac aag gtt tat atg tca ggc        48
Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15
```

```
acg gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga aag        96
Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30

cct tac gag ggg gag cag acg gta agg ctc act gtc acc aag ggc gga       144
Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly
        35                  40                  45

cct ctg cca ttt gct tgg gat att ttg tca cca cag tat cag tac gga       192
Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Tyr Gln Tyr Gly
    50                  55                  60

agc ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag       240
Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80

tag tca ttc ccg gag gga ttt aca tgg gac agg atc atg aac ttt gaa       288
    Ser Phe Pro Glu Gly Phe Thr Trp Asp Arg Ile Met Asn Phe Glu
                    85                  90                  95

gat ggt gca gtg tgt acc gtc agc aat gat tcc agc atc caa ggc aac       336
Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
                100                 105                 110

tgt ttc atc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat       384
Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
            115                 120                 125

gga cct gtt atg cag aag aag aca cag ggc tgg gaa ccc aac act gag       432
Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
        130                 135                 140

cgt ctc ctt gca cga gat gga atg ctg cta gga aac aac ttt atg gct       480
Arg Leu Leu Ala Arg Asp Gly Met Leu Leu Gly Asn Asn Phe Met Ala
    145                 150                 155

ctg aag tta gaa gga ggt ggt cac tat ttg tgt gaa ttc aaa act act       528
Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr
160                 165                 170                 175

tac aag gca aag aag cct gtg aag atg cca ggg tat cac tat gtt gac       576
Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
                180                 185                 190

cgc aaa ctg gat gta acc aat cac aac aag gat tac act tcc gtt gag       624
Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
            195                 200                 205

cgg tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                   663
Arg Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
        210                 215                 220
```

<210> 155

<211> 80

<212> PRT

<213> Platygyra sp.

<400> 155

Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1 5 10 15

Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
20 25 30

Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly
35 40 45

Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Tyr Gln Tyr Gly
50 55 60

Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65 70 75 80

<210> 156

<211> 140

<212> PRT

<213> Platygyra sp.

<400> 156

Ser Phe Pro Glu Gly Phe Thr Trp Asp Arg Ile Met Asn Phe Glu Asp
1 5 10 15

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
20 25 30

Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
35 40 45

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
50 55 60

Leu Leu Ala Arg Asp Gly Met Leu Leu Gly Asn Asn Phe Met Ala Leu
65 70 75 80

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr Tyr
85 90 95

```
Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            100                 105                 110


Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Arg
        115                 120                 125


Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    130                 135                 140


<210>  157

<211>  660

<212>  DNA

<213>  Platygyra sp.



<220>

<221>  CDS

<222>  (1)..(660)



<400>  157
agt gtg atc gct aca caa atg acc tac aag gtt tat atg tca ggc acg        48
Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga aag cct        96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
                20                  25                  30

tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggc gga cct       144
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
            35                  40                  45

ctg cca ttt gct tgg gat att tta tca cca cag tgt cag tac gga aac       192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Asn
        50                  55                  60

ata cca ttc acc aag tac cct gaa gac gtc cct gac tat gta aag cag       240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Val Pro Asp Tyr Val Lys Gln
65                      70                  75              80

tca ttc ccg gag gga ttt aca tgg gag agg atc atg aac ttt gaa gat       288
Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac tgt       336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110
```

```
ttc acc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga       384
Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtg atg cag aag aag aca cag ggc tgg gaa ccc cac tct gag cgt       432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu Arg
    130                 135                 140

ctc ttt gca cgg ggt gga atg ctg ata gga aac aac ttt atg gct ctg       480
Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

aag tta gaa gga ggc ggt cac tat ttg tgt gga ttc aaa act act tac       528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Gly Phe Lys Thr Thr Tyr
                165                 170                 175

aag gca aag aag ccc gtg aag atg cca ggg tat cat tat gtt gac cgc       576
Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aaa ctg gat gta acc aat cac aac aag gat tac att tcc gtt gag cag       624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Ile Ser Val Glu Gln
        195                 200                 205

tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                       660
Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
```

<210> 158

<211> 220

<212> PRT

<213> Platygyra sp.

<400> 158

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Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Asn
    50                  55                  60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Val Pro Asp Tyr Val Lys Gln
65                  70                  75                  80
```

```
Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu Arg
    130                 135                 140

Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Gly Phe Lys Thr Thr Tyr
                165                 170                 175

Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Ile Ser Val Glu Gln
        195                 200                 205

Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220

<210>  159

<211>  660

<212>  DNA

<213>  Platygyra sp.


<220>

<221>  CDS

<222>  (1)..(660)


<400>  159
agt gtg atc gct aca caa atg acc tac aag gtt tat atg tca ggc acg        48
Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15
```

```
gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga aag cct         96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggc gga cct        144
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att tta tca cca cag tgt cag tac gga aac        192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Asn
    50                  55                  60

ata cca ttc acc aag tac cct gaa gac gtc cct gac tat gta aag cag        240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Val Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc ccg gag gga ttt aca tgg gag ggg atc atg aac ttt gaa gat        288
Ser Phe Pro Glu Gly Phe Thr Trp Glu Gly Ile Met Asn Phe Glu Asp
                85                  90                  95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac tgt        336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

ttc acc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga        384
Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtg atg cag aag aag aca cag ggc tgg gaa ccc cac tct gag cgt        432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu Arg
    130                 135                 140

ctc ttt gca cgg ggt gga atg ctg ata gga aac aac ttt atg gct ctg        480
Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

aag tta gaa gga ggc ggt cac tat ttg tgt gga ttc aaa act act tac        528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Gly Phe Lys Thr Thr Tyr
                165                 170                 175

aag gca aag aag cct gtg aag atg cca ggg tat cat tat gtt gac cgc        576
Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aaa ctg gat gta acc aat cac aac aag gat tac att tcc gtt gag cag        624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Ile Ser Val Glu Gln
        195                 200                 205

tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                        660
Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
```

<210> 160

<211> 220

<212> PRT

<213> Platygyra sp.

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<400>  160

Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Asn
    50                  55                  60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Val Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

Ser Phe Pro Glu Gly Phe Thr Trp Glu Gly Ile Met Asn Phe Glu Asp
                85                  90                  95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu Arg
    130                 135                 140

Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Gly Phe Lys Thr Thr Tyr
                165                 170                 175

Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Ile Ser Val Glu Gln
        195                 200                 205

Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
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<210>  161

<211>  660

<212>  DNA

<213>  Pavona decussata


<220>

<221>  CDS

<222>  (1)..(660)


<400>  161
agt gtg atc gct aca caa atg acc tac aag gtt tat atg tca ggc acg         48
Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

gtc aat gga cac tac ttt gag gtt gaa ggc gat gga aaa gga gag cct         96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Glu Pro
            20                  25                  30

tac gag ggg gag cag acg gta agg ctc act gtc aca aag ggc gga cct        144
Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att tta tca cca cag tat cag tac gga agc        192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Tyr Gln Tyr Gly Ser
    50                  55                  60

ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag cag        240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc ccg gaa gga tat aca tgg gag agg atc atg aac ttt gaa gat        288
Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

ggt gct gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac tgt        336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

ttc atc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga        384
Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtg acg cag aag aag aca cag ggc tgg gaa ccc aac act gag cgt        432
Pro Val Thr Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt atg gct ctg        480
Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160
```

```
aag tta gaa gga ggc ggt cac tat ttg tgt gaa ttc aaa tcg act tac      528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

aag gca aag aag act gtg aag atg cca ggg tat cac tat gtt gac cgc      576
Lys Ala Lys Lys Thr Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aaa ctg gat gta acc aat cac aac aag gat tac act tcc gtt gag cag      624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                      660
Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220


<210>  162

<211>  220

<212>  PRT

<213>  Pavona decussata


<400>  162

Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15


Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Glu Pro
            20                  25                  30


Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45


Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Tyr Gln Tyr Gly Ser
    50                  55                  60


Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80


Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95


Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110


Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125
```

```
Pro Val Thr Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

Lys Ala Lys Lys Thr Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220

<210>  163

<211>  663

<212>  DNA

<213>  Pavona decussata


<220>

<221>  CDS

<222>  (1)..(663)


<400>  163
atg agt gtg atc gct aca caa atg acc tac aag gtt tat atg tca ggc        48
Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15

acg gtc aat gga cac tac ttt gag gtt gaa ggc gat gga aaa gga aag        96
Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30

cct tac gag ggg gag cag acg gta agg ctc act gtc aca aag ggc gga       144
Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly
        35                  40                  45

cct ctg cca ttt gct tgg gat att tta tca cca cag tat cag tac gga       192
Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Tyr Gln Tyr Gly
    50                  55                  60
```

```
agc ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta tag     240
Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val
65                  70                  75

cag tca ttc ccg gaa gga tat aca tgg gag agg atc atg aac ttt gaa     288
Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu
80                  85                  90                  95

gat ggt gct gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac     336
Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
                100                 105                 110

tgt ttc atc tac cat gtc aag ttt tct ggt ttg aac ttt cct ccc aat     384
Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
            115                 120                 125

gga cct gtg atg cag aag aag aca cag ggc tgg gaa ccc aac act gag     432
Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
        130                 135                 140

cgt ctc ttt gca cga gat gga ttg ctg ata gga aac aac ttt atg gct     480
Arg Leu Phe Ala Arg Asp Gly Leu Leu Ile Gly Asn Asn Phe Met Ala
    145                 150                 155

ctg aag tta gaa gaa ggc ggt cac tat ttg tgt gaa ttc aaa tcg act     528
Leu Lys Leu Glu Glu Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr
160                 165                 170                 175

tac aag gca aag aag act gcg aag atg cca ggg tat cac tat gtt gac     576
Tyr Lys Ala Lys Lys Thr Ala Lys Met Pro Gly Tyr His Tyr Val Asp
                180                 185                 190

cgc aaa ctg gat gta acc aat cac aac aag gat tac act tcc gtt gag     624
Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
            195                 200                 205

cag tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                 663
Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
        210                 215                 220


<210>  164

<211>  79

<212>  PRT

<213>  Pavona decussata


<400>  164

Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15


Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30
```

```
Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly
        35                  40                  45

Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Tyr Gln Tyr Gly
    50                  55                  60

Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val
65                  70                  75

<210>  165

<211>  141

<212>  PRT

<213>  Pavona decussata


<400>  165

Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu
1               5                   10                  15

Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            20                  25                  30

Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        35                  40                  45

Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
    50                  55                  60

Arg Leu Phe Ala Arg Asp Gly Leu Leu Ile Gly Asn Asn Phe Met Ala
65                  70                  75                  80

Leu Lys Leu Glu Glu Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr
                85                  90                  95

Tyr Lys Ala Lys Lys Thr Ala Lys Met Pro Gly Tyr His Tyr Val Asp
            100                 105                 110

Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
        115                 120                 125

Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    130                 135                 140
```

<210> 166

<211> 663

<212> DNA

<213> Pavona decussata

<220>

<221> CDS

<222> (1)..(663)

<400> 166

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atg agt gtg atc gct aca caa gtg acc tac aag gtt tat atg tca ggc          48
Met Ser Val Ile Ala Thr Gln Val Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15

acg gtc aat gga cac tac ttt gag gtt gaa ggc gat gga aaa gga aag          96
Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30

cct tac gag ggg gag caa acg gta agg ctc act gtc aca aag ggc gga         144
Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly
        35                  40                  45

cct ctg cca ttt gct tgg gat att tta tca cca cag tat cag tac gga         192
Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Tyr Gln Tyr Gly
    50                  55                  60

agc ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag         240
Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80

cag tca ttc ccg gaa gga tat aca tgg gag agg atc atg aac ttt gaa         288
Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

gat ggt gct gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac         336
Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110

tgt ttc atc tac cat gtc aag ttt tct ggt ttg aac ttt cct ccc aat         384
Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125

gga cct gtg atg cag aag aag aca cag ggc tgg gaa ccc aac act gag         432
Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
    130                 135                 140

cgt ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt atg gct         480
Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160
```

```
ctg aag tta gaa gga ggc ggt cac tat ttg tgt gaa ttc aaa tcg act        528
Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr
                165                 170                 175

tac aag gca aag aag act gtg aag atg cca ggg tat cac tat gtt gac        576
Tyr Lys Ala Lys Lys Thr Val Lys Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190

cgc aaa ctg gat gta acc aat cac aac aag gat tac act tcc gtt gag        624
Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
        195                 200                 205

cag tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                    663
Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220


<210>  167

<211>  221

<212>  PRT

<213>  Pavona decussata


<400>  167

Met Ser Val Ile Ala Thr Gln Val Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15


Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30


Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly
        35                  40                  45


Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Tyr Gln Tyr Gly
    50                  55                  60


Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80


Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95


Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110


Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125
```

```
Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
    130                 135                 140

Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160

Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr
                165                 170                 175

Tyr Lys Ala Lys Lys Thr Val Lys Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190

Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
        195                 200                 205

Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220

<210>  168

<211>  660

<212>  DNA

<213>  Pavona decussata


<220>

<221>  CDS

<222>  (1)..(660)


<400>  168
agt gtg atc gct aca caa atg acc tac aag gtt tat atg tca ggc acg       48
Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

gtc aat gga cac tac ttt gag gtt gaa ggc gat gga aaa gga aag cct       96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

tac gag ggg gag cag acg gta agg ctc act gtc aca aag ggc gga cct      144
Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att tta tca cca cag tat cag tac gga agc      192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Tyr Gln Tyr Gly Ser
    50                  55                  60
```

```
ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag cag       240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc ccg gaa gga tat aca tgg gag ggg atc atg aac ttt gaa gat       288
Ser Phe Pro Glu Gly Tyr Thr Trp Glu Gly Ile Met Asn Phe Glu Asp
                85                  90                  95

ggt gct gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac tgt       336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

ttc atc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga       384
Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtg atg cag aag aag aca cag ggc tgg gaa ccc aac act gag cgt       432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt atg gct ctg       480
Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

aag tta gaa gga ggc ggt cac tat ttg tgt gaa ttc aaa tcg act tac       528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

aag gca aag aag act gtg aag atg cca ggg tat cac tat gtt gac cgc       576
Lys Ala Lys Lys Thr Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aaa ctg gtt gta acc aat cac aac aag gat tac act tcc gtt gag cag       624
Lys Leu Val Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                       660
Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220


<210>  169

<211>  220

<212>  PRT

<213>  Pavona decussata


<400>  169

Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15


Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30
```

```
Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Tyr Gln Tyr Gly Ser
    50                  55                  60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

Ser Phe Pro Glu Gly Tyr Thr Trp Glu Gly Ile Met Asn Phe Glu Asp
                85                  90                  95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

Lys Ala Lys Lys Thr Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

Lys Leu Val Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
```

<210> 170

<211> 663

<212> DNA

<213> Montipora sp.

<220>

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<221>  CDS

<222>  (1)..(663)


<400>  170
atg agt gtg atc gct aca caa atg acc tac aag gtt tat atg tca ggc        48
Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15

acg gtc aat gga cac tac ttt gag gtt gaa ggc gat gga aaa gga aag        96
Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30

cct tac gaa ggg gag cag acg gta agg ctc act gtc aca aag ggc gga       144
Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly
        35                  40                  45

cct ctg cca ttt gct tgg gat att tta tca cca cag tat cag tac gga       192
Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Tyr Gln Tyr Gly
    50                  55                  60

agc ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag       240
Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80

cag tca ttc ccg gaa gga tat aca tgg gag agg atc atg aac ttt gaa       288
Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

gat ggt gca gtg tgt gct gtc agc aat gat tcc agc atc caa ggc aac       336
Asp Gly Ala Val Cys Ala Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110

tgt ttc atc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat       384
Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125

gga cct gtg atg caa aag aag aca cag ggc tgg gaa ccc aac act gag       432
Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
    130                 135                 140

cgt ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt atg gct       480
Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160

ctg aag tta gaa gga ggc ggt cac tat ttg tgt gaa ttc aaa tct act       528
Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr
                165                 170                 175

tac aag gca aag aag cct gtg aag atg cca ggg tat cac tat gtt gac       576
Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190

cgc aaa ctg gat gta acc aat cac aac aag gat tac act tcc gtt gag       624
Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
        195                 200                 205
```

```
cag tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                    663
Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220


<210>  171

<211>  221

<212>  PRT

<213>  Montipora sp.



<400>  171

Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15


Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30


Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly
        35                  40                  45


Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Tyr Gln Tyr Gly
    50                  55                  60


Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80


Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95


Asp Gly Ala Val Cys Ala Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110


Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125


Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
    130                 135                 140


Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160


Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr
                165                 170                 175
```

Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
180 185 190

Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
195 200 205

Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
210 215 220

<210> 172

<211> 663

<212> DNA

<213> Montipora sp.

<220>

<221> CDS

<222> (1)..(663)

<400> 172
atg agt gtg agc gct aca caa atg acc tac aag gtt tat atg tca ggc 48
Met Ser Val Ser Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1 5 10 15

acg gtc aat gga cac tac ttt gag gtt gaa ggc gat gga aaa gga aag 96
Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
20 25 30

cct tac gaa ggg gag cag acg gta agg ctc act gtc aca aag ggc gga 144
Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly
35 40 45

cct ctg cca ttt gct tgg gat att tta tca cca cag tat cag tac gga 192
Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Tyr Gln Tyr Gly
50 55 60

agc ata cca ttc acc aag tac cct gaa gac atc cct ggc tat gta aag 240
Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Gly Tyr Val Lys
65 70 75 80

cag tca ttc ccg gaa gga tat aca tgg gag agg atc atg aac ttt gaa 288
Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu
85 90 95

gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac 336
Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
100 105 110

```
tgt ttc atc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat       384
Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125

gga cct gtg atg caa aaa aag aca caa ggc tgg gaa ccc aac act gag       432
Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
    130                 135                 140

cgt ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt atg gct       480
Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160

ctg aag tta gaa gga ggc ggt cac tat ttg tgt gaa ttc aaa tct act       528
Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr
                165                 170                 175

tac aag gca aag aag cct gtg aag atg cca ggg tat cac tat gtt gac       576
Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190

cgc aaa ctg gat gta acc aat cac aac aag gat tac act tcc gtt ggg       624
Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Gly
        195                 200                 205

cag tgt gaa att tcc att gcc ccc aaa cct gtg gtc gcc                   663
Gln Cys Glu Ile Ser Ile Ala Pro Lys Pro Val Val Ala
    210                 215                 220
```

<210> 173

<211> 221

<212> PRT

<213> Montipora sp.

<400> 173

```
Met Ser Val Ser Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15

Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30

Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly
        35                  40                  45

Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Tyr Gln Tyr Gly
    50                  55                  60

Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Gly Tyr Val Lys
65                  70                  75                  80
```

```
Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110

Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125

Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
    130                 135                 140

Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160

Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr
                165                 170                 175

Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190

Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Gly
        195                 200                 205

Gln Cys Glu Ile Ser Ile Ala Pro Lys Pro Val Val Ala
    210                 215                 220
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<210> 174

<211> 660

<212> DNA

<213> Montipora sp.

<220>

<221> CDS

<222> (1)..(660)

<400> 174

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agt gtg atc gct aca caa atg acc tac aag gtt tat atg tca ggc acg        48
Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15
```

```
gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga aag cct        96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggc gga cct       144
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att tta tca cca cag tgt cag tac gga agc       192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Ser
    50                  55                  60

ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag cag       240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc ccg gag gga ttt aca tgg gag agg atc atg aac ttt gaa gat       288
Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac tgt       336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

ttc acc tac cat gtc aag ttc tct ggt ttg aac ttt cct cct aat gga       384
Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtg atg cag aag aag aca cag ggc tgg gaa ccc cac tct gag cgt       432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu Arg
    130                 135                 140

ctc ttt gca cgg ggt gga atg ctg ata gga aac aac ttt atg gct ctg       480
Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

aag tta gaa gga ggc ggt cac tat ttg tgt gaa ttc aaa act act tac       528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr Tyr
                165                 170                 175

aag gca aag aag cct gtg aag atg cca ggg tat cat tat gtt gac cgc       576
Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aaa ctg gat gta acc aat cac aac aag gat tac act tcc gtt gag cag       624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                       660
Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
```

<210> 175

<211> 220

<212> PRT

<213> Montipora sp.

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<400>  175

Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Ser
    50                  55                  60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu Arg
    130                 135                 140

Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr Tyr
                165                 170                 175

Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
```

<210> 176

<211> 660

<212> DNA

<213> Montipora sp.

<220>

<221> CDS

<222> (1)..(660)

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<400>  176
agt gtg atc gtt aca caa atg acc tac aag gtt tat atg tca ggc acg        48
Ser Val Ile Val Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

gtc aat gga cac tac ttt gag gtt gaa ggc gat gga aaa gga aag cct        96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

tac gaa ggg gag cag acg gta agg ctc act gtc aca aag ggc gga ccc       144
Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att tta tca cca cag tat cag tac gga agc       192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Tyr Gln Tyr Gly Ser
    50                  55                  60

ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag cag       240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc ccg gaa gga tat aca tgg gag agg atc atg aac ttt gaa gat       288
Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac tgt       336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

ttc atc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga       384
Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtg atg cag aag aag aca cag ggc tgg gaa ccc aac act gag cgt       432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt atg gct ctg       480
Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160
```

```
aag tta gaa gga ggc ggt cac tat ttg tgt gaa ttc aaa tct act tac       528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

aag gca aag aag cct gtg aag atg cca ggg tat cac tat gtt gac cgc       576
Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aaa ctg gat gta acc aat cac aac aag gat tac acc tcc gtt gag cag       624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                       660
Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220


<210>  177

<211>  220

<212>  PRT

<213>  Montipora sp.


<400>  177

Ser Val Ile Val Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Tyr Gln Tyr Gly Ser
    50                  55                  60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125
```

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
130 135 140

Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145 150 155 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
165 170 175

Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
180 185 190

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
195 200 205

Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
210 215 220

<210> 178

<211> 701

<212> DNA

<213> Acanthastria sp.

<400> 178
tccgttatcg ctaaacagat gaccgcttca acgttaagtt gacaacagga agcacgacgg 60

agactgcagt cccgtacgcg cgaacgggat acctgggatt tatcaagaga acagatttca 120

cgcagacaga tggagcccgg catgacgcgt tatttgtggt tggccctctt gaagaaacca 180

tgatattgcg tggtatgagg tatcacccgg tagatatcga gaacacagtg acgagatgtc 240

atcgatcaat ctgtgaaagt gcggtcttca cgatgacaaa cctacttgtg gtagcagtgg 300

agcttgatgc agatgaacgc gaggcacttg acgtggttcc gctggtgacg acatccgtac 360

tgaatgaaca gcaacttgtc gtaggggtgg tggtagtggt tgaccctggc gtagtcccga 420

tcaattctcg cggagagaaa caacggatgc atctgaggga cgggttcctg ggggaccagt 480

tggatcctat ctacgtggcg tataatatgt agacacctca ctgcttagtt tcgtaattga 540

attgtgtcgt agttttttta aatgacaatt aatagacaag tttgaaattg actgtagcgc 600

taggtttagg tataaactag cgtttggtaa ggcaattatg acaggaacta ctgtcacgcg 660

tgacgcgaga ccgtcacttt acacgcaaac ctgtggtcgc c 701

<210> 179

<211> 701

<212> DNA

<213> Green Pocillopora

<400> 179
tccgttatcg ctaaacagat gaccgcttca acgttaagtt gacaacagga agcacgacgg 60

agactgcagt cccgtacgcg cgaacgggat acctgggatt tatcaagaga acagatttca 120

cgcagacaga tggagcccgg catgacgcgt tatttgtggt tggccctctt gaagaaacca 180

tgatattgcg tggtatgagg tatcacccgg tagatatcga gaacacagtg acgagatgtc 240

atcgatcaat ctgtgaaagt gcggtcttca cgatgacaaa cctacttgtg gtagcagtgg 300

agcttgatgc agatgaacgc gaggcacttg acgtggttcc gctggtgacg acatccgtac 360

tgaatgaaca gcaacttgtc gtaggggtgg tggtagtggt tgaccctggt gtagtcccga 420

tcaattctcg cggagagaaa caacggatgc atctgaggga cgggttcctg gggaccagt 480

tggatcctat ctacgtggcg tataatatgt agacacctca ctgcttaatt ttcgtaattg 540

aattgtgtcg tagttttttt aaatgacaac taatagacag tttgaaattg actgtagcgc 600

taggtttagg tataaactag cgtttggtaa ggcaattatg acaggaatta ctgtcacgcg 660

tgacgcgaga ccgtcacttt acacgcaaac ctgtggtcgc c 701

<210> 180

<211> 701

<212> DNA

<213> Green Pocillopora

<220>

<221> misc_feature

<222> (634)..(634)

<223> n = any nucleotide

<220>

<221> misc_feature

<222> (640)..(640)

<223> n = any nucleotide

<400> 180
tccgttatcg ctaaacagat gaccgcttca acgttaagtt gacaacagga agcacgacgg 60

agactgcagt cccgtacgcg cgaacgggat acctgggatt tatcaagaga acagatttca 120

cgcagacaga tggagcccgg catgacgcgt tatttgtggt tggccctctt gaagaaacca 180

tgatattgcg tggtatgagg tatcacccgg tagatatcga gaacacagtg acgagatgtc 240

atcgatcaat ctgtgaaagt gcggtcttca cgatgacaaa cctacttgtg gtagcagtgg 300

agcttgatgc agatgaacgc gaggcacttg acgtggttcc gctggtgacg acatccgtac 360

tgaatgaaca gcaacttgtc gtaggggtgg tggtagtggt tgaccctggc gtagtcccga 420

tcaattctcg cggagagaaa caacggatgc atctgaggga cgggttcctg ggggaccagt 480

tggatcctat ctacgtggcg tataatatgt agacacctca ctgcttagtt tcgtaattga 540

attgtgtcgt agttttttta aatgacaatt aatagacaag tttgaaattg actgtagcgc 600

taggtttagg tataaactag cgtttggtaa ggcnattatn acaggaacta ctgtcacgcg 660

tgacgcgaga ccgtcacttt acacgcaaac ctgtggtcgc c 701

<210> 181

<211> 701

<212> DNA

<213> Green Pocillopora

<400> 181
tccgttatcg ctaaacagat gaccgcttca ccgttaagtt gacaacagga agcacgacgg 60

agactgcagt cccgtacgcg cgaacgggat acctgggatt tatcaagaga acagatttca 120

cgcagacagg tggagcccgg catgacgcgt tatttgtggt tggccctctt gaagaaacca 180

tgatattgcg tggtatgagg tatcacccgg tagatatcga gaacacagtg acgagatgtc 240

atcgatcaat ctgtgaaagt gcggtcttca cgatgacaaa cctacttgtg gtagcagtgg 300

agcttgatgc agatgaacgc gaggcacttg acgtggttcc gctggtgacg acatccgtac 360

tgaatgaaca gcaacttgtc gtaggggtgg tggtagtggt tgaccctggt gtagtcccga 420

tcaattctcg cggagagaaa caacggatgc atctgaggga cgggttcctg ggggaccagt 480

tggatcctat ctacgtggcg tataatatgt agacacctca ctgcttagtt tcgtaattga 540

attgtgtcgt agttttttta aatgacaatt aatagacaag tttgaaattg actgtagcgc 600

taggtttagg tataaactag cgtttggtaa ggcaattatg acaggaatta ctgtcacgcg 660

tgacgcgaga ccgtcacttc acacgcaaac ctgtggtcgc c 701

<210> 182

<211> 701

<212> DNA

<213> Millepora sp. (Hydrozoan)

<400> 182
tccgttatcg ctaaacagat gaccgcttca acgttaagtt gacaacagga agcacgacgg 60

agactgcagt cccgtacgcg cgaacgggat acctgggatt tatcaagaga acagatttca 120

cgcagacagg tggagcccgg catgacgcgt tatttgtggt tggccctctt gaagaaacca 180

tgatattgcg tggtatgagg tatcacccgg tagatatcga gaacacagtg acgagatgtc 240

atcgatcaat ctgtgaaagt gcggtcttca cgatgacaaa cctacttgtg gtagcagtgg 300

agcttgatgc agatgaacgc gaggcacttg acgtggttcc gctggtgacg acatccgtac 360

tgtatgaaca gcaacttgtc gtaggggtgg tggtagtggt tgaccctggt gtagtcccga 420

tcaattctcg cggagagaaa caacggatgc atctgaggga cgggttcctg ggggaccagt 480

tggatcctat ctacgtggcg tataatatgt agacacctca ctgcttagtt tcgtaattga 540

attgtgtcgt agttttttta aatgacaatt aatagacaag tttgaaattg actgtagcgc 600

taggtttagg tataaactag cgtttggtaa ggcaattatg acaggaatta ctgtcacgcg 660

tgacgcgaga ccgtcacttc acacgcaaac ctgtggtcgc c 701

<210> 183

<211> 701

<212> DNA

<213> Pavona decussaca

<220>

<221> CDS

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<222>  (1)..(699)


<400>  183
tcc gtt atc gct aaa cag atg acc gct tca acg tta agt tga caa cag        48
Ser Val Ile Ala Lys Gln Met Thr Ala Ser Thr Leu Ser     Gln Gln
1               5                   10                      15

gaa gca cga cgg aga ctg cag tcc cgt acg cgc gaa cgg gat acc tgg        96
Glu Ala Arg Arg Arg Leu Gln Ser Arg Thr Arg Glu Arg Asp Thr Trp
                20                  25                  30

gat tta tca aga gaa cag att tca cgc aga cag atg gag ccc ggc atg       144
Asp Leu Ser Arg Glu Gln Ile Ser Arg Arg Gln Met Glu Pro Gly Met
            35                  40                  45

acg cgt tat ttg tgg ttg gcc ctc ttg aag aaa cca tga tat tgc gtg       192
Thr Arg Tyr Leu Trp Leu Ala Leu Leu Lys Lys Pro     Tyr Cys Val
        50                  55                      60

gta tga ggt atc acc cgg tag ata tcg aga aca cag tga cga gat gtc       240
Val     Gly Ile Thr Arg     Ile Ser Arg Thr Gln     Arg Asp Val
            65                      70                      75

atc gat caa tct gtg aaa gtg cgg tct tca cga tga caa acc tac ttg       288
Ile Asp Gln Ser Val Lys Val Arg Ser Ser Arg     Gln Thr Tyr Leu
                80                  85                      90

tgg tag cag tgg agc ttg atg cag atg aac gcg agg cac ttg acg tgg       336
Trp     Gln Trp Ser Leu Met Gln Met Asn Ala Arg His Leu Thr Trp
                95                  100                     105

ttc cgc tgg tga cga cat ccg tac tga atg aac agc aac ttg tcg tag       384
Phe Arg Trp     Arg His Pro Tyr     Met Asn Ser Asn Leu Ser
                    110                     115

ggg tgg tgg tag tgg ttg acc ctg gcg tag tcc cga tca att ctc gcg       432
Gly Trp Trp     Trp Leu Thr Leu Ala     Ser Arg Ser Ile Leu Ala
    120                     125                     130

gag aga aac aac gga tgc atc tga ggg acg ggt tcc tgg ggg acc agt       480
Glu Arg Asn Asn Gly Cys Ile     Gly Thr Gly Ser Trp Gly Thr Ser
        135                         140                 145

tgg atc cta tct acg tgg cgt ata ata tgt aga cac ctc act gct tag       528
Trp Ile Leu Ser Thr Trp Arg Ile Ile Cys Arg His Leu Thr Ala
        150                 155                     160

ttt cgt aat tga att gtg tcg tag ttt ttt taa atg aca att aat aga       576
Phe Arg Asn     Ile Val Ser     Phe Phe     Met Thr Ile Asn Arg
        165                         170                     175

caa gtt tga aat tga ctg tag cgc tag gtt tag gta taa act agc gtt       624
Gln Val     Asn     Leu     Arg     Val     Val     Thr Ser Val
                            180                             185

tgg taa ggc aat tat gac agg aac tac tgt cac gcg tga cgc gag acc       672
Trp     Gly Asn Tyr Asp Arg Asn Tyr Cys His Ala     Arg Glu Thr
                    190                 195
```

```
gtc act tta cac gca aac ctg tgg tcg cc                          701
Val Thr Leu His Ala Asn Leu Trp Ser
200                 205


<210>  184

<211>  13

<212>  PRT

<213>  Pavona decussaca



<400>  184

Ser Val Ile Ala Lys Gln Met Thr Ala Ser Thr Leu Ser
1               5                   10


<210>  185

<211>  46

<212>  PRT

<213>  Pavona decussaca



<400>  185

Gln Gln Glu Ala Arg Arg Arg Leu Gln Ser Arg Thr Arg Glu Arg Asp
1               5                   10                  15


Thr Trp Asp Leu Ser Arg Glu Gln Ile Ser Arg Arg Gln Met Glu Pro
            20                  25                  30


Gly Met Thr Arg Tyr Leu Trp Leu Ala Leu Leu Lys Lys Pro
        35                  40                  45

<210>  186

<211>  4

<212>  PRT

<213>  Pavona decussaca



<400>  186

Tyr Cys Val Val
1
```

<210> 187

<211> 4

<212> PRT

<213> Pavona decussaca

<400> 187

```
Gly Ile Thr Arg
1
```

<210> 188

<211> 5

<212> PRT

<213> Pavona decussaca

<400> 188

```
Ile Ser Arg Thr Gln
1               5
```

<210> 189

<211> 14

<212> PRT

<213> Pavona decussaca

<400> 189

```
Arg Asp Val Ile Asp Gln Ser Val Lys Val Arg Ser Ser Arg
1               5                   10
```

<210> 190

<211> 5

<212> PRT

<213> Pavona decussaca

<400> 190

Gln Thr Tyr Leu Trp
1 5

<210> 191

<211> 17

<212> PRT

<213> Pavona decussaca

<400> 191

Gln Trp Ser Leu Met Gln Met Asn Ala Arg His Leu Thr Trp Phe Arg
1 5 10 15

Trp

<210> 192

<211> 4

<212> PRT

<213> Pavona decussaca

<400> 192

Arg His Pro Tyr
1

<210> 193

<211> 6

<212> PRT

<213> Pavona decussaca

<400> 193

Met Asn Ser Asn Leu Ser
1 5

<210> 194

<211> 5

<212> PRT

<213> Pavona decussaca

<400> 194

```
Trp Leu Thr Leu Ala
1               5
```

<210> 195

<211> 13

<212> PRT

<213> Pavona decussaca

<400> 195

```
Ser Arg Ser Ile Leu Ala Glu Arg Asn Asn Gly Cys Ile
1               5                   10
```

<210> 196

<211> 23

<212> PRT

<213> Pavona decussaca

<400> 196

```
Gly Thr Gly Ser Trp Gly Thr Ser Trp Ile Leu Ser Thr Trp Arg Ile
1               5                   10                  15

Ile Cys Arg His Leu Thr Ala
            20
```

<210> 197

<211> 7

<212> PRT

<213> Pavona decussaca

<400> 197

```
Met Thr Ile Asn Arg Gln Val
1               5


<210>  198

<211>  4

<212>  PRT

<213>  Pavona decussaca


<400>  198

Thr Ser Val Trp
1


<210>  199

<211>  10

<212>  PRT

<213>  Pavona decussaca


<400>  199

Gly Asn Tyr Asp Arg Asn Tyr Cys His Ala
1               5                   10


<210>  200

<211>  12

<212>  PRT

<213>  Pavona decussaca


<400>  200

Arg Glu Thr Val Thr Leu His Ala Asn Leu Trp Ser
1               5                   10


<210>  201

<211>  231

<212>  PRT

<213>  coral
```

<400> 201

Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1 5 10 15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
20 25 30

Tyr Glu Gly Glu Gln Thr Val Arg Leu Ala Val Thr Lys Gly Gly Pro
35 40 45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Ser
50 55 60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65 70 75 80

Ser Phe Pro Gly Arg Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
85 90 95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
100 105 110

Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
115 120 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
130 135 140

Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145 150 155 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
165 170 175

Lys Ala Arg Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
180 185 190

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
195 200 205

Arg Glu Ile Ser Ile Ala Arg Lys Pro Leu Val Ala Cys Cys Phe Phe
210 215 220

Arg Val Lys Ser Arg His Lys
225 230

<210> 202

<211> 235

<212> PRT

<213> coral

<400> 202

```
Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Leu Pro
            20                  25                  30

Tyr Glu Gly Gly Gln Thr Val Arg Leu Ala Val Thr Lys Gly Gly Pro
        35                  40                  45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Ser
    50                  55                  60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

Ser Phe Pro Gly Arg Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

Phe Ile Tyr His Val Lys Arg Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

Lys Leu Asp Val Thr Asn His Asn Leu Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala Cys Arg Phe Phe
    210                 215                 220

Arg Val Lys Ser Arg His Lys Tyr Ala Val Ala
225                 230                 235
```

<210> 203

<211> 49

<212> DNA

<213> oligonucleotide

<400> 203
tgagagaact agtctcgagc tctagaacaa gcttttttt ttttttttt 49

<210> 204

<211> 41

<212> DNA

<213> oligonucleotide

<400> 204
cagggcgcgc catgggatcc gttatcgcta aacagatgac c 41

<210> 205

<211> 38

<212> DNA

<213> oligonucleotide

<400> 205
gggttaatta agctgcaggg cgaccacagg tttgcgtg 38

<210> 206

<211> 18

<212> DNA

<213> oligonucleotide

<400> 206
cccgaaaagt gccacctg 18

<210> 207

<211> 19

<212> DNA

<213> oligonucleotide

<400> 207
gttctgaggt cattactgg 19

<210> 208

<211> 20

<212> DNA

<213> oligonucleotide

<400> 208
tcagggtact tggtgaatgg 20

<210> 209

<211> 669

<212> DNA

<213> Acropora sp

<400> 209
ggatccgtta tcgctaaaca gatgacctac aaggtttata tgtcaggcac ggtcaatgga 60

cactactttg aggtcgaagg cgatggaaaa ggaaagcctt acgaggggga gcagacggta 120

aagctcactg tcaccaaggg tggacctctg ccatttgctt gggatatttt atcaccacag 180

tcacagtacg gaagcatacc attcaccaag taccctgaag acatcccgga ctatgtaaag 240

cagtcattcc cggagggata tacatgggag aggatcatga actttgaaga tggtgcagtg 300

tgtactgtca gcaatgactc cagcatccaa ggcaactgtt tcatctacca tgtcaagttc 360

tctggtttga actttcctcc caatggacct gttatgcaga agaagacaca gggctgggaa 420

cccaacactg agcgtctctt tgcacgagat ggaatgctga taggaaacaa ctttatggct 480

ctgaagttag aaggaggtgg tcactatttg tgtgaattca aatctactta caaggcaaag 540

aagcctgtga agatgccagg gtatcactat gttgaccgca aactggatgt aaccaatcac 600

aacaaggatt acacttccgt tgagcagtgt gaaatttcca ttgcacgcaa acctgtggtc 660

gccctgcag 669

<210> 210

<211> 222

<212> PRT

<213> Acropora sp

<400> 210

```
Gly Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15

Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30
```

```
Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly
        35                  40                  45

Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly
    50                  55                  60

Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80

Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110

Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125

Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
    130                 135                 140

Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Leu
145                 150                 155                 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala Leu Gln
    210                 215                 220
```

<210> 211

<211> 669

<212> DNA

<213> Discosoma sp

<400> 211

```
ggatccgtta tcgctaaaca gatgacctac aaagtttata tgtcaggcac ggtcaatgga      60

cactactttg aggtcgaagg cgatggaaaa ggaaagcctt acgaggggga gcagacggta     120

aggctgactg tcaccaaggg cggacctctg ccatttgctt gggatatttt atcaccacag     180

tcacagtacg gaagcatacc attcaccaag taccctgaag acatccctga ctatgtaaag     240

cagtcattcc cggagggata tacatgggag aggatcatga actttgaaga tggtgcagtg     300

tgtactgtca gcaatgattc cagcatccaa ggcaactgtt tcatctacca tgtcaagttc     360

tctggtttga actttcctcc caatggacct gttatgcaga agaagacaca gggctgggaa     420
```

```
cccaacactg agcgtctctt agcacgagat ggaatgctga taggaaacaa ctttatggct     480

ctgaagttag aaggaggtgg tcactatttg tgtgaattca aatctactta caaggcaagg     540

aagcctgtga agatgccagg gtatcactat gttgaccgca aactggatgt aaccaatcac     600

aacaaggatt acacttccgt tgagcagcgt gaaatttcca ttgcacgcaa acctgtggtc     660

gccctgcag                                                             669
```

<210> 212

<211> 222

<212> PRT

<213> Discosoma sp

<400> 212

```
Gly Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15

Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30

Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly
        35                  40                  45

Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly
    50                  55                  60

Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80

Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110

Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125

Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
    130                 135                 140

Arg Leu Leu Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Leu
145                 150                 155                 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

Lys Ala Arg Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205
```

```
Arg Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala Leu Gln
    210                 215                 220
```

<210> 213

<211> 669

<212> DNA

<213> Sinularia sp

<400> 213

```
ggatccgtta tcgctaaaca gatgacctac aaggtttata tgtcaggcac ggtcaatgga      60

cactactttg aggtcgaagg cgatggaaaa ggaaagcctt acgaggggga gcagacggta     120

aagctcactg tcaccaaggg tggacctctg ccatttgctt gggatatttt atcaccacag     180

tcacagtacg gaagcatacc attcaccaag taccctgaag acatcccgga ctatgtaaag     240

cagtcattcc cggaggggta tacatgggag aggatcatga actttgaaga tggtgcagtg     300

tgtactgtca gcaatgactc cagcatccaa ggcaactgtt tcatctacca tgtcaagttc     360

tctggtttga actttccttc caatggacct gttatgcaga agaagacaca gggctgggaa     420

cccaacactg agcgtctctt tgcacgagat ggaatgctga taggaaacaa ctttatggct     480

ctgaagttag aaggaggtgg tcactatttg tgtgaattca aatctactta caaggcaaag     540

aagcctgtga agatgccagg gtatcactat gttgaccgca aactggatgt aaccaatcac     600

aacaaggatt acacttccgt tgagcagtgt gaaatttcca ttgcacgcaa acctttggtc     660

gccctgcag                                                             669
```

<210> 214

<211> 223

<212> PRT

<213> Sinularia sp

<400> 214

```
Gly Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15

Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30

Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly
        35                  40                  45
```

Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly
    50   55   60

Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65   70   75   80

Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu
                85   90   95

Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100   105   110

Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Ser Asn
        115   120   125

Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
    130   135   140

Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145   150   155   160

Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr
                165   170   175

Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
            180   185   190

Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
        195   200   205

Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Leu Val Ala Leu Gln
    210   215   220

<210> 215

<211> 669

<212> DNA

<213> Tubastrea sp

<400> 215
ggatccgtta tcgctaaaca gatgacctac aaggtttata tgtcaggcac ggtcaatgga 60

cactactttg aggtcgaagg cgatggaaaa ggaaagcctt acgaggggga gcagacggta 120

aagctcactg tcaccaaggg tggacctctg ccatttgctt gggatatttt atcaccacag 180

tcacagtacg gaagcatacc attcaccaag taccctgaag acatcccgga ctatgtaaag 240

cagtcattcc cggagggata tacatgggag aggatcatga actttgaaga tggtgcagtg 300

tgtactgtca gcaatgactc cagcatccaa ggcaactgtt tcatctacca tgtcaagttc 360

tctggtttga actttcctcc caatggacct gttatgcaga agaagacaca gggctgggaa 420

cccaacactg agcgtctctt tgcacgagat ggaatgctga taggaaacaa ctttatggct 480

ctgaagttag aaggaggtgg tcactatttg tgtgaattca aatctactta caaggcaaag 540

```
aagcctgtga agatgccagg gtatcactat gttgaccgca aactggatgt aaccaatcac     600

aacaaggatt acacttccgt tgagcagtgt gaaatttcca ttgcgcgcaa acctgtggtc     660

gccctgcag                                                              669


<210>  216

<211>  223

<212>  PRT

<213>  Tubastrea sp



<400>  216

Gly Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15

Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30

Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly
        35                  40                  45

Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly
    50                  55                  60

Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80

Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110

Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125

Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
    130                 135                 140

Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160

Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr
                165                 170                 175

Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190

Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
        195                 200                 205

Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala Leu Gln
    210                 215                 220
```

<210> 217

<211> 669

<212> DNA

<213> Discosoma sp

<400> 217
ggatccgtta tcgctaaaca gatgacctac aaggtttata tgtcaggcac ggtcaatgga 60

cactactttg aggtcgaagg cgatggaaaa ggaaagcctt acgaggggga gcagacggta 120

aggctggctg tcaccaaggg cggacctctg ccatttgctt gggatatttt atcaccacag 180

tgtcagtacg gaagcatacc attcaccaag taccctgaag acatccctga ctatgtaaag 240

cagtcattcc cggagggatt tacatgggag aggatcatga actttgaaga tggtgcagtg 300

tgtcctgtca gcaatgattc cagcatccaa ggcaactgtt tcatctacca tgtcaagttc 360

tctggtttga actttcctcc caatggacct gttatgcaga agaagacaca gggctgggaa 420

ccccactctg agcgtctctt tgcacgagac ggaatgctga taggaaacac ctttatggct 480

ctgaagttag aaggaggcgg tcactatttg tgtgaattca aaactactta caaggcaaag 540

aagcctgtga agatgccagg gtatcattat gttgaccgca aactggatgt aatcaatcac 600

aacaaggatt acacttccgt tgagcagtgt gaaatttcca ttgcacgcaa acctgtggtc 660

gccctgcag 669

<210> 218

<211> 223

<212> PRT

<213> Discosoma sp

<400> 218

Gly Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1 5 10 15

Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
20 25 30

Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Ala Val Thr Lys Gly Gly
35 40 45

Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly
50 55 60

```
Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80

Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

Asp Gly Ala Val Cys Pro Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110

Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125

Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu
    130                 135                 140

Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Thr Phe Met Ala
145                 150                 155                 160

Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr
                165                 170                 175

Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190

Arg Lys Leu Asp Val Ile Asn His Asn Lys Asp Tyr Thr Ser Val Glu
        195                 200                 205

Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala Leu Gln
    210                 215                 220

<210>  219

<211>  555

<212>  DNA

<213>  Sinularia sp


<400>  219
acggtaaggc tggctgtcac caagggcgga cctctgccat ttgcttggga tattttatca      60

ccacagtgtc agtacggaag cataccattc accaagtacc ttgaagacat ccctgactat     120

gtaaagcagt cattcccgga gggatttaca tgggagagga tcatgaactt tgaagatggt     180

gcagtgtgta ctgtcagcaa tgattccagc atccaaggca actgtttcat ctaccatgtc     240

aagttctctg gtttgaactt tcctcccaat ggacctgtta tgcagaagaa gacacagggc     300

tgggaaccca acactgagcg tctctttgca cgagatggaa tgctgatagg aaacaacttt     360

atggctctaa agttagaggg aggtggtcac tatttgtgtg aattcaaatc tacttacaag     420

gcaaagaagc ctgtgaagat gccagggtat cactatgttg accgcaaact ggatgtaacc     480

aatcacaaca aggattacac ttccgttgag cagtgtgaaa tttccattgc acgcaaacct     540

ttggtcgccc tgcag                                                      555
```

<210> 220

<211> 223

<212> PRT

<213> Sinularia sp

<400> 220

```
Gly Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15

Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30

Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Ala Val Thr Lys Gly Gly
        35                  40                  45

Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly
    50                  55                  60

Ser Ile Pro Phe Thr Lys Tyr Leu Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80

Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110

Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125

Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
    130                 135                 140

Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160

Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr
                165                 170                 175

Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190

Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
        195                 200                 205

Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Leu Val Ala Leu Gln
    210                 215                 220
```

<210> 221

<211> 669

<212> DNA

<213> Tubastrea sp

<400> 221
ggatccgtta tcgctaaaca gatgacctac aaggtttata tgtcaggcac ggtcaatgga 60

cactactttg aggtcgaagg cgatggaaaa ggaaagcctt acgaggggga gcagacggta 120

aggctggctg tcaccaaggg cggacctctg ccatttgctt gggatatttt atcaccacag 180

tgtcagtacg gaagcatacc attcaccaag taccctgaag acatccctga ctatgtaaag 240

cggtcattcc cggagggatt tacatgggag aggatcatga actttgaaga tggtgcagtg 300

tgtactgtca gcaatgattc cagcatccaa ggcaactgtt tcatctacca tgtcaagttc 360

tctggtttga actttcctcc caatggacct gttatgcaga agaagacaca gggctgggaa 420

ccccactctg agcgtctctt tgcacgagac ggaatgctga taggaaacaa ctttatggct 480

ctgaagttag aaggaggcgg tcactatttg tgtgaattca aaactactta caaggcaaag 540

aagcctgtga agatgccagg gtatcattat gttgaccgca aactggatgt aatcaatcac 600

aacaaggatt acacttccgt tgagcagtgt gaaatttcca ttgcacgcaa acctgtggtc 660

gccctgcag 669

<210> 222

<211> 223

<212> PRT

<213> Tubastrea sp

<400> 222

```
Gly Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15

Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30

Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Ala Val Thr Lys Gly Gly
        35                  40                  45

Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly
    50                  55                  60

Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80

Arg Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95
```

```
Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110

Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125

Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu
    130                 135                 140

Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160

Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr
                165                 170                 175

Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190

Arg Lys Leu Asp Val Ile Asn His Asn Lys Asp Tyr Thr Ser Val Glu
        195                 200                 205

Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala Leu Gln
    210                 215                 220
```

<210> 223

<211> 46

<212> DNA

<213> oligonucleotide

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<400> 223
cagggcgcgc caaggagata taacaatggc ttcctcagtt ctttcc              46
```

<210> 224

<211> 33

<212> DNA

<213> oligonucleotide

```
<400> 224
cactggatcc gcattgcact cttccgccgt tgc                            33
```

<210> 225

<211> 45

<212> DNA

<213> oligonucleotide

<400> 225
gcatggcgcg ccaaggagat ataacaatga agactaatct ttttc 45

<210> 226

<211> 34

<212> DNA

<213> oligonucleotide

<400> 226
gcatggatcc gaattcggcc gaggataatg atag 34

<210> 227

<211> 45

<212> DNA

<213> oligonucleotide

<400> 227
gcatggcgcg ccaaggagat ataacaatga agactaatct ttttc 45

<210> 228

<211> 34

<212> DNA

<213> oligonucleotide

<400> 228
gcatggatcc gaattcggcc gaggataatg atag 34

<210> 229

<211> 46

<212> DNA

<213> oligonucleotide

<400> 229
gatcttaatt aaagctcatc atgctgcagg gcgaccacag gtttgc 46

<210> 230

<211> 42

<212> DNA

<213> oligonucleotide

<400> 230
gcatctgcag gtcgccacca gtaaaggaga agaacttttc ac 42

<210> 231

<211> 39

<212> DNA

<213> oligonucleotide

<400> 231
ctgattaatt aattatttgt atagttcatc catgccatg 39

<210> 232

<211> 55

<212> DNA

<213> oligonucleotide

<400> 232
cagggcgcgc caaggagata taacaatggg atccgttatc gctaaacaga tgacc 55

<210> 233

<211> 45

<212> DNA

<213> oligonucleotide

<400> 233
ggctctagaa aggagatata caatgtccgt tatcgctaaa cagat 45

<210> 234

<211> 45

<212> DNA

<213> oligonucleotide

<400> 234
ggctctagaa aggagatata caatgtccgt tatcgctaaa cagat 45

<210> 235

<211> 50

<212> DNA

<213> oligonucleotide

<400> 235
ggcaagcttt cagtggtggt ggtggtggtg ggcgaccaca ggtttgcgtg 50

<210> 236

<211> 221

<212> PRT

<213> coral

<400> 236

```
Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15

Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30

Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly
        35                  40                  45

Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly
    50                  55                  60

Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80

Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110

Cys Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125
```

Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser Ser Glu
130 135 140

His Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn His Met Ala
145 150 155 160

Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr
165 170 175

Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
180 185 190

Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
195 200 205

Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
210 215 220

<210> 237

<211> 221

<212> PRT

<213> coral

<400> 237

Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1 5 10 15

Thr Val Asn Gly His Tyr Phe Glu Val Gln Gly Asp Gly Lys Gly Lys
20 25 30

Pro Tyr Glu Glu Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly
35 40 45

Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly
50 55 60

Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65 70 75 80

Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu
85 90 95

Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
100 105 110

Cys Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
115 120 125

Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
130 135 140

Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145 150 155 160

Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr
165 170 175

Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
180 185 190

Arg Lys Leu Asp Val Thr Asn His Asn Ile Asp Tyr Thr Ser Val Glu
195 200 205

Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
210 215 220

<210> 238

<211> 226

<212> PRT

<213> coral

<400> 238

Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1 5 10 15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
20 25 30

Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly Pro
35 40 45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
50 55 60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65 70 75 80

Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
85 90 95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
100 105 110

Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
115 120 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
130 135 140

Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145 150 155 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
165 170 175

Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr Val Asp Arg
180 185 190

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
195 200 205

Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala Trp Cys Phe Phe
210 215 220

Arg Val
225

<210> 239

<211> 220

<212> PRT

<213> coral

<400> 239

Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1 5 10 15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
20 25 30

Tyr Glu Gly Glu Gln Thr Val Arg Leu Ala Val Thr Lys Gly Gly Pro
35 40 45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Ser
50 55 60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65 70 75 80

Ser Phe Pro Gly Arg Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
85 90 95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
100 105 110

Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
115 120 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
130 135 140

Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145 150 155 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
165 170 175

Lys Ala Arg Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
180 185 190

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
195 200 205

```
Arg Glu Ile Ser Ile Ala Arg Lys Pro Leu Val Ala
    210                 215                 220

<210>  240

<211>  230

<212>  PRT

<213>  coral



<400>  240

Met Ser Cys Ser Lys Asn Val Ile Lys Glu Phe Met Arg Phe Lys Val
1               5                   10                  15

Arg Met Glu Gly Thr Val Asn Gly His Glu Phe Glu Ile Lys Gly Glu
            20                  25                  30

Gly Glu Gly Arg Pro Tyr Glu Gly His Cys Ser Val Lys Leu Met Val
        35                  40                  45

Thr Lys Gly Gly Pro Leu Pro Phe Ala Phe Asp Ile Leu Ser Pro Gln
    50                  55                  60

Phe Gln Tyr Gly Ser Lys Val Tyr Val Lys His Pro Ala Asp Ile Pro
65                  70                  75                  80

Asp Tyr Lys Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val
                85                  90                  95

Met Asn Phe Glu Asp Gly Gly Val Val Thr Val Ser Gln Asp Ser Ser
            100                 105                 110

Leu Lys Asp Gly Cys Phe Ile Tyr Glu Val Lys Phe Ile Gly Val Asn
        115                 120                 125

Phe Pro Ser Asp Gly Pro Val Met Gln Arg Arg Thr Arg Gly Trp Glu
    130                 135                 140

Ala Ser Ser Glu Arg Leu Tyr Pro Arg Asp Gly Val Leu Lys Gly Asp
145                 150                 155                 160

Ile His Met Ala Leu Arg Leu Glu Gly Gly Gly His Tyr Leu Val Glu
                165                 170                 175

Phe Lys Ser Ile Tyr Met Val Lys Lys Pro Ser Val Gln Leu Pro Gly
            180                 185                 190

Tyr Tyr Tyr Val Asp Ser Lys Leu Asp Met Thr Ser His Asn Glu Asp
        195                 200                 205

Tyr Thr Val Val Glu Gln Tyr Glu Lys Thr Gln Gly Arg His His Pro
    210                 215                 220

Phe Ile Lys Pro Leu Gln
225                 230
```

<210> 241

<211> 225

<212> PRT

<213> coral

<400> 241

```
Met Arg Ser Ser Lys Asn Val Ile Lys Glu Phe Met Arg Phe Lys Val
1               5                   10                  15

Arg Met Glu Gly Thr Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu
            20                  25                  30

Gly Glu Gly Arg Pro Tyr Glu Gly His Asn Thr Val Lys Leu Lys Val
        35                  40                  45

Thr Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln
    50                  55                  60

Phe Gln Tyr Gly Asn Lys Val Tyr Val Lys His Pro Ala Asp Ile Pro
65                  70                  75                  80

Asp Tyr Lys Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Trp
                85                  90                  95

Met Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser
            100                 105                 110

Leu Gln Asp Gly Cys Phe Ile Tyr Lys Val Lys Phe Ile Gly Val Asn
        115                 120                 125

Phe Pro Ser Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu
    130                 135                 140

Ala Ser Thr Lys Arg Leu Tyr Pro Arg Asp Gly Val Leu Lys Gly Glu
145                 150                 155                 160

Ile His Lys Ala Leu Lys Leu Lys Asp Gly Gly His Tyr Leu Val Glu
                165                 170                 175

Phe Lys Ser Ile Tyr Met Ala Lys Lys Pro Val Gln Leu Pro Gly Tyr
            180                 185                 190

Tyr Tyr Val Asp Ser Lys Leu Asp Ile Thr Ser His Asn Glu Asp Tyr
        195                 200                 205

Thr Ile Val Glu Gln Tyr Glu Arg Thr Glu Gly Arg His His Leu Phe
    210                 215                 220

Leu
225
```

<210> 242

<211> 230

<212> PRT

<213> coral

<400> 242

```
Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
                165                 170                 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
            180                 185                 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
        195                 200                 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
    210                 215                 220

Thr Ala Ala Gly Ile Thr
225                 230
```

<210> 243

<211> 818

<212> DNA

<213> Aequorea victoria

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<400>  243
ggatccaagg agatataaca atgaagacta atctttttct ctttctcatc ttttcacttc      60

tcctatcatt atcctcggcc gaattcagta aaggagaaga acttttcact ggagttgtcc     120

caattcttgt tgaattagat ggtgatgtta atgggcacaa attttctgtc agtggagagg     180

gtgaaggtga tgcaacatac ggaaaactta cccttaaatt tatttgcact actggaaaac     240

tacctgttcc atggccaaca cttgtcacta ctttctctta tggtgttcaa tgcttttcaa     300

gatacccaga tcatatgaag cggcacgact tcttcaagag cgccatgcct gagggatacg     360

tgcaggagag gaccatcttc ttcaaggacg acgggaacta caagacacgt gctgaagtca     420

agtttgaggg agacaccctc gtcaacagga tcgagcttaa gggaatcgat ttcaaggagg     480

acggaaacat cctcggccac aagttggaat acaactacaa ctcccacaac gtatacatca     540

tggcagacaa acaaaagaat ggaatcaaag ttaacttcaa aattagacac aacattgaag     600

atggaagcgt tcaactagca gaccattatc aacaaaatac tccaattggc gatggccctg     660

tccttttacc agacaaccat tacctgtcca cacaatctgc cctttcgaaa gatcccaacg     720

aaaagagaga ccacatggtc cttcttgagt ttgtaacagc tgctgggatt acacatggca     780

tggatgaact atacaaacat gatgagcttt aagagctc                              818


<210>  244

<211>  263

<212>  PRT

<213>  Aequorea victoria


<400>  244

Met Lys Thr Asn Leu Phe Leu Phe Leu Ile Phe Ser Leu Leu Leu Ser
1               5                   10                  15

Leu Ser Ser Ala Glu Phe Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
            20                  25                  30

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
        35                  40                  45

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
    50                  55                  60

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
65                  70                  75                  80

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
                85                  90                  95
```

```
Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
            100                 105                 110

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
        115                 120                 125

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
    130                 135                 140

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
145                 150                 155                 160

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
                165                 170                 175

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
            180                 185                 190

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
        195                 200                 205

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
    210                 215                 220

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
225                 230                 235                 240

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
                245                 250                 255

Leu Tyr Lys His Asp Glu Leu
            260
```

<210> 245

<211> 235

<212> PRT

<213> Acropora aspera

<400> 245

```
Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

Tyr Glu Gly Glu Gln Thr Val Arg Leu Ala Val Thr Lys Gly Gly Pro
        35                  40                  45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Ser
    50                  55                  60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80
```

```
Ser Phe Pro Gly Arg Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala Cys Arg Phe Phe
    210                 215                 220

Arg Val Lys Ser Arg His Lys Val Ala Val Ala
225                 230                 235

<210>  246

<211>  232

<212>  PRT

<213>  Acropora aspera


<400>  246

Met Ala Ser Phe Leu Lys Lys Thr Met Pro Phe Lys Thr Thr Ile Glu
1               5                   10                  15

Gly Thr Val Asn Gly His Tyr Phe Lys Cys Thr Gly Lys Gly Glu Gly
            20                  25                  30

Asn Pro Phe Glu Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly
        35                  40                  45

Gly Pro Leu Pro Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr
    50                  55                  60

Gly Ser Lys Thr Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe
65                  70                  75                  80

Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr
                85                  90                  95
```

```
Glu Asp Gly Gly Phe Leu Thr Ala His Gln Asp Thr Ser Leu Asp Gly
            100                 105                 110

Asp Cys Leu Val Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro Ala
        115                 120                 125

Asp Gly Pro Val Met Gln Asn Lys Ala Gly Arg Trp Glu Pro Ala Thr
    130                 135                 140

Glu Ile Val Tyr Glu Val Asp Gly Val Leu Arg Gly Gln Ser Leu Met
145                 150                 155                 160

Ala Leu Lys Cys Pro Gly Gly Arg His Leu Thr Cys His Leu His Thr
                165                 170                 175

Thr Tyr Arg Ser Lys Lys Pro Ala Ser Ala Leu Lys Met Pro Gly Phe
            180                 185                 190

His Phe Glu Asp His Arg Ile Glu Ile Met Glu Glu Val Glu Lys Gly
        195                 200                 205

Lys Cys Tyr Lys Gln Tyr Glu Ala Ala Val Gly Arg Tyr Cys Asp Ala
    210                 215                 220

Ala Pro Ser Lys Leu Gly His Asn
225                 230
```

<210> 247

<211> 51

<212> DNA

<213> oligonucleotide

<400> 247
cgcgccaagg agatataaca atgagaggat cgcatcacca tcaccatcac g 51

<210> 248

<211> 51

<212> DNA

<213> oligonucleotide

<400> 248
gatccgtgat ggtgatggtg atgcgatcct ctcattgtta tatctccttg g 51

<210> 249

<211> 47

<212> DNA

<213> oligonucleotide

<400> 249
ctgattaatt aaagctcatc atgtttgtat agttcatcca tgccatg 47

<210> 250

<211> 34

<212> DNA

<213> oligonucleotide

<400> 250
gtgtgtactg tcagccagga ttccagcatc caag 34

<210> 251

<211> 32

<212> DNA

<213> oligonucleotide

<400> 251
ctgtcagcaa tgatatcagc atccaaggca ac 32

<210> 252

<211> 44

<212> DNA

<213> oligonucleotide

<400> 252
ggatccatcg ccaccatgtc taaaggtgaa gaattattca ctgg 44

<210> 253

<211> 34

<212> DNA

<213> oligonucleotide

<400> 253

cagctgttat ttgtacaatt catccatacc atgg 34

<210> 254

<211> 41

<212> DNA

<213> oligonucleotide

<400> 254
cgggatccat cgccaccatg aggtcttcca agaatgttat c 41

<210> 255

<211> 31

<212> DNA

<213> oligonucleotide

<400> 255
gaggatccgc ggccgctaaa ggaacagatg g 31

<210> 256

<211> 38

<212> DNA

<213> oligonucleotide

<400> 256
gaagatctaa aacaatgagt gtgatcgcta cacaaatg 38

<210> 257

<211> 35

<212> DNA

<213> oligonucleotide

<400> 257
tatcaaatcg ccggcgtcag gcgaccacag gtttg 35

<210> 258

<211> 30

<212> DNA

<213> oligonucleotide

<400> 258
agatctgtgt tgtgacgcaa ctgcaactcc 30

<210> 259

<211> 39

<212> DNA

<213> oligonucleotide

<400> 259
gtgatcagcg gatcccttca atttagaaag caattgttc 39

<210> 260

<211> 25

<212> DNA

<213> oligonucleotide

<400> 260
cctctatata ttacgcacca tattc 25

<210> 261

<211> 22

<212> DNA

<213> oligonucleotide

<400> 261
atacgtgacg acattggtag tc 22

<210> 262

<211> 15

<212> PRT

<213> coral

<220>

<221> misc_feature

<222> (15)..(15)

<223> x = any amino acid

<400> 262

```
Ser Pro Pro Asp Tyr Thr Leu Glu Phe Pro Lys Lys Xaa Val Ala
1               5                   10                  15
```

<210> 263

<211> 15

<212> PRT

<213> coral

<400> 263

```
Ser Pro Pro Asp Tyr Thr Leu Glu Arg Pro Lys Lys Gly Val Ala
1               5                   10                  15
```

<210> 264

<211> 24

<212> PRT

<213> coral

<400> 264

```
Asp Ser Ser Pro Glu Ser Tyr Leu Lys Asn Gly Ile Ala Glu Glu Met
1               5                   10                  15

Lys Thr Asp Val Met Glu Gly Ile
            20
```

<210> 265

<211> 22

<212> PRT

<213> coral

<400> 265

```
Ser Tyr Leu Pro Asn Gly Ile Ala Glu Glu Met Lys Thr Asp Leu Met
1               5                   10                  15

Glu Gly Ile Val Asn Gly
            20
```

<210> 266

<211> 22

<212> PRT

<213> coral

<400> 266

```
Ser Leu Tyr Gln Asn Gly Ile Ala Glu Glu Met Lys Thr Asp Leu Met
1               5                   10                  15

Glu Gly Ile Val Asn Gly
            20
```

<210> 267

<211> 20

<212> DNA

<213> oligonucleotide

<400> 267

```
atggaaggga tagtcgatgg                                                   20
```

<210> 268

<211> 20

<212> DNA

<213> oligonucleotide

<400> 268

```
atggaaggga ttgtcgatgg                                                   20
```

<210> 269

<211> 20

<212> DNA

<213> oligonucleotide

<400> 269
atggaaggga tcgtcgatgg 20

<210> 270

<211> 19

<212> DNA

<213> oligonucleotide

<400> 270
cctcgacaat cccttccat 19

<210> 271

<211> 19

<212> DNA

<213> oligonucleotide

<400> 271
cctcgacgat cccttccat 19

```
agc ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag       240
Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80

cag tca ttc ccg gag gga ttt aca tgg gag agg atc atg aac ttt gaa       288
Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac       336
Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110

tgt ttc acc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat       384
Cys Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125

gga cct gtg atg cag aag aag aca cag ggc tgg gaa ccc cac tct gag       432
Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu
    130                 135                 140

cgt ctc ttt gca cgg ggt gga atg ctg ata gga aac aac ttt atg gct       480
Arg Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160

ctg aag tta gaa gga ggc ggt cac tat ttg tgt gaa ttc aaa act act       528
Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr
                165                 170                 175

tac aag gca aag aag cct gtg aag atg cca ggg tat cat tat gtt gac       576
Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190

cgc aaa ctg gat gta acc aat cac aac aag gat tac act tcc gtt gag       624
Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
        195                 200                 205

cag tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                   663
Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
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<210> 129

<211> 221

<212> PRT

<213> Millepora sp.

<400> 129

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Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15

Thr Val Asp Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30
```

```
Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly
        35                  40                  45

Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly
    50                  55                  60

Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80

Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110

Cys Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125

Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu
    130                 135                 140

Arg Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160

Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr
                165                 170                 175

Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190

Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
        195                 200                 205

Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220

<210>  130

<211>  663

<212>  DNA

<213>  Millepora sp.


<220>
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<221>  CDS

<222>  (1)..(663)


<400>  130
atg agt gtg atc gct aca caa atg acc tac aag gtt tat atg tca ggc        48
Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15

acg gtc gat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga aag        96
Thr Val Asp Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30

cct tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggc gga       144
Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly
        35                  40                  45

cct ctg cca ttt gct tgg gat att tta tca cca cag tgt cag tac gga       192
Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly
    50                  55                  60

agc ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag       240
Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80

cag tca ttc ccg gag gga ttt aca tgg gag agg atc atg aac ttt gaa       288
Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

gat ggt gca gtg tgt act gtc agc aat ggt tcc agc atc caa ggc aac       336
Asp Gly Ala Val Cys Thr Val Ser Asn Gly Ser Ser Ile Gln Gly Asn
            100                 105                 110

tgt ttc acc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat       384
Cys Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125

gga cct gtg atg cag aag aag aca cag ggc tgg gaa ccc cac tct gag       432
Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu
    130                 135                 140

cgt ctc ttt gca cgg ggt gga atg ctg ata gga aac aac ttt atg gct       480
Arg Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160

ctg aag tta gga gga ggc ggt cac tat ttg tgt gaa ttc aaa act act       528
Leu Lys Leu Gly Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr
                165                 170                 175

tac agg gca aag aag cct gtg aag atg cca ggg tat cat tat gtt gac       576
Tyr Arg Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190

cgc aaa ctg gat gta acc aat cac aac aag gat tac act tcc gtt gag       624
Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
        195                 200                 205
```

```
cag tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                 663
Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
```

<210> 131

<211> 221

<212> PRT

<213> Millepora sp.

<400> 131

```
Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15

Thr Val Asp Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30

Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly
        35                  40                  45

Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly
    50                  55                  60

Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80

Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

Asp Gly Ala Val Cys Thr Val Ser Asn Gly Ser Ser Ile Gln Gly Asn
            100                 105                 110

Cys Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125

Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu
    130                 135                 140

Arg Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160

Leu Lys Leu Gly Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr
                165                 170                 175
```

Tyr Arg Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
            180   185   190

Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
        195   200   205

Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210   215   220

<210> 132

<211> 660

<212> DNA

<213> Millepora sp.

<220>

<221> CDS

<222> (1)..(660)

<400> 132
agt gtg atc gct aca caa atg acc tac aag gtt tat atg tca ggc acg 48
Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1   5   10   15

gtc gat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga aag cct 96
Val Asp Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20   25   30

tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggc gga cct 144
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35   40   45

ctg cca ttt gct tgg gat att tta tca cca cag tgt cag tac gga agc 192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Ser
    50   55   60

ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag cag 240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65   70   75   80

tca ttc ccg gag gga ttt aca tgg gag agg atc atg aac ttt gaa gat 288
Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85   90   95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac tgt 336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100   105   110

```
ttc acc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga         384
Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtg atg cag aag aag aca cag ggc tgg gaa ccc cac tct gag cgt         432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu Arg
    130                 135                 140

ctc ttt gca cgg ggt gga atg ctg ata gga aac aac ttt atg gct ctg         480
Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

aag tta gaa gga ggc ggt cac tat ttg tgt gaa ttc aaa act act tac         528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr Tyr
                165                 170                 175

aag gca aag aag cct gtg aag atg cca ggg tat cat tat gtt gac cgc         576
Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aaa ctg gat gta acc aat cac aac aag gat tac act tcc gtt gag cag         624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                         660
Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220


<210>  133

<211>  220

<212>  PRT

<213>  Millepora sp.


<400>  133

Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15


Val Asp Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30


Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45


Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Ser
    50                  55                  60


Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80
```

Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
85 90 95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
100 105 110

Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
115 120 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu Arg
130 135 140

Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145 150 155 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr Tyr
165 170 175

Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
180 185 190

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
195 200 205

Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
210 215 220

<210> 134

<211> 663

<212> DNA

<213> Porites murrayensis

<220>

<221> CDS

<222> (1)..(663)

<400> 134
atg agt gtg atc gct aca caa atg acc tac aag gtt tat atg cca ggc 48
Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Pro Gly
1 5 10 15

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acg gtc aat gga cac tac ttt gag gtt gaa ggc gat gga aaa gga aag        96
Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30

cct tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggc gga       144
Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly
    35                  40                  45

cct ctg cca ttt gct tgg gat att cta tca cca cag agt cag tac gga       192
Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly
    50                  55                  60

agc ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag       240
Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80

cag tca ttc cct gag gga tat aca tgg gag agg atc atg aac ttc gaa       288
Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggt aac       336
Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110

tgt ttc atc tac aat gtc aag ttc tct ggt ttg aac ttt cct ccc aat       384
Cys Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125

gga cct gtt atg caa aag aag aca cag ggc tgg gaa ccc aac act gag       432
Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
    130                 135                 140

cgt ctt tat gca cga gat gga atg ctg ata gga aac aac ttt atg gct       480
Arg Leu Tyr Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160

ctg aag ttg gaa gga ggt ggt cat tat ttg tgt gaa ttc aaa tct act       528
Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr
                165                 170                 175

tac aag gca aag aag cct gtg atg atg cct gga tat cac tat gtt gac       576
Tyr Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190

cgc aaa ttg gat gta acc aat cac aac aag gat tac act tcc gtt gag       624
Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
        195                 200                 205

cag tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                   663
Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
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<210> 135

<211> 221

<212> PRT

<213> Porites murrayensis

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<400>  135

Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Pro Gly
1               5                   10                  15

Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30

Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly
        35                  40                  45

Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly
    50                  55                  60

Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80

Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110

Cys Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125

Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
    130                 135                 140

Arg Leu Tyr Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160

Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr
                165                 170                 175

Tyr Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190

Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
        195                 200                 205

Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
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<210> 136

<211> 663

<212> DNA

<213> Porites murrayensis

<220>

<221> CDS

<222> (1)..(663)

<400> 136

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atg agt gtg atc gct aca caa atg acc tac aag gtt tat atg tca ggc      48
Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15

acg gtc aat gga cac tac ttt gag gtt gaa ggc gat gga aaa gga aag      96
Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30

cct tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggc gga     144
Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly
        35                  40                  45

cct ctg cca ttt gct tgg gat att cta tca cca cag agt cag tac gga     192
Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly
    50                  55                  60

agc ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag     240
Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80

cag tca ttc cct gag gga tat aca tgg gag agg atc atg aac ttc gaa     288
Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggt aac     336
Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110

tgt ttc atc tac aat gtc aag ttc tct ggt ttg aac ttt cct ccc aat     384
Cys Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125

gga cct gtt atg caa aag aag aca cag ggt tgg gaa ccc aac act gag     432
Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
    130                 135                 140

cgt ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt atg gct     480
Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160
```

```
ctg aag ttg gaa gga ggt ggt cat tat ttg tgt gaa ttc aaa tct act       528
Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr
                165                 170                 175

tac aag gca aag aag cct gtg atg atg cca ggg tat cac tat gtt gac       576
Tyr Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190

cgc aaa ttg gat gta acc aat cac aac aag gat tac act tcc gtt gag       624
Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
        195                 200                 205

cag tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                   663
Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220


<210>  137

<211>  221

<212>  PRT

<213>  Porites murrayensis


<400>  137

Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15


Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30


Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly
        35                  40                  45


Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly
    50                  55                  60


Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80


Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95


Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110


Cys Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125
```

```
Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
    130                 135                 140


Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160


Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr
                165                 170                 175


Tyr Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190


Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
        195                 200                 205


Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220


<210>  138

<211>  660

<212>  DNA

<213>  Porites murrayensis



<220>

<221>  CDS

<222>  (1)..(660)



<400>  138
agt gtg atc gct aca caa atg acc tac aag gtt tat atg tca ggc acg       48
Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

gtc aat gga cac tac ttt gag gtc caa ggc gat gga aaa gga aag cct       96
Val Asn Gly His Tyr Phe Glu Val Gln Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

tac gag ggc gag cag act gta aag ctc act gtc acc aag ggc gga cct      144
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg ccc ttt gct tgg gat att tta tca cct cag act cag tac gga agc      192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Thr Gln Tyr Gly Ser
    50                  55                  60
```

```
ata cca ttc acc aag tac cct gac gac atc cct gac tat gta aaa cag        240
Ile Pro Phe Thr Lys Tyr Pro Asp Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc cct gag gga tat aca tgg gag agg atc atg aag ttt gaa gat        288
Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Lys Phe Glu Asp
                85                  90                  95

ggt gca gtg tgt act gtc acc aat gac tcc agc atg caa ggc aac tgt        336
Gly Ala Val Cys Thr Val Thr Asn Asp Ser Ser Met Gln Gly Asn Cys
            100                 105                 110

ttc atc tac aat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga        384
Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtt atg cag aag aag aca cag ggc tgg gaa ccc aac act ggg cgt        432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Gly Arg
    130                 135                 140

ctt tat gca cga gat gga atg ctg ata gga aac aac ttt atg gct ctg        480
Leu Tyr Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

aag ttg gaa gga ggt ggt cat tat acc tgt gaa ttc aaa tct act tac        528
Lys Leu Glu Gly Gly Gly His Tyr Thr Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

aag gca aag aag cct gtg atg atg cct gga tat cac tat gtt gac cgc        576
Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aaa ttg gat gta acc aat cac aac aag gat tac act tcc gtt gag cag        624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                        660
Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220


<210>  139

<211>  220

<212>  PRT

<213>  Porites murrayensis


<400>  139

Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15


Val Asn Gly His Tyr Phe Glu Val Gln Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30
```

```
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Thr Gln Tyr Gly Ser
    50                  55                  60

Ile Pro Phe Thr Lys Tyr Pro Asp Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Lys Phe Glu Asp
                85                  90                  95

Gly Ala Val Cys Thr Val Thr Asn Asp Ser Ser Met Gln Gly Asn Cys
            100                 105                 110

Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Gly Arg
    130                 135                 140

Leu Tyr Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

Lys Leu Glu Gly Gly Gly His Tyr Thr Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
```

<210> 140

<211> 660

<212> DNA

<213> Porites murrayensis

<220>

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<221>  CDS

<222>  (1)..(660)


<400>  140
agt gtg atc gct aca caa atg acc tac aag gtt tat atg tca ggc acg        48
Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

gtc aat gga cac tac ttt gag gtt gaa ggc gat gga caa gga aag cct        96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Gln Gly Lys Pro
        20                  25                  30

tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggc gga cct       144
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
    35                  40                  45

ctg cca ttt gct tgg gat att cta tca cca cag agt cag tac gga agc       192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
    50                  55                  60

ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag cag       240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc cct gag gga tat aca tgg gag agg atc atg aac ttc gaa gat       288
Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac tgt       336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

ttc atc tac aat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga       384
Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtt atg caa aag aag aca cag ggc tgg gaa ccc aac act gag cgt       432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt atg gct ctg       480
Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

aag tcg gaa gga ggt ggt cat tat ttg tgt gaa ttc aaa tct act tac       528
Lys Ser Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

aag gca aag aag cct gtg atg atg cca ggg tat cac tat gtt gac cgc       576
Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aaa ttg gat gta acc aat cac aac aag gat tac act tcc gtt gag cag       624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205
```

tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc 660
Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
210 215 220

<210> 141

<211> 220

<212> PRT

<213> Porites murrayensis

<400> 141

Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1 5 10 15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Gln Gly Lys Pro
20 25 30

Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
35 40 45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
50 55 60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65 70 75 80

Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
85 90 95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
100 105 110

Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
115 120 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
130 135 140

Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145 150 155 160

Lys Ser Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
165 170 175

```
Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190


Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205


Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220


<210>  142

<211>  660

<212>  DNA

<213>  Porites murrayensis



<220>

<221>  CDS

<222>  (1)..(660)



<400>  142
agt gtg atc gct aca caa atg acc tac aag gtt tat atg tca ggc acg       48
Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

gtc aat gga cac tac ttt gag gtt gaa ggc gat gga aaa gga aag cct       96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggc gga cct      144
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att cta tca cca cag agt cag tac gga agc      192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
    50                  55                  60

ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag cag      240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc cct gag gga tat aca tgg gag agg atc atg aac ttc gaa gat      288
Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac tgt      336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110
```

```
ttc atc tac aat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga         384
Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtt atg caa aag aag aca cag ggc tgg gaa ccc aac aca gag cgt         432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt atg gct ctg         480
Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

aag ttg gaa gga ggt ggt cat tat ttg tgt gaa ttc aaa tct act tac         528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

aag gca aag aag cct gtg atg atg cca ggg tat cac tat gtt gac cgc         576
Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aaa ttg gat gta acc aat cac aac aag gat tac act tcc gtt gag cag         624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                         660
Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
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<210> 143

<211> 220

<212> PRT

<213> Porites murrayensis

<400> 143

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Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
    50                  55                  60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80
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Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
85 90 95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
100 105 110

Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
115 120 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
130 135 140

Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145 150 155 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
165 170 175

Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp Arg
180 185 190

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
195 200 205

Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
210 215 220

<210> 144

<211> 660

<212> DNA

<213> Pink Pocillopora

<220>

<221> CDS

<222> (1)..(660)

<400> 144
agt gtg atc gct aca caa atg acc tac aag gtt tat atg tca ggc acg 48
Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1 5 10 15

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gtc aat gga cac tac ttt gag gtt gaa ggc gat gga aaa gga aag cct      96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

tac gag ggc gag cag act gta aag ctc act gtc acc aag ggc gga cct     144
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg ccg ttt gct tgg gat att tta tca cca cag act cag tac gga agc     192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Thr Gln Tyr Gly Ser
    50                  55                  60

ata cca ttc acc aag tac cct gaa gac att cct gac tat gta aaa cag     240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc cct gag gga tat aca tgg gag agg atc atg aag ttt gaa gat     288
Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Lys Phe Glu Asp
                85                  90                  95

ggt gca gta tgt act gtc agc aat gat tcc agc atg caa ggc aac tgt     336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Met Gln Gly Asn Cys
            100                 105                 110

ttc atc tac aat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga     384
Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtt atg cag aag aag aca cag ggc tgg gaa ccc aac act gag cgt     432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

ctt tat gca cga gat gga atg ctg ata gga aac aac ttt atg gct ctg     480
Leu Tyr Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

aag ttg gaa gga ggt ggt cat tat acc tgt gaa ttc aaa tct act tac     528
Lys Leu Glu Gly Gly Gly His Tyr Thr Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

aag gca aag aag cct gtg atg atg cct gga tat cac tat gtt gac cgc     576
Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aaa ttg gat gta acc aat cac aac aag gat tac act tcc gtt gag cag     624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                     660
Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
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<210> 145

<211> 220

<212> PRT

<213> Pink Pocillopora

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<400>  145

Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Thr Gln Tyr Gly Ser
    50                  55                  60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Lys Phe Glu Asp
                85                  90                  95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Met Gln Gly Asn Cys
            100                 105                 110

Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

Leu Tyr Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

Lys Leu Glu Gly Gly Gly His Tyr Thr Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
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<210>  146

<211>  663

<212>  DNA

<213>  Pink Pocillopora


<220>

<221>  CDS

<222>  (1)..(663)


<400>  146
atg agt gtg atc gct aca caa atg acc tac aag gtt tat atg tca ggc        48
Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15

acg gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga aag        96
Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30

cct tac gag ggg gag cag acg gta agg ctg gct gtc acc aag ggc gga       144
Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Ala Val Thr Lys Gly Gly
        35                  40                  45

cct ctg cca ttt gct tgg gat att tta tca cca cag tgt cag tac gga       192
Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly
    50                  55                  60

agc ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag       240
Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80

cag tca ttc ccg gag gga ttt aca tgg gag agg atc atg aac ttt gaa       288
Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac       336
Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110

tgt ttc atc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat       384
Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125

gga cct gtt atg cag aag aag aca cag ggc tgg gaa ccc cac tct gag       432
Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu
    130                 135                 140

cgt ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt atg gct       480
Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160
```

ctg aag tta gaa gga ggc ggt cac tat ttg tgt gaa ttc aaa act act 528
Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr
165 170 175

tac aag gca aag aag cct gtg aag atg cca ggg tat cat tat gtt gac 576
Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
180 185 190

cgc aaa ctg gat gta acc aat cac aac aag gat tac act tcc gtt gag 624
Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
195 200 205

cag tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc 663
Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
210 215 220

<210> 147

<211> 221

<212> PRT

<213> Pink Pocillopora

<400> 147

Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1 5 10 15

Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
20 25 30

Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Ala Val Thr Lys Gly Gly
35 40 45

Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly
50 55 60

Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65 70 75 80

Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu
85 90 95

Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
100 105 110

Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
115 120 125

```
Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu
    130                 135                 140


Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160


Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr
                165                 170                 175


Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190


Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
        195                 200                 205


Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220


<210>  148

<211>  663

<212>  DNA

<213>  Pink Pocillopora



<220>

<221>  CDS

<222>  (1)..(663)



<400>  148
atg agt gtg atc gct aca caa atg acc tac aag gtt tat atg tca ggc       48
Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15

acg gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga aag       96
Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30

cct tac gag ggg gag cag acg gta agg ctg gct gtc acc aag ggc gga      144
Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Ala Val Thr Lys Gly Gly
        35                  40                  45

cct ctg cca ttt gct tgg gat att tta tca cca cag tgt cag tac gga      192
Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly
    50                  55                  60
```

```
agc ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag      240
Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80

cag tca ttc ccg gag gga ttt aca tgg gag agg atc atg aac ttt gaa      288
Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac      336
Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110

tgt ttc atc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat      384
Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125

gga cct gtt atg cag aag aag aca cag ggc tgg gaa ccc cac tct gag      432
Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu
    130                 135                 140

cgt ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt atg gct      480
Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160

ctg aag tta gaa gga ggc ggt cac tat ttg tgt gaa ttc aaa act act      528
Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr
                165                 170                 175

tac aag gca aag aag cct gtg aag atg cca ggg tat cat tat gtt gac      576
Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190

cgc aaa ctg gat gta acc aat cac aac aag gat tac act tcc gtt gag      624
Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
        195                 200                 205

cag tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                  663
Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220


<210>  149

<211>  221

<212>  PRT

<213>  Pink Pocillopora


<400>  149

Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15


Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30
```

```
Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Ala Val Thr Lys Gly Gly
        35                  40                  45

Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly
    50                  55                  60

Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80

Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110

Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125

Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu
    130                 135                 140

Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160

Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr
                165                 170                 175

Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190

Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
        195                 200                 205

Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220

<210>  150

<211>  660

<212>  DNA

<213>  Pink Pocillopora


<220>
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<221>  CDS

<222>  (1)..(660)


<400>  150
agt gtg atc gct aca caa atg acc tac aag gtt tat atg tca ggc acg        48
Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

gtc aat gga cac tac ttt gag gtt gaa ggc gat gga aaa gga aag cct        96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggc gga cct       144
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att cta tca cca cag agt cag tac gga agc       192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
    50                  55                  60

ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag cag       240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc cct gag gga tat aca tgg gag agg atc atg aac ttc gaa gat       288
Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac tgt       336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

ttc atc tac aat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga       384
Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtt atg caa aag aag aca cag ggc tgg gaa ccc aac act gag cgt       432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt atg gct ctg       480
Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

aag ttg gaa gga ggt ggt cat tat ttg tgt gaa ttc aaa tct act tac       528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

aag gca aag aag cct gtg atg atg cca ggg tat cac tat gtt gac cgc       576
Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aaa ttg gat gta acc aat cac aac aag gat tac act tcc gtt gag cag       624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205
```

```
tgt gag att tcc att gca cgc aaa cct gtg gtc gcc                 660
Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
```

<210> 151

<211> 220

<212> PRT

<213> Pink Pocillopora

<400> 151

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Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
    50                  55                  60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175
```

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Lys Ala Lys Lys Pro Val Met Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190


Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205


Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220


<210>  152

<211>  663

<212>  DNA

<213>  Platygyra sp.



<220>

<221>  CDS

<222>  (1)..(663)



<400>  152
atg agt gtg atc gct aca caa atg acc tac aag gtt tat atg tca ggc        48
Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15

acg gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga aag        96
Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30

cct tac gag ggg gag cgg acg gta aag ctc act gtc acc aag ggc gga       144
Pro Tyr Glu Gly Glu Arg Thr Val Lys Leu Thr Val Thr Lys Gly Gly
        35                  40                  45

cct ctg ccg ttt gct tgg gat att tta tca cca cag tgt cag tac gga       192
Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly
    50                  55                  60

aac ata cca ttc acc aag tac cct gaa gac gtc cct gac tat gta aag       240
Asn Ile Pro Phe Thr Lys Tyr Pro Glu Asp Val Pro Asp Tyr Val Lys
65                  70                  75                  80

cag tca ttc ccg gag gga ttt aca tgg gag agg atc atg aac ttt gaa       288
Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac       336
Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110
```

```
tgt ttc acc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat      384
Cys Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125

gga cct gtg atg cag aag aag aca cag ggc tgg gaa ccc cac tct gag      432
Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu
    130                 135                 140

cgt ctc ttt gca cgg ggt gga atg ctg ata gga aac aac ttt atg gct      480
Arg Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160

ctg aag tta gaa gga ggc ggt cac tat ttg tgt gga ttc aaa act act      528
Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Gly Phe Lys Thr Thr
                165                 170                 175

tac aag gca aag aag cct gtg aag atg cca ggg tat cat tat gtt gac      576
Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190

cgc aaa ctg gat gta acc aat cac aac aag gat tac att tcc gtt gag      624
Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Ile Ser Val Glu
        195                 200                 205

cag tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                  663
Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220


<210>  153

<211>  221

<212>  PRT

<213>  Platygyra sp.


<400>  153

Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15


Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30


Pro Tyr Glu Gly Glu Arg Thr Val Lys Leu Thr Val Thr Lys Gly Gly
        35                  40                  45


Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly
    50                  55                  60


Asn Ile Pro Phe Thr Lys Tyr Pro Glu Asp Val Pro Asp Tyr Val Lys
65                  70                  75                  80
```

```
Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110

Cys Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125

Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu
    130                 135                 140

Arg Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160

Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Gly Phe Lys Thr Thr
                165                 170                 175

Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190

Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Ile Ser Val Glu
        195                 200                 205

Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
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<210> 154

<211> 663

<212> DNA

<213> Platygyra sp.

<220>

<221> CDS

<222> (1)..(663)

<400> 154

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atg agt gtg atc gct aca caa atg acc tac aag gtt tat atg tca ggc      48
Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15
```

```
acg gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga aag       96
Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30

cct tac gag ggg gag cag acg gta agg ctc act gtc acc aag ggc gga      144
Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly
        35                  40                  45

cct ctg cca ttt gct tgg gat att ttg tca cca cag tat cag tac gga      192
Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Tyr Gln Tyr Gly
    50                  55                  60

agc ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag      240
Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80

tag tca ttc ccg gag gga ttt aca tgg gac agg atc atg aac ttt gaa      288
    Ser Phe Pro Glu Gly Phe Thr Trp Asp Arg Ile Met Asn Phe Glu
                    85                  90                  95

gat ggt gca gtg tgt acc gtc agc aat gat tcc agc atc caa ggc aac      336
Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
                100                 105                 110

tgt ttc atc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat      384
Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
            115                 120                 125

gga cct gtt atg cag aag aag aca cag ggc tgg gaa ccc aac act gag      432
Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
        130                 135                 140

cgt ctc ctt gca cga gat gga atg ctg cta gga aac aac ttt atg gct      480
Arg Leu Leu Ala Arg Asp Gly Met Leu Leu Gly Asn Asn Phe Met Ala
    145                 150                 155

ctg aag tta gaa gga ggt ggt cac tat ttg tgt gaa ttc aaa act act      528
Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr
160                 165                 170                 175

tac aag gca aag aag cct gtg aag atg cca ggg tat cac tat gtt gac      576
Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
                180                 185                 190

cgc aaa ctg gat gta acc aat cac aac aag gat tac act tcc gtt gag      624
Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
            195                 200                 205

cgg tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                  663
Arg Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
        210                 215                 220
```

<210> 155

<211> 80

<212> PRT

<213> Platygyra sp.

<400> 155

Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1 5 10 15

Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
20 25 30

Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly
35 40 45

Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Tyr Gln Tyr Gly
50 55 60

Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65 70 75 80

<210> 156

<211> 140

<212> PRT

<213> Platygyra sp.

<400> 156

Ser Phe Pro Glu Gly Phe Thr Trp Asp Arg Ile Met Asn Phe Glu Asp
1 5 10 15

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
20 25 30

Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
35 40 45

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
50 55 60

Leu Leu Ala Arg Asp Gly Met Leu Leu Gly Asn Asn Phe Met Ala Leu
65 70 75 80

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr Tyr
85 90 95

Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
100 105 110

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Arg
115 120 125

Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
130 135 140

<210> 157

<211> 660

<212> DNA

<213> Platygyra sp.

<220>

<221> CDS

<222> (1)..(660)

<400> 157
agt gtg atc gct aca caa atg acc tac aag gtt tat atg tca ggc acg 48
Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1 5 10 15

gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga aag cct 96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
20 25 30

tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggc gga cct 144
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
35 40 45

ctg cca ttt gct tgg gat att tta tca cca cag tgt cag tac gga aac 192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Asn
50 55 60

ata cca ttc acc aag tac cct gaa gac gtc cct gac tat gta aag cag 240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Val Pro Asp Tyr Val Lys Gln
65 70 75 80

tca ttc ccg gag gga ttt aca tgg gag agg atc atg aac ttt gaa gat 288
Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
85 90 95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac tgt 336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
100 105 110

```
ttc acc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga       384
Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtg atg cag aag aag aca cag ggc tgg gaa ccc cac tct gag cgt       432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu Arg
    130                 135                 140

ctc ttt gca cgg ggt gga atg ctg ata gga aac aac ttt atg gct ctg       480
Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

aag tta gaa gga ggc ggt cac tat ttg tgt gga ttc aaa act act tac       528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Gly Phe Lys Thr Thr Tyr
                165                 170                 175

aag gca aag aag ccc gtg aag atg cca ggg tat cat tat gtt gac cgc       576
Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aaa ctg gat gta acc aat cac aac aag gat tac att tcc gtt gag cag       624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Ile Ser Val Glu Gln
        195                 200                 205

tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                       660
Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
```

<210> 158

<211> 220

<212> PRT

<213> Platygyra sp.

<400> 158

```
Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Asn
    50                  55                  60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Val Pro Asp Tyr Val Lys Gln
65                  70                  75                  80
```

```
Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95


Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110


Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125


Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu Arg
    130                 135                 140


Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160


Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Gly Phe Lys Thr Thr Tyr
                165                 170                 175


Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190


Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Ile Ser Val Glu Gln
        195                 200                 205


Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220


<210>  159

<211>  660

<212>  DNA

<213>  Platygyra sp.



<220>

<221>  CDS

<222>  (1)..(660)



<400>  159
agt gtg atc gct aca caa atg acc tac aag gtt tat atg tca ggc acg          48
Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15
```

```
gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga aag cct            96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggc gga cct           144
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att tta tca cca cag tgt cag tac gga aac           192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Asn
    50                  55                  60

ata cca ttc acc aag tac cct gaa gac gtc cct gac tat gta aag cag           240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Val Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc ccg gag gga ttt aca tgg gag ggg atc atg aac ttt gaa gat           288
Ser Phe Pro Glu Gly Phe Thr Trp Glu Gly Ile Met Asn Phe Glu Asp
                85                  90                  95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac tgt           336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

ttc acc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga           384
Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtg atg cag aag aag aca cag ggc tgg gaa ccc cac tct gag cgt           432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu Arg
    130                 135                 140

ctc ttt gca cgg ggt gga atg ctg ata gga aac aac ttt atg gct ctg           480
Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

aag tta gaa gga ggc ggt cac tat ttg tgt gga ttc aaa act act tac           528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Gly Phe Lys Thr Thr Tyr
                165                 170                 175

aag gca aag aag cct gtg aag atg cca ggg tat cat tat gtt gac cgc           576
Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aaa ctg gat gta acc aat cac aac aag gat tac att tcc gtt gag cag           624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Ile Ser Val Glu Gln
        195                 200                 205

tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                           660
Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
```

<210> 160

<211> 220

<212> PRT

<213> Platygyra sp.

```
<400>  160

Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Asn
    50                  55                  60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Val Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

Ser Phe Pro Glu Gly Phe Thr Trp Glu Gly Ile Met Asn Phe Glu Asp
                85                  90                  95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu Arg
    130                 135                 140

Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Gly Phe Lys Thr Thr Tyr
                165                 170                 175

Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Ile Ser Val Glu Gln
        195                 200                 205

Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
```

```
<210>  161

<211>  660

<212>  DNA

<213>  Pavona decussata


<220>

<221>  CDS

<222>  (1)..(660)


<400>  161
agt gtg atc gct aca caa atg acc tac aag gtt tat atg tca ggc acg       48
Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

gtc aat gga cac tac ttt gag gtt gaa ggc gat gga aaa gga gag cct       96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Glu Pro
            20                  25                  30

tac gag ggg gag cag acg gta agg ctc act gtc aca aag ggc gga cct      144
Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att tta tca cca cag tat cag tac gga agc      192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Tyr Gln Tyr Gly Ser
    50                  55                  60

ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag cag      240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc ccg gaa gga tat aca tgg gag agg atc atg aac ttt gaa gat      288
Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

ggt gct gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac tgt      336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

ttc atc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga      384
Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtg acg cag aag aag aca cag ggc tgg gaa ccc aac act gag cgt      432
Pro Val Thr Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt atg gct ctg      480
Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160
```

```
aag tta gaa gga ggc ggt cac tat ttg tgt gaa ttc aaa tcg act tac        528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

aag gca aag aag act gtg aag atg cca ggg tat cac tat gtt gac cgc        576
Lys Ala Lys Lys Thr Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aaa ctg gat gta acc aat cac aac aag gat tac act tcc gtt gag cag        624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                        660
Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220


<210>  162

<211>  220

<212>  PRT

<213>  Pavona decussata



<400>  162

Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15


Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Glu Pro
            20                  25                  30


Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45


Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Tyr Gln Tyr Gly Ser
    50                  55                  60


Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80


Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95


Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110


Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125
```

Pro Val Thr Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
130 135 140

Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145 150 155 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
165 170 175

Lys Ala Lys Lys Thr Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
180 185 190

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
195 200 205

Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
210 215 220

<210> 163

<211> 663

<212> DNA

<213> Pavona decussata

<220>

<221> CDS

<222> (1)..(663)

<400> 163
atg agt gtg atc gct aca caa atg acc tac aag gtt tat atg tca ggc 48
Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1 5 10 15

acg gtc aat gga cac tac ttt gag gtt gaa ggc gat gga aaa gga aag 96
Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
20 25 30

cct tac gag ggg gag cag acg gta agg ctc act gtc aca aag ggc gga 144
Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly
35 40 45

cct ctg cca ttt gct tgg gat att tta tca cca cag tat cag tac gga 192
Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Tyr Gln Tyr Gly
50 55 60

```
agc ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta tag        240
Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val
65                  70                  75

cag tca ttc ccg gaa gga tat aca tgg gag agg atc atg aac ttt gaa        288
Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu
80                  85                  90                  95

gat ggt gct gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac        336
Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
                100                 105                 110

tgt ttc atc tac cat gtc aag ttt tct ggt ttg aac ttt cct ccc aat        384
Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
            115                 120                 125

gga cct gtg atg cag aag aag aca cag ggc tgg gaa ccc aac act gag        432
Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
        130                 135                 140

cgt ctc ttt gca cga gat gga ttg ctg ata gga aac aac ttt atg gct        480
Arg Leu Phe Ala Arg Asp Gly Leu Leu Ile Gly Asn Asn Phe Met Ala
    145                 150                 155

ctg aag tta gaa gaa ggc ggt cac tat ttg tgt gaa ttc aaa tcg act        528
Leu Lys Leu Glu Glu Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr
160                 165                 170                 175

tac aag gca aag aag act gcg aag atg cca ggg tat cac tat gtt gac        576
Tyr Lys Ala Lys Lys Thr Ala Lys Met Pro Gly Tyr His Tyr Val Asp
                180                 185                 190

cgc aaa ctg gat gta acc aat cac aac aag gat tac act tcc gtt gag        624
Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
            195                 200                 205

cag tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                    663
Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
        210                 215                 220
```

```
<210>  164

<211>  79

<212>  PRT

<213>  Pavona decussata


<400>  164

Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15


Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30
```

```
Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly
        35                  40                  45


Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Tyr Gln Tyr Gly
    50                  55                  60


Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val
65                  70                  75


<210>  165

<211>  141

<212>  PRT

<213>  Pavona decussata



<400>  165

Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu
1               5                   10                  15


Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            20                  25                  30


Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        35                  40                  45


Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
    50                  55                  60


Arg Leu Phe Ala Arg Asp Gly Leu Leu Ile Gly Asn Asn Phe Met Ala
65                  70                  75                  80


Leu Lys Leu Glu Glu Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr
                85                  90                  95


Tyr Lys Ala Lys Lys Thr Ala Lys Met Pro Gly Tyr His Tyr Val Asp
            100                 105                 110


Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
        115                 120                 125


Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    130                 135                 140
```

```
<210>  166

<211>  663

<212>  DNA

<213>  Pavona decussata


<220>

<221>  CDS

<222>  (1)..(663)


<400>  166
atg agt gtg atc gct aca caa gtg acc tac aag gtt tat atg tca ggc        48
Met Ser Val Ile Ala Thr Gln Val Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15

acg gtc aat gga cac tac ttt gag gtt gaa ggc gat gga aaa gga aag        96
Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30

cct tac gag ggg gag caa acg gta agg ctc act gtc aca aag ggc gga       144
Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly
        35                  40                  45

cct ctg cca ttt gct tgg gat att tta tca cca cag tat cag tac gga       192
Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Tyr Gln Tyr Gly
    50                  55                  60

agc ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag       240
Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80

cag tca ttc ccg gaa gga tat aca tgg gag agg atc atg aac ttt gaa       288
Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

gat ggt gct gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac       336
Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110

tgt ttc atc tac cat gtc aag ttt tct ggt ttg aac ttt cct ccc aat       384
Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125

gga cct gtg atg cag aag aag aca cag ggc tgg gaa ccc aac act gag       432
Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
    130                 135                 140

cgt ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt atg gct       480
Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160
```

```
ctg aag tta gaa gga ggc ggt cac tat ttg tgt gaa ttc aaa tcg act        528
Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr
                165                 170                 175

tac aag gca aag aag act gtg aag atg cca ggg tat cac tat gtt gac        576
Tyr Lys Ala Lys Lys Thr Val Lys Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190

cgc aaa ctg gat gta acc aat cac aac aag gat tac act tcc gtt gag        624
Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
        195                 200                 205

cag tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                    663
Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
```

<210> 167

<211> 221

<212> PRT

<213> Pavona decussata

<400> 167

```
Met Ser Val Ile Ala Thr Gln Val Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15

Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30

Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly
        35                  40                  45

Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Tyr Gln Tyr Gly
    50                  55                  60

Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80

Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110

Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125
```

```
Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
    130                 135                 140


Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160


Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr
                165                 170                 175


Tyr Lys Ala Lys Lys Thr Val Lys Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190


Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
        195                 200                 205


Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220


<210>  168

<211>  660

<212>  DNA

<213>  Pavona decussata



<220>

<221>  CDS

<222>  (1)..(660)



<400>  168
agt gtg atc gct aca caa atg acc tac aag gtt tat atg tca ggc acg          48
Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

gtc aat gga cac tac ttt gag gtt gaa ggc gat gga aaa gga aag cct          96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

tac gag ggg gag cag acg gta agg ctc act gtc aca aag ggc gga cct         144
Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att tta tca cca cag tat cag tac gga agc         192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Tyr Gln Tyr Gly Ser
    50                  55                  60
```

```
ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag cag      240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc ccg gaa gga tat aca tgg gag ggg atc atg aac ttt gaa gat      288
Ser Phe Pro Glu Gly Tyr Thr Trp Glu Gly Ile Met Asn Phe Glu Asp
                85                  90                  95

ggt gct gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac tgt      336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

ttc atc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga      384
Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtg atg cag aag aag aca cag ggc tgg gaa ccc aac act gag cgt      432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt atg gct ctg      480
Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

aag tta gaa gga ggc ggt cac tat ttg tgt gaa ttc aaa tcg act tac      528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

aag gca aag aag act gtg aag atg cca ggg tat cac tat gtt gac cgc      576
Lys Ala Lys Lys Thr Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aaa ctg gtt gta acc aat cac aac aag gat tac act tcc gtt gag cag      624
Lys Leu Val Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                      660
Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
```

```
<210>  169

<211>  220

<212>  PRT

<213>  Pavona decussata


<400>  169

Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15


Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30
```

```
Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Tyr Gln Tyr Gly Ser
    50                  55                  60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

Ser Phe Pro Glu Gly Tyr Thr Trp Glu Gly Ile Met Asn Phe Glu Asp
                85                  90                  95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

Lys Ala Lys Lys Thr Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

Lys Leu Val Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
```

<210> 170

<211> 663

<212> DNA

<213> Montipora sp.

<220>

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<221>  CDS

<222>  (1)..(663)


<400>  170
atg agt gtg atc gct aca caa atg acc tac aag gtt tat atg tca ggc         48
Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15

acg gtc aat gga cac tac ttt gag gtt gaa ggc gat gga aaa gga aag         96
Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30

cct tac gaa ggg gag cag acg gta agg ctc act gtc aca aag ggc gga        144
Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly
        35                  40                  45

cct ctg cca ttt gct tgg gat att tta tca cca cag tat cag tac gga        192
Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Tyr Gln Tyr Gly
    50                  55                  60

agc ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag        240
Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80

cag tca ttc ccg gaa gga tat aca tgg gag agg atc atg aac ttt gaa        288
Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

gat ggt gca gtg tgt gct gtc agc aat gat tcc agc atc caa ggc aac        336
Asp Gly Ala Val Cys Ala Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110

tgt ttc atc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat        384
Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125

gga cct gtg atg caa aag aag aca cag ggc tgg gaa ccc aac act gag        432
Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
    130                 135                 140

cgt ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt atg gct        480
Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160

ctg aag tta gaa gga ggc ggt cac tat ttg tgt gaa ttc aaa tct act        528
Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr
                165                 170                 175

tac aag gca aag aag cct gtg aag atg cca ggg tat cac tat gtt gac        576
Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190

cgc aaa ctg gat gta acc aat cac aac aag gat tac act tcc gtt gag        624
Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
        195                 200                 205
```

```
cag tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                 663
Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
```

<210> 171

<211> 221

<212> PRT

<213> Montipora sp.

<400> 171

```
Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15

Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30

Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly
        35                  40                  45

Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Tyr Gln Tyr Gly
    50                  55                  60

Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80

Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

Asp Gly Ala Val Cys Ala Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110

Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125

Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
    130                 135                 140

Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160

Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr
                165                 170                 175
```

```
Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190


Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
        195                 200                 205


Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220


<210>  172

<211>  663

<212>  DNA

<213>  Montipora sp.


<220>

<221>  CDS

<222>  (1)..(663)


<400>  172
atg agt gtg agc gct aca caa atg acc tac aag gtt tat atg tca ggc        48
Met Ser Val Ser Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15

acg gtc aat gga cac tac ttt gag gtt gaa ggc gat gga aaa gga aag        96
Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30

cct tac gaa ggg gag cag acg gta agg ctc act gtc aca aag ggc gga       144
Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly
        35                  40                  45

cct ctg cca ttt gct tgg gat att tta tca cca cag tat cag tac gga       192
Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Tyr Gln Tyr Gly
    50                  55                  60

agc ata cca ttc acc aag tac cct gaa gac atc cct ggc tat gta aag       240
Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Gly Tyr Val Lys
65                  70                  75                  80

cag tca ttc ccg gaa gga tat aca tgg gag agg atc atg aac ttt gaa       288
Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac       336
Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110
```

```
tgt ttc atc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat       384
Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125

gga cct gtg atg caa aaa aag aca caa ggc tgg gaa ccc aac act gag       432
Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
    130                 135                 140

cgt ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt atg gct       480
Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160

ctg aag tta gaa gga ggc ggt cac tat ttg tgt gaa ttc aaa tct act       528
Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr
                165                 170                 175

tac aag gca aag aag cct gtg aag atg cca ggg tat cac tat gtt gac       576
Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190

cgc aaa ctg gat gta acc aat cac aac aag gat tac act tcc gtt ggg       624
Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Gly
        195                 200                 205

cag tgt gaa att tcc att gcc ccc aaa cct gtg gtc gcc                   663
Gln Cys Glu Ile Ser Ile Ala Pro Lys Pro Val Val Ala
    210                 215                 220
```

<210> 173

<211> 221

<212> PRT

<213> Montipora sp.

<400> 173

```
Met Ser Val Ser Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15

Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30

Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly
        35                  40                  45

Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Tyr Gln Tyr Gly
    50                  55                  60

Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Gly Tyr Val Lys
65                  70                  75                  80
```

```
Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110

Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125

Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
    130                 135                 140

Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160

Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr
                165                 170                 175

Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190

Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Gly
        195                 200                 205

Gln Cys Glu Ile Ser Ile Ala Pro Lys Pro Val Val Ala
    210                 215                 220

<210>  174

<211>  660

<212>  DNA

<213>  Montipora sp.


<220>

<221>  CDS

<222>  (1)..(660)


<400>  174
agt gtg atc gct aca caa atg acc tac aag gtt tat atg tca ggc acg        48
Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15
```

```
gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga aag cct           96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggc gga cct          144
Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att tta tca cca cag tgt cag tac gga agc          192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Ser
    50                  55                  60

ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag cag          240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc ccg gag gga ttt aca tgg gag agg atc atg aac ttt gaa gat          288
Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac tgt          336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

ttc acc tac cat gtc aag ttc tct ggt ttg aac ttt cct cct aat gga          384
Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtg atg cag aag aag aca cag ggc tgg gaa ccc cac tct gag cgt          432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu Arg
    130                 135                 140

ctc ttt gca cgg ggt gga atg ctg ata gga aac aac ttt atg gct ctg          480
Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

aag tta gaa gga ggc ggt cac tat ttg tgt gaa ttc aaa act act tac          528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr Tyr
                165                 170                 175

aag gca aag aag cct gtg aag atg cca ggg tat cat tat gtt gac cgc          576
Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aaa ctg gat gta acc aat cac aac aag gat tac act tcc gtt gag cag          624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                          660
Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
```

<210> 175

<211> 220

<212> PRT

<213> Montipora sp.

```
<400>  175

Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
                20                  25                  30

Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Ser
    50                  55                  60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu Arg
    130                 135                 140

Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr Tyr
                165                 170                 175

Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
```

```
<210>  176

<211>  660

<212>  DNA

<213>  Montipora sp.


<220>

<221>  CDS

<222>  (1)..(660)


<400>  176
agt gtg atc gtt aca caa atg acc tac aag gtt tat atg tca ggc acg         48
Ser Val Ile Val Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

gtc aat gga cac tac ttt gag gtt gaa ggc gat gga aaa gga aag cct         96
Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

tac gaa ggg gag cag acg gta agg ctc act gtc aca aag ggc gga ccc        144
Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

ctg cca ttt gct tgg gat att tta tca cca cag tat cag tac gga agc        192
Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Tyr Gln Tyr Gly Ser
    50                  55                  60

ata cca ttc acc aag tac cct gaa gac atc cct gac tat gta aag cag        240
Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

tca ttc ccg gaa gga tat aca tgg gag agg atc atg aac ttt gaa gat        288
Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac tgt        336
Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

ttc atc tac cat gtc aag ttc tct ggt ttg aac ttt cct ccc aat gga        384
Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

cct gtg atg cag aag aag aca cag ggc tgg gaa ccc aac act gag cgt        432
Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt atg gct ctg        480
Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160
```

```
aag tta gaa gga ggc ggt cac tat ttg tgt gaa ttc aaa tct act tac       528
Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

aag gca aag aag cct gtg aag atg cca ggg tat cac tat gtt gac cgc       576
Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

aaa ctg gat gta acc aat cac aac aag gat tac acc tcc gtt gag cag       624
Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

tgt gaa att tcc att gca cgc aaa cct gtg gtc gcc                       660
Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220
```

<210> 177

<211> 220

<212> PRT

<213> Montipora sp.

<400> 177

```
Ser Val Ile Val Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly Pro
        35                  40                  45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Tyr Gln Tyr Gly Ser
    50                  55                  60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125
```

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
130 135 140

Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145 150 155 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
165 170 175

Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
180 185 190

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
195 200 205

Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
210 215 220

<210> 178

<211> 701

<212> DNA

<213> Acanthastria sp.

<400> 178
tccgttatcg ctaaacagat gaccgcttca acgttaagtt gacaacagga agcacgacgg 60

agactgcagt cccgtacgcg cgaacgggat acctgggatt tatcaagaga acagatttca 120

cgcagacaga tggagcccgg catgacgcgt tatttgtggt tggccctctt gaagaaacca 180

tgatattgcg tggtatgagg tatcacccgg tagatatcga gaacacagtg acgagatgtc 240

atcgatcaat ctgtgaaagt gcggtcttca cgatgacaaa cctacttgtg gtagcagtgg 300

agcttgatgc agatgaacgc gaggcacttg acgtggttcc gctggtgacg acatccgtac 360

tgaatgaaca gcaacttgtc gtaggggtgg tggtagtggt tgaccctggc gtagtcccga 420

tcaattctcg cggagagaaa caacggatgc atctgaggga cgggttcctg ggggaccagt 480

tggatcctat ctacgtggcg tataatatgt agacacctca ctgcttagtt tcgtaattga 540

attgtgtcgt agttttttta aatgacaatt aatagacaag tttgaaattg actgtagcgc 600

taggtttagg tataaactag cgtttggtaa ggcaattatg acaggaacta ctgtcacgcg 660

tgacgcgaga ccgtcacttt acacgcaaac ctgtggtcgc c 701

<210> 179

<211> 701

<212> DNA

<213> Green Pocillopora

<400> 179
tccgttatcg ctaaacagat gaccgcttca acgttaagtt gacaacagga agcacgacgg 60

agactgcagt cccgtacgcg cgaacgggat acctgggatt tatcaagaga acagatttca 120

cgcagacaga tggagcccgg catgacgcgt tatttgtggt tggccctctt gaagaaacca 180

tgatattgcg tggtatgagg tatcacccgg tagatatcga gaacacagtg acgagatgtc 240

atcgatcaat ctgtgaaagt gcggtcttca cgatgacaaa cctacttgtg gtagcagtgg 300

agcttgatgc agatgaacgc gaggcacttg acgtggttcc gctggtgacg acatccgtac 360

tgaatgaaca gcaacttgtc gtaggggtgg tggtagtggt tgaccctggt gtagtcccga 420

tcaattctcg cggagagaaa caacggatgc atctgaggga cgggttcctg ggggaccagt 480

tggatcctat ctacgtggcg tataatatgt agacacctca ctgcttaatt ttcgtaattg 540

aattgtgtcg tagttttttt aaatgacaac taatagacag tttgaaattg actgtagcgc 600

taggtttagg tataaactag cgtttggtaa ggcaattatg acaggaatta ctgtcacgcg 660

tgacgcgaga ccgtcacttt acacgcaaac ctgtggtcgc c 701

<210> 180

<211> 701

<212> DNA

<213> Green Pocillopora

<220>

<221> misc_feature

<222> (634)..(634)

<223> n = any nucleotide

<220>

<221> misc_feature

<222> (640)..(640)

<223> n = any nucleotide

<400> 180
tccgttatcg ctaaacagat gaccgcttca acgttaagtt gacaacagga agcacgacgg 60

agactgcagt cccgtacgcg cgaacgggat acctgggatt tatcaagaga acagatttca 120

cgcagacaga tggagcccgg catgacgcgt tatttgtggt tggccctctt gaagaaacca 180

tgatattgcg tggtatgagg tatcacccgg tagatatcga gaacacagtg acgagatgtc 240

atcgatcaat ctgtgaaagt gcggtcttca cgatgacaaa cctacttgtg gtagcagtgg 300

agcttgatgc agatgaacgc gaggcacttg acgtggttcc gctggtgacg acatccgtac 360

tgaatgaaca gcaacttgtc gtaggggtgg tggtagtggt tgaccctggc gtagtcccga 420

tcaattctcg cggagagaaa caacggatgc atctgaggga cgggttcctg ggggaccagt 480

tggatcctat ctacgtggcg tataatatgt agacacctca ctgcttagtt tcgtaattga 540

attgtgtcgt agttttttta aatgacaatt aatagacaag tttgaaattg actgtagcgc 600

taggtttagg tataaactag cgtttggtaa ggcnattatn acaggaacta ctgtcacgcg 660

tgacgcgaga ccgtcacttt acacgcaaac ctgtggtcgc c 701

<210> 181

<211> 701

<212> DNA

<213> Green Pocillopora

<400> 181
tccgttatcg ctaaacagat gaccgcttca ccgttaagtt gacaacagga agcacgacgg 60

agactgcagt cccgtacgcg cgaacgggat acctgggatt tatcaagaga acagatttca 120

cgcagacagg tggagcccgg catgacgcgt tatttgtggt tggccctctt gaagaaacca 180

tgatattgcg tggtatgagg tatcacccgg tagatatcga gaacacagtg acgagatgtc 240

atcgatcaat ctgtgaaagt gcggtcttca cgatgacaaa cctacttgtg gtagcagtgg 300

agcttgatgc agatgaacgc gaggcacttg acgtggttcc gctggtgacg acatccgtac 360

tgaatgaaca gcaacttgtc gtaggggtgg tggtagtggt tgaccctggt gtagtcccga 420

tcaattctcg cggagagaaa caacggatgc atctgaggga cgggttcctg ggggaccagt 480

tggatcctat ctacgtggcg tataatatgt agacacctca ctgcttagtt tcgtaattga 540

attgtgtcgt agttttttta aatgacaatt aatagacaag tttgaaattg actgtagcgc 600

taggtttagg tataaactag cgtttggtaa ggcaattatg acaggaatta ctgtcacgcg 660

tgacgcgaga ccgtcacttc acacgcaaac ctgtggtcgc c 701

<210> 182

<211> 701

<212> DNA

<213> Millepora sp. (Hydrozoan)

<400> 182
tccgttatcg ctaaacagat gaccgcttca acgttaagtt gacaacagga agcacgacgg 60

agactgcagt cccgtacgcg cgaacgggat acctgggatt tatcaagaga acagatttca 120

cgcagacagg tggagcccgg catgacgcgt tatttgtggt tggccctctt gaagaaacca 180

tgatattgcg tggtatgagg tatcacccgg tagatatcga gaacacagtg acgagatgtc 240

atcgatcaat ctgtgaaagt gcggtcttca cgatgacaaa cctacttgtg gtagcagtgg 300

agcttgatgc agatgaacgc gaggcacttg acgtggttcc gctggtgacg acatccgtac 360

tgtatgaaca gcaacttgtc gtaggggtgg tggtagtggt tgaccctggt gtagtcccga 420

tcaattctcg cggagagaaa caacggatgc atctgaggga cgggttcctg ggggaccagt 480

tggatcctat ctacgtggcg tataatatgt agacacctca ctgcttagtt tcgtaattga 540

attgtgtcgt agttttttta aatgacaatt aatagacaag tttgaaattg actgtagcgc 600

taggtttagg tataaactag cgtttggtaa ggcaattatg acaggaatta ctgtcacgcg 660

tgacgcgaga ccgtcacttc acacgcaaac ctgtggtcgc c 701

<210> 183

<211> 701

<212> DNA

<213> Pavona decussaca

<220>

<221> CDS

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<222>  (1)..(699)


<400>  183
tcc gtt atc gct aaa cag atg acc gct tca acg tta agt tga caa cag       48
Ser Val Ile Ala Lys Gln Met Thr Ala Ser Thr Leu Ser     Gln Gln
1               5                   10                      15

gaa gca cga cgg aga ctg cag tcc cgt acg cgc gaa cgg gat acc tgg       96
Glu Ala Arg Arg Arg Leu Gln Ser Arg Thr Arg Glu Arg Asp Thr Trp
                20                  25                  30

gat tta tca aga gaa cag att tca cgc aga cag atg gag ccc ggc atg      144
Asp Leu Ser Arg Glu Gln Ile Ser Arg Arg Gln Met Glu Pro Gly Met
            35                  40                  45

acg cgt tat ttg tgg ttg gcc ctc ttg aag aaa cca tga tat tgc gtg      192
Thr Arg Tyr Leu Trp Leu Ala Leu Leu Lys Lys Pro     Tyr Cys Val
        50                  55                      60

gta tga ggt atc acc cgg tag ata tcg aga aca cag tga cga gat gtc      240
Val     Gly Ile Thr Arg     Ile Ser Arg Thr Gln     Arg Asp Val
            65                      70                      75

atc gat caa tct gtg aaa gtg cgg tct tca cga tga caa acc tac ttg      288
Ile Asp Gln Ser Val Lys Val Arg Ser Ser Arg     Gln Thr Tyr Leu
                80                  85                      90

tgg tag cag tgg agc ttg atg cag atg aac gcg agg cac ttg acg tgg      336
Trp     Gln Trp Ser Leu Met Gln Met Asn Ala Arg His Leu Thr Trp
                    95                  100                 105

ttc cgc tgg tga cga cat ccg tac tga atg aac agc aac ttg tcg tag      384
Phe Arg Trp     Arg His Pro Tyr     Met Asn Ser Asn Leu Ser
                    110                     115

ggg tgg tgg tag tgg ttg acc ctg gcg tag tcc cga tca att ctc gcg      432
Gly Trp Trp     Trp Leu Thr Leu Ala     Ser Arg Ser Ile Leu Ala
    120                     125                     130

gag aga aac aac gga tgc atc tga ggg acg ggt tcc tgg ggg acc agt      480
Glu Arg Asn Asn Gly Cys Ile     Gly Thr Gly Ser Trp Gly Thr Ser
        135                     140                 145

tgg atc cta tct acg tgg cgt ata ata tgt aga cac ctc act gct tag      528
Trp Ile Leu Ser Thr Trp Arg Ile Ile Cys Arg His Leu Thr Ala
        150                 155                 160

ttt cgt aat tga att gtg tcg tag ttt ttt taa atg aca att aat aga      576
Phe Arg Asn     Ile Val Ser     Phe Phe     Met Thr Ile Asn Arg
        165                         170                     175

caa gtt tga aat tga ctg tag cgc tag gtt tag gta taa act agc gtt      624
Gln Val     Asn     Leu     Arg     Val     Val     Thr Ser Val
                            180                             185

tgg taa ggc aat tat gac agg aac tac tgt cac gcg tga cgc gag acc      672
Trp     Gly Asn Tyr Asp Arg Asn Tyr Cys His Ala     Arg Glu Thr
                    190                 195
```

```
gtc act tta cac gca aac ctg tgg tcg cc                            701
Val Thr Leu His Ala Asn Leu Trp Ser
200                 205


<210>  184

<211>  13

<212>  PRT

<213>  Pavona decussaca



<400>  184

Ser Val Ile Ala Lys Gln Met Thr Ala Ser Thr Leu Ser
1               5                   10


<210>  185

<211>  46

<212>  PRT

<213>  Pavona decussaca



<400>  185

Gln Gln Glu Ala Arg Arg Arg Leu Gln Ser Arg Thr Arg Glu Arg Asp
1               5                   10                  15


Thr Trp Asp Leu Ser Arg Glu Gln Ile Ser Arg Arg Gln Met Glu Pro
            20                  25                  30


Gly Met Thr Arg Tyr Leu Trp Leu Ala Leu Leu Lys Lys Pro
        35                  40                  45


<210>  186

<211>  4

<212>  PRT

<213>  Pavona decussaca



<400>  186

Tyr Cys Val Val
1
```

<210> 187

<211> 4

<212> PRT

<213> Pavona decussaca

<400> 187

```
Gly Ile Thr Arg
1
```

<210> 188

<211> 5

<212> PRT

<213> Pavona decussaca

<400> 188

```
Ile Ser Arg Thr Gln
1               5
```

<210> 189

<211> 14

<212> PRT

<213> Pavona decussaca

<400> 189

```
Arg Asp Val Ile Asp Gln Ser Val Lys Val Arg Ser Ser Arg
1               5                   10
```

<210> 190

<211> 5

<212> PRT

<213> Pavona decussaca

<400> 190

```
Gln Thr Tyr Leu Trp
1               5


<210>  191

<211>  17

<212>  PRT

<213>  Pavona decussaca


<400>  191

Gln Trp Ser Leu Met Gln Met Asn Ala Arg His Leu Thr Trp Phe Arg
1               5                   10                  15

Trp


<210>  192

<211>  4

<212>  PRT

<213>  Pavona decussaca


<400>  192

Arg His Pro Tyr
1

<210>  193

<211>  6

<212>  PRT

<213>  Pavona decussaca


<400>  193

Met Asn Ser Asn Leu Ser
1               5

<210>  194

<211>  5
```

<212> PRT

<213> Pavona decussaca

<400> 194

```
Trp Leu Thr Leu Ala
1               5
```

<210> 195

<211> 13

<212> PRT

<213> Pavona decussaca

<400> 195

```
Ser Arg Ser Ile Leu Ala Glu Arg Asn Asn Gly Cys Ile
1               5                   10
```

<210> 196

<211> 23

<212> PRT

<213> Pavona decussaca

<400> 196

```
Gly Thr Gly Ser Trp Gly Thr Ser Trp Ile Leu Ser Thr Trp Arg Ile
1               5                   10                  15

Ile Cys Arg His Leu Thr Ala
            20
```

<210> 197

<211> 7

<212> PRT

<213> Pavona decussaca

<400> 197

```
Met Thr Ile Asn Arg Gln Val
1               5


<210>  198

<211>  4

<212>  PRT

<213>  Pavona decussaca


<400>  198

Thr Ser Val Trp
1


<210>  199

<211>  10

<212>  PRT

<213>  Pavona decussaca


<400>  199

Gly Asn Tyr Asp Arg Asn Tyr Cys His Ala
1               5                   10


<210>  200

<211>  12

<212>  PRT

<213>  Pavona decussaca


<400>  200

Arg Glu Thr Val Thr Leu His Ala Asn Leu Trp Ser
1               5                   10


<210>  201

<211>  231

<212>  PRT

<213>  coral
```

```
<400>  201

Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
            20                  25                  30

Tyr Glu Gly Glu Gln Thr Val Arg Leu Ala Val Thr Lys Gly Gly Pro
        35                  40                  45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Ser
    50                  55                  60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

Ser Phe Pro Gly Arg Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

Lys Ala Arg Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

Arg Glu Ile Ser Ile Ala Arg Lys Pro Leu Val Ala Cys Cys Phe Phe
    210                 215                 220

Arg Val Lys Ser Arg His Lys
225                 230

<210>  202

<211>  235

<212>  PRT

<213>  coral


<400>  202
```

```
Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1               5                   10                  15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Leu Pro
            20                  25                  30

Tyr Glu Gly Gly Gln Thr Val Arg Leu Ala Val Thr Lys Gly Gly Pro
        35                  40                  45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Ser
    50                  55                  60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65                  70                  75                  80

Ser Phe Pro Gly Arg Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
                85                  90                  95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
            100                 105                 110

Phe Ile Tyr His Val Lys Arg Ser Gly Leu Asn Phe Pro Pro Asn Gly
        115                 120                 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
    130                 135                 140

Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145                 150                 155                 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

Lys Leu Asp Val Thr Asn His Asn Leu Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala Cys Arg Phe Phe
    210                 215                 220

Arg Val Lys Ser Arg His Lys Tyr Ala Val Ala
225                 230                 235

<210>  203

<211>  49

<212>  DNA

<213>  oligonucleotide


<400>  203
tgagagaact agtctcgagc tctagaacaa gctttttttt tttttttt                   49


<210>  204
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<211> 41

<212> DNA

<213> oligonucleotide

<400> 204
cagggcgcgc catgggatcc gttatcgcta aacagatgac c 41

<210> 205

<211> 38

<212> DNA

<213> oligonucleotide

<400> 205
gggttaatta agctgcaggg cgaccacagg tttgcgtg 38

<210> 206

<211> 18

<212> DNA

<213> oligonucleotide

<400> 206
cccgaaaagt gccacctg 18

<210> 207

<211> 19

<212> DNA

<213> oligonucleotide

<400> 207
gttctgaggt cattactgg 19

<210> 208

<211> 20

<212> DNA

<213> oligonucleotide

<400> 208
tcagggtact tggtgaatgg 20

<210> 209

<211> 669

<212> DNA

<213> Acropora sp

<400> 209
ggatccgtta tcgctaaaca gatgacctac aaggtttata tgtcaggcac ggtcaatgga 60

cactactttg aggtcgaagg cgatggaaaa ggaaagcctt acgaggggga gcagacggta 120

aagctcactg tcaccaaggg tggacctctg ccatttgctt gggatatttt atcaccacag 180

tcacagtacg gaagcatacc attcaccaag taccctgaag acatcccgga ctatgtaaag 240

cagtcattcc cggagggata tacatgggag aggatcatga actttgaaga tggtgcagtg 300

tgtactgtca gcaatgactc cagcatccaa ggcaactgtt tcatctacca tgtcaagttc 360

tctggtttga actttcctcc caatggacct gttatgcaga agaagacaca gggctgggaa 420

cccaacactg agcgtctctt tgcacgagat ggaatgctga taggaaacaa ctttatggct 480

ctgaagttag aaggaggtgg tcactatttg tgtgaattca aatctactta caaggcaaag 540

aagcctgtga agatgccagg gtatcactat gttgaccgca aactggatgt aaccaatcac 600

aacaaggatt acacttccgt tgagcagtgt gaaatttcca ttgcacgcaa acctgtggtc 660

gccctgcag 669

<210> 210

<211> 222

<212> PRT

<213> Acropora sp

<400> 210

Gly Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1 5 10 15

Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
20 25 30

```
Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly
        35                  40                  45

Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly
    50                  55                  60

Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80

Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110

Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125

Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
    130                 135                 140

Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Leu
145                 150                 155                 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205

Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala Leu Gln
    210                 215                 220

<210>  211

<211>  669

<212>  DNA

<213>  Discosoma sp


<400>  211
ggatccgtta tcgctaaaca gatgacctac aaagtttata tgtcaggcac ggtcaatgga      60

cactactttg aggtcgaagg cgatggaaaa ggaaagcctt acgaggggga gcagacggta     120

aggctgactg tcaccaaggg cggacctctg ccatttgctt gggatatttt atcaccacag     180

tcacagtacg gaagcatacc attcaccaag taccctgaag acatccctga ctatgtaaag     240

cagtcattcc cggagggata tacatgggag aggatcatga actttgaaga tggtgcagtg     300

tgtactgtca gcaatgattc cagcatccaa ggcaactgtt tcatctacca tgtcaagttc     360

tctggtttga actttcctcc caatggacct gttatgcaga agaagacaca gggctgggaa     420
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```
cccaacactg agcgtctctt agcacgagat ggaatgctga taggaaacaa ctttatggct     480

ctgaagttag aaggaggtgg tcactatttg tgtgaattca aatctactta caaggcaagg     540

aagcctgtga agatgccagg gtatcactat gttgaccgca aactggatgt aaccaatcac     600

aacaaggatt acacttccgt tgagcagcgt gaaatttcca ttgcacgcaa acctgtggtc     660

gccctgcag                                                              669
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<210> 212

<211> 222

<212> PRT

<213> Discosoma sp

<400> 212

```
Gly Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15

Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30

Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly
        35                  40                  45

Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly
    50                  55                  60

Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80

Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110

Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125

Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
    130                 135                 140

Arg Leu Leu Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Leu
145                 150                 155                 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
                165                 170                 175

Lys Ala Arg Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
            180                 185                 190

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
        195                 200                 205
```

Arg Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala Leu Gln
    210   215   220

<210> 213

<211> 669

<212> DNA

<213> Sinularia sp

<400> 213
ggatccgtta tcgctaaaca gatgacctac aaggtttata tgtcaggcac ggtcaatgga 60

cactactttg aggtcgaagg cgatggaaaa ggaaagcctt acgaggggga gcagacggta 120

aagctcactg tcaccaaggg tggacctctg ccatttgctt gggatatttt atcaccacag 180

tcacagtacg gaagcatacc attcaccaag taccctgaag acatcccgga ctatgtaaag 240

cagtcattcc cggaggggta tacatgggag aggatcatga actttgaaga tggtgcagtg 300

tgtactgtca gcaatgactc cagcatccaa ggcaactgtt tcatctacca tgtcaagttc 360

tctggtttga actttccttc caatggacct gttatgcaga agaagacaca gggctgggaa 420

cccaacactg agcgtctctt tgcacgagat ggaatgctga taggaaacaa ctttatggct 480

ctgaagttag aaggaggtgg tcactatttg tgtgaattca aatctactta caaggcaaag 540

aagcctgtga agatgccagg gtatcactat gttgaccgca aactggatgt aaccaatcac 600

aacaaggatt acacttccgt tgagcagtgt gaaatttcca ttgcacgcaa acctttggtc 660

gccctgcag 669

<210> 214

<211> 223

<212> PRT

<213> Sinularia sp

<400> 214

Gly Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1   5   10   15

Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20   25   30

Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly
        35   40   45

```
Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly
    50                  55                  60

Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                      80

Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110

Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Ser Asn
        115                 120                 125

Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
    130                 135                 140

Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160

Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr
                165                 170                 175

Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190

Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
        195                 200                 205

Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Leu Val Ala Leu Gln
    210                 215                 220
```

<210> 215

<211> 669

<212> DNA

<213> Tubastrea sp

```
<400> 215
ggatccgtta tcgctaaaca gatgacctac aaggtttata tgtcaggcac ggtcaatgga      60

cactactttg aggtcgaagg cgatggaaaa ggaaagcctt acgaggggga gcagacggta     120

aagctcactg tcaccaaggg tggacctctg ccatttgctt gggatatttt atcaccacag     180

tcacagtacg gaagcatacc attcaccaag taccctgaag acatcccgga ctatgtaaag     240

cagtcattcc cggagggata tacatgggag aggatcatga actttgaaga tggtgcagtg     300

tgtactgtca gcaatgactc cagcatccaa ggcaactgtt tcatctacca tgtcaagttc     360

tctggtttga actttcctcc caatggacct gttatgcaga agaagacaca gggctgggaa     420

cccaacactg agcgtctctt tgcacgagat ggaatgctga taggaaacaa ctttatggct     480

ctgaagttag aaggaggtgg tcactatttg tgtgaattca aatctactta caaggcaaag     540
```

```
aagcctgtga agatgccagg gtatcactat gttgaccgca aactggatgt aaccaatcac     600

aacaaggatt acacttccgt tgagcagtgt gaaatttcca ttgcgcgcaa acctgtggtc     660

gccctgcag                                                             669


<210>  216

<211>  223

<212>  PRT

<213>  Tubastrea sp



<400>  216

Gly Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15

Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30

Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly
        35                  40                  45

Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly
    50                  55                  60

Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80

Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110

Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125

Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
    130                 135                 140

Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160

Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr
                165                 170                 175

Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190

Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
        195                 200                 205

Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala Leu Gln
    210                 215                 220
```

<210> 217

<211> 669

<212> DNA

<213> Discosoma sp

<400> 217
```
ggatccgtta tcgctaaaca gatgacctac aaggtttata tgtcaggcac ggtcaatgga      60

cactactttg aggtcgaagg cgatggaaaa ggaaagcctt acgaggggga gcagacggta     120

aggctggctg tcaccaaggg cggacctctg ccatttgctt gggatatttt atcaccacag     180

tgtcagtacg gaagcatacc attcaccaag taccctgaag acatccctga ctatgtaaag     240

cagtcattcc cggagggatt tacatgggag aggatcatga actttgaaga tggtgcagtg     300

tgtcctgtca gcaatgattc cagcatccaa ggcaactgtt tcatctacca tgtcaagttc     360

tctggtttga actttcctcc caatggacct gttatgcaga agaagacaca gggctgggaa     420

ccccactctg agcgtctctt tgcacgagac ggaatgctga taggaaacac ctttatggct     480

ctgaagttag aaggaggcgg tcactatttg tgtgaattca aaactactta caaggcaaag     540

aagcctgtga agatgccagg gtatcattat gttgaccgca aactggatgt aatcaatcac     600

aacaaggatt acacttccgt tgagcagtgt gaaatttcca ttgcacgcaa acctgtggtc     660

gccctgcag                                                              669
```

<210> 218

<211> 223

<212> PRT

<213> Discosoma sp

<400> 218

```
Gly Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15

Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30

Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Ala Val Thr Lys Gly Gly
        35                  40                  45

Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly
    50                  55                  60
```

Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65 70 75 80

Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu
85 90 95

Asp Gly Ala Val Cys Pro Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
100 105 110

Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
115 120 125

Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu
130 135 140

Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Thr Phe Met Ala
145 150 155 160

Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr
165 170 175

Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
180 185 190

Arg Lys Leu Asp Val Ile Asn His Asn Lys Asp Tyr Thr Ser Val Glu
195 200 205

Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala Leu Gln
210 215 220

<210> 219

<211> 555

<212> DNA

<213> Sinularia sp

<400> 219
acggtaaggc tggctgtcac caagggcgga cctctgccat ttgcttggga tattttatca 60

ccacagtgtc agtacggaag cataccattc accaagtacc ttgaagacat ccctgactat 120

gtaaagcagt cattcccgga gggatttaca tgggagagga tcatgaactt tgaagatggt 180

gcagtgtgta ctgtcagcaa tgattccagc atccaaggca actgtttcat ctaccatgtc 240

aagttctctg gtttgaactt tcctcccaat ggacctgtta tgcagaagaa gacacagggc 300

tgggaaccca acactgagcg tctctttgca cgagatggaa tgctgatagg aaacaacttt 360

atggctctaa agttagaggg aggtggtcac tatttgtgtg aattcaaatc tacttacaag 420

gcaaagaagc ctgtgaagat gccagggtat cactatgttg accgcaaact ggatgtaacc 480

aatcacaaca aggattacac ttccgttgag cagtgtgaaa tttccattgc acgcaaacct 540

ttggtcgccc tgcag 555

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<210>  220

<211>  223

<212>  PRT

<213>  Sinularia sp



<400>  220

Gly Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15

Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30

Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Ala Val Thr Lys Gly Gly
        35                  40                  45

Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly
    50                  55                  60

Ser Ile Pro Phe Thr Lys Tyr Leu Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80

Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110

Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125

Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
    130                 135                 140

Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160

Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr
                165                 170                 175

Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190

Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
        195                 200                 205

Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Leu Val Ala Leu Gln
    210                 215                 220

<210>  221

<211>  669

<212>  DNA
```

<213> Tubastrea sp

<400> 221
ggatccgtta tcgctaaaca gatgacctac aaggtttata tgtcaggcac ggtcaatgga 60

cactactttg aggtcgaagg cgatggaaaa ggaaagcctt acgaggggga gcagacggta 120

aggctggctg tcaccaaggg cggacctctg ccatttgctt gggatatttt atcaccacag 180

tgtcagtacg gaagcatacc attcaccaag taccctgaag acatccctga ctatgtaaag 240

cggtcattcc cggagggatt tacatgggag aggatcatga actttgaaga tggtgcagtg 300

tgtactgtca gcaatgattc cagcatccaa ggcaactgtt tcatctacca tgtcaagttc 360

tctggtttga actttcctcc caatggacct gttatgcaga agaagacaca gggctgggaa 420

ccccactctg agcgtctctt tgcacgagac ggaatgctga taggaaacaa ctttatggct 480

ctgaagttag aaggaggcgg tcactatttg tgtgaattca aaactactta caaggcaaag 540

aagcctgtga agatgccagg gtatcattat gttgaccgca aactggatgt aatcaatcac 600

aacaaggatt acacttccgt tgagcagtgt gaaatttcca ttgcacgcaa acctgtggtc 660

gccctgcag 669

<210> 222

<211> 223

<212> PRT

<213> Tubastrea sp

<400> 222

Gly Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1 5 10 15

Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
20 25 30

Pro Tyr Glu Gly Glu Gln Thr Val Arg Leu Ala Val Thr Lys Gly Gly
35 40 45

Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly
50 55 60

Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65 70 75 80

Arg Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu
85 90 95

```
Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110

Cys Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125

Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro His Ser Glu
    130                 135                 140

Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160

Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr
                165                 170                 175

Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190

Arg Lys Leu Asp Val Ile Asn His Asn Lys Asp Tyr Thr Ser Val Glu
        195                 200                 205

Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala Leu Gln
    210                 215                 220
```

<210> 223

<211> 46

<212> DNA

<213> oligonucleotide

<400> 223
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caggggcgcgc caaggagata taacaatggc ttcctcagtt ctttcc                    46
```

<210> 224

<211> 33

<212> DNA

<213> oligonucleotide

<400> 224
```
cactggatcc gcattgcact cttccgccgt tgc                                   33
```

<210> 225

<211> 45

<212> DNA

<213> oligonucleotide

```
<400>  225
gcatggcgcg ccaaggagat ataacaatga agactaatct ttttc                     45


<210>  226

<211>  34

<212>  DNA

<213>  oligonucleotide


<400>  226
gcatggatcc gaattcggcc gaggataatg atag                                 34


<210>  227

<211>  45

<212>  DNA

<213>  oligonucleotide


<400>  227
gcatggcgcg ccaaggagat ataacaatga agactaatct ttttc                     45


<210>  228

<211>  34

<212>  DNA

<213>  oligonucleotide


<400>  228
gcatggatcc gaattcggcc gaggataatg atag                                 34


<210>  229

<211>  46

<212>  DNA

<213>  oligonucleotide


<400>  229
gatcttaatt aaagctcatc atgctgcagg gcgaccacag gtttgc                    46
```

```
<210>  230

<211>  42

<212>  DNA

<213>  oligonucleotide


<400>  230
gcatctgcag gtcgccacca gtaaaggaga agaacttttc ac                        42

<210>  231

<211>  39

<212>  DNA

<213>  oligonucleotide


<400>  231
ctgattaatt aattatttgt atagttcatc catgccatg                            39

<210>  232

<211>  55

<212>  DNA

<213>  oligonucleotide


<400>  232
cagggcgcgc caaggagata taacaatggg atccgttatc gctaaacaga tgacc          55

<210>  233

<211>  45

<212>  DNA

<213>  oligonucleotide


<400>  233
ggctctagaa aggagatata caatgtccgt tatcgctaaa cagat                     45

<210>  234

<211>  45
```

<212> DNA

<213> oligonucleotide

<400> 234
```
ggctctagaa aggagatata caatgtccgt tatcgctaaa cagat                 45
```

<210> 235

<211> 50

<212> DNA

<213> oligonucleotide

<400> 235
```
ggcaagcttt cagtggtggt ggtggtggtg ggcgaccaca ggtttgcgtg            50
```

<210> 236

<211> 221

<212> PRT

<213> coral

<400> 236

```
Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15

Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
            20                  25                  30

Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly
        35                  40                  45

Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly
    50                  55                  60

Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80

Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110

Cys Phe Thr Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125
```

```
Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser Ser Glu
    130                 135                 140

His Leu Phe Ala Arg Gly Gly Met Leu Ile Gly Asn Asn His Met Ala
145                 150                 155                 160

Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr
                165                 170                 175

Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
            180                 185                 190

Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
        195                 200                 205

Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
    210                 215                 220

<210>  237

<211>  221

<212>  PRT

<213>  coral


<400>  237

Met Ser Val Ile Ala Thr Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1               5                   10                  15

Thr Val Asn Gly His Tyr Phe Glu Val Gln Gly Asp Gly Lys Gly Lys
            20                  25                  30

Pro Tyr Glu Glu Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly
        35                  40                  45

Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly
    50                  55                  60

Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65                  70                  75                  80

Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu
                85                  90                  95

Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
            100                 105                 110

Cys Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
        115                 120                 125

Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
    130                 135                 140

Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145                 150                 155                 160
```

Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr
165 170 175

Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
180 185 190

Arg Lys Leu Asp Val Thr Asn His Asn Ile Asp Tyr Thr Ser Val Glu
195 200 205

Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala
210 215 220

<210> 238

<211> 226

<212> PRT

<213> coral

<400> 238

Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1 5 10 15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
20 25 30

Tyr Glu Gly Glu Gln Thr Val Arg Leu Thr Val Thr Lys Gly Gly Pro
35 40 45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly Ser
50 55 60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65 70 75 80

Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
85 90 95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
100 105 110

Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
115 120 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
130 135 140

Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145 150 155 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
165 170 175

Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr Val Asp Arg
180 185 190

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
195 200 205

Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala Trp Cys Phe Phe
210 215 220

Arg Val
225

<210> 239

<211> 220

<212> PRT

<213> coral

<400> 239

Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1 5 10 15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
20 25 30

Tyr Glu Gly Glu Gln Thr Val Arg Leu Ala Val Thr Lys Gly Gly Pro
35 40 45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Ser
50 55 60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65 70 75 80

Ser Phe Pro Gly Arg Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
85 90 95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
100 105 110

Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
115 120 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
130 135 140

Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145 150 155 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
165 170 175

Lys Ala Arg Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
180 185 190

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
195 200 205

```
Arg Glu Ile Ser Ile Ala Arg Lys Pro Leu Val Ala
    210                 215                 220

<210>  240

<211>  230

<212>  PRT

<213>  coral



<400>  240

Met Ser Cys Ser Lys Asn Val Ile Lys Glu Phe Met Arg Phe Lys Val
1               5                   10                  15

Arg Met Glu Gly Thr Val Asn Gly His Glu Phe Glu Ile Lys Gly Glu
            20                  25                  30

Gly Glu Gly Arg Pro Tyr Glu Gly His Cys Ser Val Lys Leu Met Val
        35                  40                  45

Thr Lys Gly Gly Pro Leu Pro Phe Ala Phe Asp Ile Leu Ser Pro Gln
    50                  55                  60

Phe Gln Tyr Gly Ser Lys Val Tyr Val Lys His Pro Ala Asp Ile Pro
65                  70                  75                  80

Asp Tyr Lys Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val
                85                  90                  95

Met Asn Phe Glu Asp Gly Gly Val Val Thr Val Ser Gln Asp Ser Ser
            100                 105                 110

Leu Lys Asp Gly Cys Phe Ile Tyr Glu Val Lys Phe Ile Gly Val Asn
        115                 120                 125

Phe Pro Ser Asp Gly Pro Val Met Gln Arg Arg Thr Arg Gly Trp Glu
    130                 135                 140

Ala Ser Ser Glu Arg Leu Tyr Pro Arg Asp Gly Val Leu Lys Gly Asp
145                 150                 155                 160

Ile His Met Ala Leu Arg Leu Glu Gly Gly Gly His Tyr Leu Val Glu
                165                 170                 175

Phe Lys Ser Ile Tyr Met Val Lys Lys Pro Ser Val Gln Leu Pro Gly
            180                 185                 190

Tyr Tyr Tyr Val Asp Ser Lys Leu Asp Met Thr Ser His Asn Glu Asp
        195                 200                 205

Tyr Thr Val Val Glu Gln Tyr Glu Lys Thr Gln Gly Arg His His Pro
    210                 215                 220

Phe Ile Lys Pro Leu Gln
225                 230
```

<210> 241

<211> 225

<212> PRT

<213> coral

<400> 241

```
Met Arg Ser Ser Lys Asn Val Ile Lys Glu Phe Met Arg Phe Lys Val
1               5                   10                  15

Arg Met Glu Gly Thr Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu
            20                  25                  30

Gly Glu Gly Arg Pro Tyr Glu Gly His Asn Thr Val Lys Leu Lys Val
        35                  40                  45

Thr Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln
    50                  55                  60

Phe Gln Tyr Gly Asn Lys Val Tyr Val Lys His Pro Ala Asp Ile Pro
65                  70                  75                  80

Asp Tyr Lys Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Trp
                85                  90                  95

Met Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser
            100                 105                 110

Leu Gln Asp Gly Cys Phe Ile Tyr Lys Val Lys Phe Ile Gly Val Asn
        115                 120                 125

Phe Pro Ser Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu
    130                 135                 140

Ala Ser Thr Lys Arg Leu Tyr Pro Arg Asp Gly Val Leu Lys Gly Glu
145                 150                 155                 160

Ile His Lys Ala Leu Lys Leu Lys Asp Gly Gly His Tyr Leu Val Glu
                165                 170                 175

Phe Lys Ser Ile Tyr Met Ala Lys Lys Pro Val Gln Leu Pro Gly Tyr
            180                 185                 190

Tyr Tyr Val Asp Ser Lys Leu Asp Ile Thr Ser His Asn Glu Asp Tyr
        195                 200                 205

Thr Ile Val Glu Gln Tyr Glu Arg Thr Glu Gly Arg His His Leu Phe
    210                 215                 220

Leu
225
```

<210> 242

<211> 230

<212> PRT

<213> coral

<400> 242

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
210 215 220

Thr Ala Ala Gly Ile Thr
225 230

<210> 243

<211> 818

<212> DNA

<213> Aequorea victoria

<400> 243
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tcctatcatt atcctcggcc gaattcagta aaggagaaga acttttcact ggagttgtcc 120

caattcttgt tgaattagat ggtgatgtta atgggcacaa attttctgtc agtggagagg 180

gtgaaggtga tgcaacatac ggaaaactta cccttaaatt tatttgcact actggaaaac 240

tacctgttcc atggccaaca cttgtcacta ctttctctta tggtgttcaa tgcttttcaa 300

gatacccaga tcatatgaag cggcacgact tcttcaagag cgccatgcct gagggatacg 360

tgcaggagag gaccatcttc ttcaaggacg acgggaacta caagacacgt gctgaagtca 420

agtttgaggg agacaccctc gtcaacagga tcgagcttaa gggaatcgat ttcaaggagg 480

acggaaacat cctcggccac aagttggaat acaactacaa ctcccacaac gtatacatca 540

tggcagacaa acaaaagaat ggaatcaaag ttaacttcaa aattagacac aacattgaag 600

atggaagcgt tcaactagca gaccattatc aacaaaatac tccaattggc gatggccctg 660

tccttttacc agacaaccat tacctgtcca cacaatctgc cctttcgaaa gatcccaacg 720

aaaagagaga ccacatggtc cttcttgagt ttgtaacagc tgctgggatt acacatggca 780

tggatgaact atacaaacat gatgagcttt aagagctc 818

<210> 244

<211> 263

<212> PRT

<213> Aequorea victoria

<400> 244

Met Lys Thr Asn Leu Phe Leu Phe Leu Ile Phe Ser Leu Leu Leu Ser
1 5 10 15

Leu Ser Ser Ala Glu Phe Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
20 25 30

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
35 40 45

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
50 55 60

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
65 70 75 80

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
85 90 95

Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
100 105 110

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
115 120 125

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
130 135 140

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
145 150 155 160

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
165 170 175

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
180 185 190

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
195 200 205

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
210 215 220

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
225 230 235 240

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
245 250 255

Leu Tyr Lys His Asp Glu Leu
260

<210> 245

<211> 235

<212> PRT

<213> Acropora aspera

<400> 245

Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr
1 5 10 15

Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro
20 25 30

Tyr Glu Gly Glu Gln Thr Val Arg Leu Ala Val Thr Lys Gly Gly Pro
35 40 45

Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Cys Gln Tyr Gly Ser
50 55 60

Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln
65 70 75 80

Ser Phe Pro Gly Arg Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu Asp
85 90 95

Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys
100 105 110

Phe Ile Tyr His Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn Gly
115 120 125

Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu Arg
130 135 140

Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala Leu
145 150 155 160

Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr
165 170 175

Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp Arg
180 185 190

Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu Gln
195 200 205

Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala Cys Arg Phe Phe
210 215 220

Arg Val Lys Ser Arg His Lys Val Ala Val Ala
225 230 235

<210> 246

<211> 232

<212> PRT

<213> Acropora aspera

<400> 246

Met Ala Ser Phe Leu Lys Lys Thr Met Pro Phe Lys Thr Thr Ile Glu
1 5 10 15

Gly Thr Val Asn Gly His Tyr Phe Lys Cys Thr Gly Lys Gly Glu Gly
20 25 30

Asn Pro Phe Glu Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly
35 40 45

Gly Pro Leu Pro Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr
50 55 60

Gly Ser Lys Thr Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe
65 70 75 80

Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr
85 90 95

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Glu Asp Gly Gly Phe Leu Thr Ala His Gln Asp Thr Ser Leu Asp Gly
            100                 105                 110

Asp Cys Leu Val Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro Ala
        115                 120                 125

Asp Gly Pro Val Met Gln Asn Lys Ala Gly Arg Trp Glu Pro Ala Thr
    130                 135                 140

Glu Ile Val Tyr Glu Val Asp Gly Val Leu Arg Gly Gln Ser Leu Met
145                 150                 155                 160

Ala Leu Lys Cys Pro Gly Gly Arg His Leu Thr Cys His Leu His Thr
                165                 170                 175

Thr Tyr Arg Ser Lys Lys Pro Ala Ser Ala Leu Lys Met Pro Gly Phe
            180                 185                 190

His Phe Glu Asp His Arg Ile Glu Ile Met Glu Glu Val Glu Lys Gly
        195                 200                 205

Lys Cys Tyr Lys Gln Tyr Glu Ala Ala Val Gly Arg Tyr Cys Asp Ala
    210                 215                 220

Ala Pro Ser Lys Leu Gly His Asn
225                 230
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<210> 247

<211> 51

<212> DNA

<213> oligonucleotide

<400> 247
cgcgccaagg agatataaca atgagaggat cgcatcacca tcaccatcac g 51

<210> 248

<211> 51

<212> DNA

<213> oligonucleotide

<400> 248
gatccgtgat ggtgatggtg atgcgatcct ctcattgtta tatctccttg g 51

<210> 249

<211> 47

<212> DNA

<213> oligonucleotide

<400> 249
ctgattaatt aaagctcatc atgtttgtat agttcatcca tgccatg 47

<210> 250

<211> 34

<212> DNA

<213> oligonucleotide

<400> 250
gtgtgtactg tcagccagga ttccagcatc caag 34

<210> 251

<211> 32

<212> DNA

<213> oligonucleotide

<400> 251
ctgtcagcaa tgatatcagc atccaaggca ac 32

<210> 252

<211> 44

<212> DNA

<213> oligonucleotide

<400> 252
ggatccatcg ccaccatgtc taaaggtgaa gaattattca ctgg 44

<210> 253

<211> 34

<212> DNA

<213> oligonucleotide

<400> 253

cagctgttat ttgtacaatt catccatacc atgg 34

<210> 254

<211> 41

<212> DNA

<213> oligonucleotide

<400> 254
cgggatccat cgccaccatg aggtcttcca agaatgttat c 41

<210> 255

<211> 31

<212> DNA

<213> oligonucleotide

<400> 255
gaggatccgc ggccgctaaa ggaacagatg g 31

<210> 256

<211> 38

<212> DNA

<213> oligonucleotide

<400> 256
gaagatctaa aacaatgagt gtgatcgcta cacaaatg 38

<210> 257

<211> 35

<212> DNA

<213> oligonucleotide

<400> 257
tatcaaatcg ccggcgtcag gcgaccacag gtttg 35

<210> 258

<211> 30

<212> DNA

<213> oligonucleotide

<400> 258
agatctgtgt tgtgacgcaa ctgcaactcc 30

<210> 259

<211> 39

<212> DNA

<213> oligonucleotide

<400> 259
gtgatcagcg gatcccttca atttagaaag caattgttc 39

<210> 260

<211> 25

<212> DNA

<213> oligonucleotide

<400> 260
cctctatata ttacgcacca tattc 25

<210> 261

<211> 22

<212> DNA

<213> oligonucleotide

<400> 261
atacgtgacg acattggtag tc 22

<210> 262

<211> 15

<212> PRT

<213> coral

<220>

<221> misc_feature

<222> (15)..(15)

<223> x = any amino acid

<400> 262

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Ser Pro Pro Asp Tyr Thr Leu Glu Phe Pro Lys Lys Xaa Val Ala
1               5                   10                  15
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<210> 263

<211> 15

<212> PRT

<213> coral

<400> 263

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Ser Pro Pro Asp Tyr Thr Leu Glu Arg Pro Lys Lys Gly Val Ala
1               5                   10                  15
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<210> 264

<211> 24

<212> PRT

<213> coral

<400> 264

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Asp Ser Ser Pro Glu Ser Tyr Leu Lys Asn Gly Ile Ala Glu Glu Met
1               5                   10                  15

Lys Thr Asp Val Met Glu Gly Ile
            20
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<210> 265

<211> 22

<212> PRT

<213> coral

<400> 265

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Ser Tyr Leu Pro Asn Gly Ile Ala Glu Glu Met Lys Thr Asp Leu Met
1               5                   10                  15

Glu Gly Ile Val Asn Gly
            20
```

<210> 266

<211> 22

<212> PRT

<213> coral

<400> 266

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Ser Leu Tyr Gln Asn Gly Ile Ala Glu Glu Met Lys Thr Asp Leu Met
1               5                   10                  15

Glu Gly Ile Val Asn Gly
            20
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<210> 267

<211> 20

<212> DNA

<213> oligonucleotide

<400> 267

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atggaaggga tagtcgatgg                                                  20
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<210> 268

<211> 20

<212> DNA

<213> oligonucleotide

<400> 268

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atggaaggga ttgtcgatgg                                                  20
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<210> 269

<211> 20

<212> DNA

<213> oligonucleotide

<400> 269
atggaaggga tcgtcgatgg 20

<210> 270

<211> 19

<212> DNA

<213> oligonucleotide

<400> 270
cctcgacaat cccttccat 19

<210> 271

<211> 19

<212> DNA

<213> oligonucleotide

<400> 271
cctcgacgat cccttccat 19